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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver is described. Also described are single exon nucleic acid probes expressed in the Fetal liver and their use in methods for detecting gene expression.

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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_FETAL_LIVER.txt,
25 created 24 January 2001, having 25,630,231 bytes. The
Sequence Listing contained in said file on said disc is
incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

Fetal liver and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known a priori with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only a priori biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches - and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species - there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 . The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
20 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies. There is a need for methods and apparatus that permit prediction of
25 diseases of the liver, particularly those diseases with polygenic etiology, from diagnosis of fetal liver.

Summary of the Invention

30 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
35 expression of putative genes identified within genomic

sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified
5 within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon
10 microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver, comprising a
15 plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

25 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
30 Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

35 Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,129 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

 Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is is addressably disposed upon a substrate.

 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate,
cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is
provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with
the first aspect of the invention.

In one embodiment, a genome-derived single-exon
microarray is packaged together with such an ordered set of
amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative
embodiments, the ordered set of amplifiable probes is
packaged separately from the genome-derived single exon
microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 12,674 - 25,129, wherein the fragment
hybridizes at high stringency to an expressed human gene.
In particular embodiments, the invention provides single
exon probes comprising SEQ ID Nos. 1 - 12,673.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
human Fetal liver which is a nucleic acid molecule
comprising a nucleotide sequence as set out in any of SEQ
ID NOs.: 1 - 12,673 or a complementary sequence or a
30 fragment thereof wherein said probe hybridizes at high
stringency to a nucleic acid expressed in the human Fetal
liver.

In one embodiment, a single exon nucleic acid
probe in accordance with the third aspect comprises a
35 nucleotide sequence as set out in any of SEQ ID NOs.:

12,674 - 25,129 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring
5 human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,130 - 37,156 or a complementary sequence or a fragment thereof wherein said probe
10 hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous
15 nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb,
25 preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or
30 PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first
35 member of a specific binding pair. Suitable fluorescent

labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single
5 exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks
10 homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance
15 with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is
20 provided a method of measuring gene expression in a sample derived from human Fetal liver, comprising:

contacting the single exon microarray in
accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said
25 first collection of nucleic acids derived from mRNA of human Fetal liver; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is
30 provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably
35 labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the Fetal liver of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,129 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,674 - 25,129, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,673.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ

ID NOS.: 25,130 - 37,156.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 25,130 - 37,156, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary

planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in
5 aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid
10 intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising
15 SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence
20 directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence
25 of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a
30 PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence
35 bioinformatically predicted to encode a portion of a

natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual

object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional
5 information.

Brief Description of the Drawings

10 The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the
15 functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the
20 process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution,
30 among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or
35 more but not all tested tissues ("1" - "9"), or expressed

in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained

in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100
5 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger
10 contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was
15 erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession,
20 species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will
25 be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

30 Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the
35 National Institutes of Health and is maintained by the

National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
5 eukaryotic organisms will also prove useful as genomic
sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
10 are predicted to have a biological function as specified by
the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
15 regulating message degradation after transcription into
mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

20 The particular genomic sequence to be input into
process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
25 given genomic region. In such case, the input often will
be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
30 experimental confirmation is identified. Experimental
confirmation can involve physical and/or bioinformatic
assay. Where the subsequent experimental assay is
bioinformatic, rather than physical, there are fewer
constraints on the sequences that can be tested, and in
35 this latter case therefore process 300 can output the

entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or

interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

5 FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

10 The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene
15 prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding
20 regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences
25 and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be
30 determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements
35 of the subsequent analytical method. Alternatively, or in

addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate
5 criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

10 Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any
15 given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

20 Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given
25 BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated
30 into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are
35 typically updated on a frequent, even hourly, basis. Thus,

as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query

criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

5 Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

 Preprocessing 24 suitable for most approaches and
10 methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like.
15 Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence,
20 vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

25 Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies
30 a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

35 Once identified, undesired sequence can be

removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".

- 5 Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of
10 highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can
15 also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.
20 Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion
25 from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the
30 informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include,
35 but are not limited to, encoding protein, regulating

transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic
5 recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for
10 identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the
15 novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative
20 coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more
25 software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

30 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region,
35 2% of the data analyzed; GENEFINDER was second, calling 1%;

and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although
5 discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be
10 repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as
15 well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated
20 and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene
25 prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way,
30 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be
35 identified is coding of protein sequence, and a first used

approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative
5 sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

10 Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and
15 approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be
20 identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into
25 putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-
30 specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative
35 exon length, sequence GC content, existence of possible

secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using
5 amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance
10 of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested
15 experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for
20 experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred
25 embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention
30 provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of
35 nucleic acid microarray, the genome-derived single exon

nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by
5 process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture
10 the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying
15 length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the
20 methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can
25 alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or
30 intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about
35 300, 400 or 500 bp in length, can be amplified. However, it

has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for

amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see

above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include

5 polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can

10 also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as

15 described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by

20 presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version

25 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using

30 ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of

35 the present invention, a plurality of *E. coli* genes can

readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified
5 product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
10 complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

15 Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined,
20 including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon,
25 and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No.
30 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however,
35 provide certain useful advantages, including high

throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure

expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse

transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector

sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence.

10 With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater

15 specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain

20 artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific

25 primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such

30 "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon

35 microarray of the present invention can be made without

such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, 5 in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved 10 using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of 15 differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used 20 for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention 25 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the 30 exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides 35 the additional opportunity to assay prespliced RNA, and

thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely
5 constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be
10 performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered
15 (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the
20 genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the
25 microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed
30 on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the
35 melting temperature of probes hybridized to their

complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the
5 microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ*
10 synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

15 The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

20 Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome
25 has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

30 Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as
35 *Saccharomyces cerevisiae*, particularly in genomic sequence

drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of
5 novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is
10 performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the
15 putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed
20 for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the
25 reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

30 mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be
35 measured) is reverse transcribed in the presence of

nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically
5 fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to
10 standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage,
15 to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it
20 is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally
25 as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially
30 identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well
35 of a microtiter dish. Although a 96 well microtiter plate

can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions
5 (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of
10 individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific
5' primers used for genomic amplification can have a first
15 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the
20 amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of
25 agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of
30 probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable
35 media that provide probe identification and addressing

information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

5 If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not
10 required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived
15 microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

20 Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be
25 identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases,
30 such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any
35 sequence query algorithm, such as BLAST ("basic local

alignment search tool"). The results of such query - including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence -
5 can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process
10 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the
15 record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored
20 locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at
25 which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present
30 invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being
35 annotated (hereinafter, the "annotated sequence"). Given

the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity

or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

5 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

10 Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction.

15 Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be

20 made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

 As earlier described, increased predictive reliability can be achieved by requiring consensus among

25 methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

 Although FIG. 3 shows three series of

30 horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

35 Furthermore, field 81 can be used to show

predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as
5 a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including
10 interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right
15 borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of
20 annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing
25 an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using
30 genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during
35 amplification and designed to permit reamplification of the

probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity

has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to

indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

5 Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized
10 mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*.
15 BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by
20 DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates
25 unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of
30 such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present
35 invention rapidly produce functional information from

genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 12,673 of these ORFs in Fetal liver.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in Fetal liver is currently available for use in measuring the level of its ORF's expression in Fetal liver.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies.

For example, cirrhosis is a major public health problem. In the industrialized world, it is among the top

ten causes of death; among patients aged 45 to 65, it is the third leading cause of death. The high prevalence is largely the result of alcohol abuse, but other major contributors include chronic hepatitis, biliary disease and iron overload. Approximately 10-15% are cryptogenic.

Cirrhosis is a broad description encompassing the common end stage of many forms of liver injury. Many patients with cirrhosis will remain asymptomatic for years, while others show generalized weakness, anorexia, malaise, and weight loss or, occasionally, more severe symptoms.

The progression from fibrosis, an early consequence of liver disease, to cirrhosis, and the specific histologic morphology that characterizes cirrhosis depend on the extent of injury, the presence of continuing damage, and the response of the liver to damage. The liver may be injured acutely and severely (e.g. necrosis with hepatitis), moderately over months or years (e.g. biliary tract obstruction and chronic active hepatitis), or modestly but continuously (e.g. alcohol abuse).

During the repair process, new vessels connecting the hepatic artery and portal vein to the hepatic venules form within the fibrous sheath that surrounds the surviving nodules of liver cells. These vessels restore the intrahepatic circulatory pathway, but provide relatively low-volume, high-pressure drainage that is less efficient than normal and results in increased portal vein pressure (portal hypertension). Thus, cirrhosis is not static and its features depend on the disease activity and stage.

As cirrhosis is the end stage of many forms of liver disease, many genes have been identified that can contribute to the development of cirrhosis. These include, e.g., the genes responsible for Wilson disease (Online Mendelian Inheritance of Man ("OMIM") 277900), type IV glycogen storage disease (OMIM 232500), galactosemia (OMIM

230400), and a deficiency of alpha-1-antitrypsin (OMIM 107400). There is substantial evidence, however, for as yet uncharacterized loci which cause cirrhosis.

For example, Iber and Maddrey, Prog. Liver Dis. 2: 290-302 (1965), reviewed 13 previously reported families and 8 new to this study, each with 2 or more affected members. They pointed out that, with a single exception, the multiple cases were in the same generation. Within a given family, the age of onset, clinical course, and biopsy findings were very similar, but there were wide differences between families.

Kalra et al., Hum. Hered. 32:170-175 (1982) studied the families of 220 cases of Indian childhood cirrhosis and 70 families of age-matched controls. The hypotheses of autosomal recessive, partial sex-linkage, and doubly recessive inheritance were found untenable and the authors concluded that multifactorial inheritance was most plausible. Lefkowitz et al., New Eng. J. Med. 307:271-277 (1982) described 4 white American sibs who died between ages 4.5 and 6 years of cirrhosis that closely resembled that of the childhood cirrhosis of Asiatic Indians.

Another example of uncharacterized loci which cause cirrhosis are those related to the risk of alcoholism.

Cloninger, Science 236:410-416 (1987), defined two separate types of alcoholism. According to these definitions, type 1 alcohol abuse has its usual onset after the age of 25 years and is characterized by severe psychological dependence and guilt. Type 1 occurs in both men and women and requires both genetic and environmental factors to become manifest. By contrast, type 2 alcohol abuse has its onset before the age of 25; persons with this type of alcoholism are characterized by their inability to abstain from alcohol and by frequent aggressive and antisocial behavior. Type 2 alcoholism is rarely found in

women and is much more heritable.

Despite considerable effort to identify genes related to the risk of alcoholism, relatively few genes have been identified. Some of this work has suggested a
5 relationship between the metabolism of dopamine and alcoholism. Blum et al., J.A.M.A. 263:2055-2060 (1990) and Bolos et al., J.A.M.A. 264:3156-3160 (1990) investigated the relationship of the dopamine D2 receptor (DRD2; OMIM 126450) to alcoholism, but the sample size was small and
10 their results were inconclusive. However, Tiihonen et al., Molec. Psychiat. 4, 286-289 (1999), found a markedly higher frequency in a population of type 1 alcoholics of the low activity allele of the enzyme catechol-O-methyltransferase (COMT, OMIM 116790), which has a crucial role in the
15 metabolism of dopamine, suggesting a role for dopamine metabolism in increased risk of alcoholism. For a brief review of recent progress toward the identification of genes related to risk for alcoholism see Buck, Genome 9:927-928 (1998).

20 As another example, multiple genes have been shown to predispose to hyperlipoproteinemia or hyperlipidemia. Much attention has been focused on these disorders because there is a strong association of hyperlipidemia, especially hypercholesterolemia, with
25 development of coronary artery disease. Coronary artery disease accounts for at least 25% of all deaths in the United States. Coronary artery disease results when the arteries supplying the heart muscle become occluded by plaques composed of lipids like cholesterol, blood clotting
30 components and blood cells.

The major plasma lipids circulate bound to proteins as macromolecular complexes called lipoproteins. Although closely interrelated, the major lipoprotein classes - chylomicron, very-low-density lipoprotein (VLDL),
35 low-density lipoprotein (LDL), and high-density lipoprotein

(HDL) - are usually classified in terms of physicochemical properties (e.g., density after centrifugation).

Chylomicrons, the largest lipoproteins, carry exogenous triglyceride from the intestine via the thoracic duct to the venous system and into peripheral sites. VLDL carries endogenous triglyceride primarily from the liver to the same peripheral sites for storage or use. Lipases quickly degrade the triglyceride in VLDL to produce intermediate density lipoproteins (IDL) and within 2 to 6 h, IDL is degraded further to generate LDL, which has a plasma half-life of 2 to 3 days. While the overall fate of LDL is unclear, the liver is responsible for removing approximately 70% and active receptor sites have been found on the surfaces of hepatocytes.

Several monogenic conditions that lead to elevated levels of one or more serum lipoproteins have been defined and the responsible gene identified, including, e.g., hyperlipoproteinemia type I (OMIM 238600), familial hypercholesterolemia (OMIM 143890), and familial defective apolipoprotein B (OMIM 107730). However, in many cases the etiology is unknown and there is strong evidence for additional uncharacterized loci.

For example, Zuliani et al., *Arterioscler. Thromb. Vasc. Biol.* 19:802-809 (1999) identified a Sardinian family with a recessive form of hypercholesterolemia with the clinical features of familial hypercholesterolemia (OMIM 603813), and found that previously identified genes were not responsible for this disorder. They proposed that in this new lipid disorder, a recessive defect causes a selective impairment of the LDL receptor function in the liver. Ciccarese et al., *Am. J. Hum. Genet.* 66:453-460 (2000) recently mapped this novel disease locus.

Another example is designated familial combined hyperlipidemia (OMIM 144250) which affects approximately 1-

2% of the population in the Western world. This disorder can have its basis in mutation in several novel genes, two of which have been mapped to chromosome 1 (Pajukanta et al., Nature Genet. 18:369-373 (1998)) and chromosome 11 (Aouizerat et al., Am. J. Hum. Genet. 65, 397-412 (1999)). The high frequency of this disorder suggests that most, if not all, hyperlipidemias are of multifactorial genetic etiology.

As yet a further example, primary sclerosing cholangitis (PSC) is a disorder characterized by a patchy obliterative inflammatory fibrosis of the large bile ducts. Chronic inflammation leads to extensive bile duct strictures, cholestasis, and gradual progression to biliary cirrhosis. PSC occurs most often in young men and is commonly associated with inflammatory bowel disease, especially ulcerative colitis. The onset is usually insidious, with gradual, progressive fatigue, pruritus, and jaundice. There is no specific therapy for sclerosing cholangitis, and liver transplantation is the only apparent cure.

The etiology of PSC is not known, but both genetic and immunologic abnormalities have been implicated. However, the frequency of HLA-B8 and HLA-DT2, which are associated with a number of autoimmune diseases, is higher in PSC than normal individuals. Prochazka et al., New Eng. J. Med. 322:1842-1844 (1990) found that 100% of 29 patients with primary sclerosing cholangitis carried the HLA-DRw52a antigen, which is normally present in 35% of the population.

As a still further example, sarcoidosis is a disease of unknown cause characterized by non-caseating granulomas in one or more organ systems. These granulomas may resolve completely or proceed to fibrosis. The disorder is systemic, but the liver is affected in approximately 75% of cases. Sarcoidosis occurs mainly in persons aged 20 to

40 yr and is most common in Northern Europeans and American blacks. The lifetime risk of developing sarcoidosis is particularly high among Swedish men (1.15%), Swedish women (1.6%), and African Americans (2.4%).

5 The much greater frequency in African Americans relative to the United States population overall suggests a genetic contribution to etiology. Early research studying familial aggregation indicated that the disease may have a nongenetic basis because the family pattern did not conform
10 to a simple Mendelian mode of inheritance (Allison, Sth. Med. J. 57: 27-32 (1964)). However, Headings et al., Ann. N.Y. Acad. Sci. 278:377-385 (1976) favored multifactorial genetic inheritance of susceptibility. Nowack et al., Arch. Intern. Med. 147:481-483 (1987), found an unusually
15 high frequency of HLA-DR5 in a study of 440 patients with sarcoidosis in Marburg, Germany. They also concluded that the role of an environmental or infectious agent triggering sarcoidosis cannot be envisaged without considering genetically linked cofactors.

20 Other significant diseases of liver are also believed to have a genetic, typically polygenic, etiologic component. These diseases include, e.g., primary biliary cirrhosis, Zellweger syndrome, cholestasis-lymphedema syndrome, Alstrom syndrome, primary pulmonary
25 hypertension, Berardinelli-Seip congenital lipodystrophy, iron overload in Africa, neonatal cholestatic hepatitis, autosomal recessive KID syndrome, familial hypotransferrinemia, type I congenital dyserythropoietic anemia, porphyria variegata, Finnish lactic acidosis with
30 hepatic hemosiderosis, Rotor syndrome, essential hypertension, ARC syndrome, type II conjugated hyperbilirubinemia, Lambert syndrome, ichthyosis congenita with biliary atresia, Kabuki make-up syndrome, Meckel syndrome, cerebral aneurysm-cirrhosis syndrome, glycogen
35 storage diseases, polycystic kidney and hepatic disease,

isolated Caroli disease, trisomy 18-like syndrome, Osler-Rendu-Weber syndrom 3, fatal intrahepatic cholestasis, Coach syndrome, type C Niemann-Pick disease, hereditary persistence of fetal hemoglobin and hepatocellular cancer.

5 Altered responses to a variety of infectious agents that target the liver, especially acute viral hepatitis, have also been shown or are suspected to have genetic bases or contributions. In addition to differential susceptibility to primary infectious agents, 10 these altered responses include predisposition to complicating conditions following contact with particular infectious agents. These include, e.g., development of hepatocellular carcinoma 2 correlated with Hepatitis B infection, and severe hepatic fibrosis following 15 *Schistosoma mansoni* infection.

 The central role of the liver in drug metabolism results in exposure of this organ to a large variety of potentially toxic chemical agents and metabolites. These include naturally occurring plant alkaloids and mycotoxins, 20 industrial chemicals, and, additionally, pharmacologic agents used in treating disease. The range of manifestations of toxin- and drug-induced liver disease are virtually as broad as the range of acute and chronic disorders and have also been shown or suspected to have 25 genetic bases or contributions.

 Such interactions between drugs and genotype have been shown in the response, e.g., to the anticonvulsant phenytoin, which can cause severe hepatitis-like disease in individuals who are impaired in the ability to detoxify a 30 metabolite of phenytoin in the liver, and in the response to the drug sodium valproate, which can produce severe hepatotoxicity in certain individuals. The abnormal responses to both of these drugs are believed to be influenced by underlying genetic factors.

35 The human genome-derived single exon nucleic acid

probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human liver, particularly those diseases with polygenic etiology. With each of the single
5 exon probes described herein shown to be expressed at detectable levels in human liver, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

10 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders, such as cirrhosis), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression
15 profiles known to be characteristic of a given liver disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
20 patient's liver to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly, using nucleic acids obtained directly or indirectly from transcripts expressed by liver of individuals with known liver disease. Methods for
25 quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single
30 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of liver disease to be assessed through the massively parallel determination of
35 altered copy number, deletion, or mutation in the patient's

genome of exons known to be expressed in human liver. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

5 The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

10 It should be appreciated, however, that the probes of the present invention, for which expression in the Fetal liver has been demonstrated are useful for both measurement in the Fetal liver and for survey of expression in other tissues.

15 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
20 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
25 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
30 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
35 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
5 for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. Nature 405,
10 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct
15 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for
20 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of
25 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

30 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
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"Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile

and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

10 The invention particularly provides genome-derived single-exon probes known to be expressed in Fetal liver. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity
15 sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA
20 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes
25 can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a
30 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known
35 amplification technique. One such technique additional to

PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
5 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
10 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be
15 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
20 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
25 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
30 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
35 single exon microarray of the present invention, the

genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however - that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,674 - 25,129, respectively, for probe SEQ ID NOS. 1 - 12,673. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,674 - 25,129 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS, in a

humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in

both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
5 sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or
10 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution
15 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

20 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or
25 enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for
30 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

35 When provided as a collection of plural

individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is
5 obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second,
10 different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen
15 for the common attribute of expression in the human Fetal liver.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell
20 type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF
25 by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to
30 provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-
35 derived single-exon nucleic acid microarrays comprising a

plurality of probes known to be expressed in human Fetal liver. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group
5 consisting of SEQ ID NOS.: 1 - 12,673.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of
10 probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the
15 same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with
20 a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to
25 their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 12,673 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,674 - 25,129, that encodes
30 a protein domain. Thus, each of SEQ ID NOS. 1 - 12,673 can be used, or that portion thereof in SEQ ID NOS. 12,674 - 25,129 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and Maniatis et al.

35 Additionally, kits are available commercially

that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,674 - 25,129. Such amino acid sequences are set out in SEQ ID NOS: 25,130 - 37,156. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

30

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

35 Preparation of Single Exon Microarrays from ORFs Predicted

in Human Genomic Sequence

Bioinformatics Results

5 All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

10 After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden
15 Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

20 The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of
25 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed.
30 That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two
35 criteria: (1) any 7 consecutive exons within a 25 kb window

were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon

to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular

Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of

the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., Nature Genet. 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

10

Table 1

| Function of Predicted ORFs As Deduced From Comparative Sequence Analysis | | | |
|--|---------|---------|---|
| Total | V6 chip | V7 chip | Function Predicted from Comparative Sequence Analysis |
| 211 | 96 | 115 | Receptor |
| 120 | 43 | 77 | Zinc Finger |
| 30 | 11 | 19 | Homeobox |
| 25 | 9 | 16 | Transcription Factor |
| 17 | 11 | 7 | Transcription |
| 118 | 57 | 61 | Structural |
| 95 | 39 | 56 | Kinase |
| 36 | 18 | 18 | Phosphatase |
| 83 | 31 | 52 | Ribosomal |
| 45 | 19 | 26 | Transport |
| 21 | 17 | 14 | Growth Factor |
| 17 | 12 | 5 | Cytochrome |
| 50 | 33 | 17 | Channel |

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

5 Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 10 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message 15 pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial 20 sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 25 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II 30 enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. 35 Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 μ l hybridization solution
5 containing 50% formamide, 5X SSC, 0.2 μ g/ μ l poly(dA), 0.2 μ g/ μ l human c₀t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC,
10 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics
15 Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference
20 permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact,
25 both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when
30 signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is
35 presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-

05 to $1e-99$; black: E values $> 1e-05$).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective
5 tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

10 It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested
15 tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence
20 databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

25 Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The
30 data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and
35 shows in blue the normalized Cy3 signal intensity for all

sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

5 As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

10 However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes
15 will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and
20 further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach
25 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis
30 of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene
35 expression panel 24 human cDNAs) (OriGene Technologies,

Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

| Function of the Most Highly Expressed Genes Expressed Only in Brain | | | | |
|---|--------------------|-------------------|------------------------------------|--|
| Microarray Sequence Name | Normal ized Signal | Expressi on Ratio | Homology to EST present in GenBank | Gene Function as described by GenBank |
| AP000217-1 | 5.2 | +7.7 | High | S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system |
| AP000047-1 | 2.3 | | High | Unknown Function |
| AC006548-9 | 1.7 | | High | Similar to mouse membrane glyco-protein M6, expressed in central nervous system |
| AC007245-5 | 1.5 | | High | Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21 |
| L44140-4 | 1.2 | +2.0 | High | Endothelial actin-binding protein found in nonmuscle filamin |

| | | | | |
|------------|-----|------|------|--|
| AC004689-9 | 1.2 | +3.5 | High | Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases |
| AL031657-1 | 1.2 | +3.0 | High | Unknown function/ Contains the anhyrin motif, a common protein sequence motif |
| AC009266-2 | 1.1 | +3.7 | Low | Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain |
| AP000086-1 | 1.0 | +2.7 | Low | Unknown, very poor homology to collagen |
| AC004689-3 | 1.0 | | High | Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases |

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip
 sequences included a translation elongation factor 1 α
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
 chromosome RNA-binding motif (Chai et al., *Genomics*
 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in
 trisomy 21 (Down's syndrome), showed high expression in
 both brain and heart, in agreement with the literature
 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we
 selected the BAC AC006064 to be included on the array.
 This BAC was known to contain the GAPDH gene, and thus
 could be used as a control for the ORF selection process.
 The gene finding and exon selection algorithms resulted in
 15 choosing 25 exons from BAC AC006064 for spotting onto the
 array, of which four were drawn from the GAPDH gene. Table
 3 shows the comparison of the average expression ratio for
 the 4 exons from BAC006064 compared with the average
 expression ratio for 5 different dilutions of a
 20 commercially available GAPDH cDNA (Clontech).

Table 3

| Comparison of Expression Ratio, for each tissue, of GAPDH | | |
|--|------------------|------------------|
| | AC006064 (n = 4) | Control (n = 5) |
| Bone Marrow | -1.81 \pm 0.11 | -1.85 \pm 0.08 |
| Brain | -1.41 \pm 0.11 | -1.17 \pm 0.05 |
| BT474 | 1.85 \pm 0.09 | 1.66 \pm 0.12 |
| Fetal Liver | -1.62 \pm 0.07 | -1.41 \pm 0.05 |
| HBL100 | 1.32 \pm 0.05 | 2.64 \pm 0.12 |
| Heart | 1.16 \pm 0.09 | 1.56 \pm 0.10 |
| HeLa | 1.11 \pm 0.06 | 1.30 \pm 0.15 |
| Liver | -1.62 \pm 0.22 | -2.07 \pm |

| | | |
|----------|--------------|--------------|
| Lung | -4.95 ± 0.93 | -3.75 ± 0.21 |
| Placenta | -3.56 ± 0.25 | -3.52 ± 0.43 |

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again
5 demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray
10 experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding
20 programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual
25 display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

30 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION
5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene
10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the
15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease
20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,
25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in Fetal liver tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 12,673 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 12,673 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,673. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the
30 exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 12,674 - 25,129, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human Fetal liver and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human Fetal liver tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 12,674 to 25,129 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:" from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The
5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each
10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs
15 in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for
20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as
25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

30 Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for
35 analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 12,673) and probe exon (SEQ ID NOs.: 12,674 - 25,129, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Fetal liver

Table 4 (526 pages) presents expression, homology, and functional information for the genome-derived single exon
5 probes that are expressed significantly in human Fetal liver.

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human Fetal liver comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,674 - 25,129.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single-exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,673 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human Fetal liver.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,674 - 25,129 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
10 of SEQ ID NOs.: 25,130 - 37,156, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one
25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human Fetal liver, comprising:

contacting the microarray of claim 12, with a first
collection of detectably labeled nucleic acids,
said first collection of nucleic acids derived
from mRNA of human Fetal liver; and then
10 measuring the label detectably bound to each probe of
said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:

15 algorithmically predicting at least one exon from
genomic sequence of said eukaryote; and then
detecting specific hybridization of detectably labeled
nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
20 from mRNA from the Fetal liver of said eukaryote, said
probe is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:

identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
then
measuring the expression of each of said exons in a
plurality of tissues and/or cell types using
hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 25,129 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 25,129.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 25,130 - 37,156.

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--------------------|
| 475 | 13108 | 26600 | 4.41 | | | | |
| 822 | 13535 | 26053 | 9.9 | | | | |
| 1083 | 13688 | | 2.9 | | | | |
| 1345 | 13940 | 26462 | 10.32 | | | | |
| 1656 | 14248 | 26782 | 2.59 | | | | |
| 1678 | 14270 | 26803 | 5.03 | | | | |
| 1763 | 14353 | 26899 | 1.73 | | | | |
| 1785 | 14375 | 26919 | 0.89 | | | | |
| 1792 | 14382 | 26927 | 9.24 | | | | |
| 1935 | 14519 | 27075 | 1.21 | | | | |
| 2021 | 14803 | 27168 | 3.24 | | | | |
| 2210 | 14786 | 27360 | 4.38 | | | | |
| 2318 | 14890 | 27465 | 2.04 | | | | |
| 2607 | 15169 | 27735 | 0.89 | | | | |
| 2607 | 15169 | 27736 | 0.89 | | | | |
| 3220 | 15832 | 28311 | 1.65 | | | | |
| 3496 | 16101 | 28576 | 1.22 | | | | |
| 3598 | 16170 | 28652 | 10.28 | | | | |
| 3617 | 16220 | | 0.8 | | | | |
| 3718 | 16319 | 28787 | 0.97 | | | | |
| 4020 | 16818 | | 0.84 | | | | |
| 4275 | 16881 | 29310 | 1.53 | | | | |
| 4348 | 16835 | 29378 | 8.4 | | | | |
| 4368 | 16955 | 29396 | 0.74 | | | | |
| 4368 | 16955 | 29397 | 0.74 | | | | |
| 4430 | 17016 | | 1.3 | | | | |
| 4662 | 17537 | 29879 | 1.04 | | | | |
| 5007 | 17580 | | 0.59 | | | | |
| 5054 | 17627 | 30071 | 0.81 | | | | |
| 5197 | 17762 | 30187 | 5.95 | | | | |
| 5212 | 17777 | 30198 | 1.32 | | | | |
| 5462 | 18097 | 30415 | 2.1 | | | | |
| 5462 | 18097 | 30416 | 2.1 | | | | |
| 5615 | 18244 | | 5.64 | | | | |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--------------------|
| 5783 | 18408 | | 8.03 | | | | |
| 5859 | 18244 | | 4.85 | | | | |
| 5910 | 18532 | 31267 | 0.84 | | | | |
| 5915 | 18537 | 31262 | 3.16 | | | | |
| 6173 | 24758 | 31552 | 1.41 | | | | |
| 6200 | 18810 | 31578 | 1.66 | | | | |
| 6548 | 19146 | | 1.28 | | | | |
| 6668 | 19264 | 32067 | 1 | | | | |
| 6668 | 19264 | 32068 | 1 | | | | |
| 7179 | 19711 | 32558 | 1.13 | | | | |
| 7179 | 19711 | 32660 | 1.13 | | | | |
| 7441 | 19965 | 32831 | 1.4 | | | | |
| 7441 | 19965 | 32832 | 1.4 | | | | |
| 8005 | 20547 | 33451 | 1.65 | | | | |
| 8422 | 20962 | 33878 | 1.45 | | | | |
| 8794 | 21333 | 34267 | 0.57 | | | | |
| 8794 | 21333 | 34258 | 0.57 | | | | |
| 9453 | 21979 | 34931 | 4.94 | | | | |
| 9681 | 22180 | 35155 | 0.78 | | | | |
| 9798 | 22294 | 35277 | 1.19 | | | | |
| 9838 | 22431 | 35408 | 1.03 | | | | |
| 10214 | 22709 | 35702 | 0.48 | | | | |
| 10214 | 22709 | 35703 | 0.48 | | | | |
| 10326 | 22820 | 35815 | 0.65 | | | | |
| 10326 | 22820 | 35816 | 0.65 | | | | |
| 10563 | 23098 | | 3.06 | | | | |
| 10725 | 24788 | 36288 | 2.46 | | | | |
| 10906 | 23425 | | 2.99 | | | | |
| 11238 | 23769 | 36827 | 2.73 | | | | |
| 11336 | 23034 | 36043 | 1.87 | | | | |
| 11336 | 23034 | 36044 | 1.87 | | | | |
| 11374 | 23826 | | 2.59 | | | | |
| 12117 | 24376 | | 2.18 | | | | |
| 12439 | 24578 | 30814 | 1.6 | | | | |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6203 | 18813 | 31593 | 14.37 | 9.8E+00 | AJ239028.1 | NT | Homo sapiens LSS gene, partial, exons 16, 18, 17 and 18 |
| 7948 | 20490 | 33400 | 1.65 | 9.8E+00 | U32716.1 | NT | Haemophilus influenzae Rd section 31 of 163 of the complete genome |
| 9658 | 22157 | 35128 | 0.47 | 9.8E+00 | Y18930.1 | NT | Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2 |
| 9658 | 22157 | 35129 | 0.47 | 9.8E+00 | Y18930.1 | NT | Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2 |
| 7073 | 18845 | 32483 | 0.8 | 9.8E+00 | AF065630.1 | NT | Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1 |
| 7073 | 18845 | 32484 | 0.8 | 9.8E+00 | AF065630.1 | NT | Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1 |
| 10319 | 22813 | 35808 | 1.22 | 9.6E+00 | AF242432.1 | NT | Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds |
| 10319 | 22813 | 35809 | 1.22 | 9.6E+00 | AF242432.1 | NT | Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds |
| 2689 | 15247 | 27814 | 1.14 | 9.4E+00 | L11433.1 | NT | Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds |
| 2689 | 15247 | 27815 | 1.14 | 9.4E+00 | L11433.1 | NT | Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds |
| 2950 | 15568 | 28040 | 3.19 | 9.4E+00 | AB043785.1 | NT | Mus musculus AT3 gene for antithrombin, complete cds |
| 8042 | 20594 | 33491 | 0.86 | 9.3E+00 | AF130990.1 | NT | Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4 |
| 8933 | 21471 | 34390 | 3.48 | 9.3E+00 | P11210 | SWISSPROT | IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP88) |
| 5500 | 18134 | 30543 | 2.82 | 9.1E+00 | AF065609.1 | NT | Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product |
| 5500 | 18134 | 30544 | 2.82 | 9.1E+00 | AF065609.1 | NT | Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product |
| 9351 | 21865 | 30544 | 0.9 | 9.0E+00 | P08241 | SWISSPROT | RHODOPSIN |
| 8186 | 18796 | 31564 | 5.12 | 8.9E+00 | BE071806.1 | EST_HUMAN | 601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3' |
| 6517 | 19117 | 31907 | 1.9 | 8.7E+00 | AB019788.1 | NT | Cynops pyrogastrus CpTbx3 premature mRNA, partial cds |
| 6517 | 19117 | 31908 | 1.9 | 8.7E+00 | AB019788.1 | NT | Cynops pyrogastrus CpTbx3 premature mRNA, partial cds |
| 465 | 13099 | 25590 | 1.66 | 8.4E+00 | 5031804 | NT | Homo sapiens insulin receptor substrate 1 (IRS1) mRNA |
| 9376 | 20315 | 33217 | 3.8 | 8.1E+00 | AJ131719.1 | NT | Zea mays mRNA for legumain-like protease (sec2a) |
| 11048 | 23561 | | 2.47 | 8.0E+00 | P41820 | SWISSPROT | BREFELDIN A RESISTANCE PROTEIN |
| 8082 | 20633 | | 0.76 | 7.6E+00 | Z21489.1 | NT | African swine fever virus NP1450L gene encoding RNA polymerase largest subunit |
| 7384 | 19910 | | 1.95 | 7.5E+00 | AL445065.1 | NT | Thermoplasma acidophilum complete genome; segment 3/5 |
| 8302 | 20843 | 33764 | 1.54 | 7.5E+00 | P35441 | SWISSPROT | THROMBOSPONDIN 1 PRECURSOR |
| 8302 | 20843 | 33765 | 1.54 | 7.5E+00 | P35441 | SWISSPROT | THROMBOSPONDIN 1 PRECURSOR |
| 5968 | 18589 | 31324 | 3.35 | 7.4E+00 | BF700517.1 | EST_HUMAN | 6021288/8F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285508 5' |
| 8688 | 21227 | 34147 | 2.63 | 7.4E+00 | P04829 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8688 | 21227 | 34148 | 2.63 | 7.4E+00 | P04629 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 3008 | 15622 | 28089 | 3.19 | 7.2E+00 | L12051.1 | NT | Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds |
| 3008 | 15622 | 28100 | 3.19 | 7.2E+00 | L12051.1 | NT | Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds |
| 7097 | 18688 | 32507 | 0.7 | 7.2E+00 | BE178080.1 | EST_HUMAN | RCO-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA |
| 7203 | 19734 | 32585 | 1.22 | 7.1E+00 | P28168 | SWISSPROT | ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1) |
| 7203 | 19734 | 32586 | 1.22 | 7.1E+00 | P28168 | SWISSPROT | ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1) |
| 9516 | 22016 | | 7.98 | 7.1E+00 | AL161595.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91 |
| 11283 | 23791 | 36848 | 3.2 | 7.1E+00 | P05850 | SWISSPROT | HYPOTHETICAL 17.3 KDA PROTEIN IN MIRDA-PHFB INTERGENIC REGION |
| 9882 | 22389 | 35387 | 3.35 | 7.0E+00 | P48610 | SWISSPROT | ARGININE KINASE (AK) |
| 11129 | 23637 | 36879 | 1.87 | 7.0E+00 | O22469 | SWISSPROT | WD-40 REPEAT PROTEIN MS3 |
| 8225 | 20768 | 33884 | 4.06 | 6.9E+00 | P35679 | SWISSPROT | 60S RIBOSOMAL PROTEIN L4 (L2) |
| 10253 | 22748 | 35738 | 1.2 | 6.8E+00 | P44834 | SWISSPROT | DNA MISMATCH REPAIR PROTEIN MUTS |
| 7848 | 20391 | 33283 | 1.38 | 6.8E+00 | W03412.1 | EST_HUMAN | z007c11.1 Scores melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291860 5' |
| 7849 | 20391 | 33284 | 1.38 | 6.8E+00 | W03412.1 | EST_HUMAN | z007c11.1 Scores melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291860 5' |
| 9080 | 21597 | | 1.13 | 6.8E+00 | P36307 | SWISSPROT | OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8] |
| 10110 | 22605 | 35595 | 3.85 | 6.8E+00 | Q03570 | SWISSPROT | HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III |
| 5488 | 18122 | | 0.69 | 6.6E+00 | Q89028 | SWISSPROT | CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT) |
| 9886 | 22481 | 35465 | 1.89 | 6.6E+00 | Q8ZE07 | SWISSPROT | URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) |
| 9886 | 22481 | 35468 | 1.89 | 6.6E+00 | Q8ZE07 | SWISSPROT | URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) |
| 11008 | 23522 | | 2.13 | 6.6E+00 | Q10309 | SWISSPROT | PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C |
| 9108 | 21844 | 34594 | 7.21 | 6.5E+00 | P03374 | SWISSPROT | ENV POLYPEPTIDE [CONTAINS: COAT PROTEIN GP82; COAT PROTEIN GP36] |
| 10208 | 22701 | 35695 | 0.49 | 6.5E+00 | BE866001.1 | EST_HUMAN | 601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3980989 5' |
| 9857 | 22158 | 35127 | 1.11 | 6.2E+00 | AY010901.1 | NT | Schizaphyllum commune unknown mRNA |
| 10455 | 22949 | 35958 | 0.53 | 6.2E+00 | 6754621 | NT | Mus musculus maritimoside 2, alpha B1 (Mar2b1), mRNA |
| 7102 | 19872 | 32511 | 1.34 | 6.0E+00 | BE780163.1 | EST_HUMAN | 601468031F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871303 5' |
| 9730 | 22228 | 35205 | 0.46 | 6.0E+00 | AP000008.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt. position (877) |
| 10407 | 22901 | 35898 | 0.6 | 6.0E+00 | AE001862.1 | NT | Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2 |
| 10407 | 22901 | 35897 | 0.6 | 6.0E+00 | AE001862.1 | NT | Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2 |
| 6843 | 19239 | 32042 | 6.87 | 5.8E+00 | AF155142.1 | NT | Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk18) genes, complete cds |
| 3578 | 16180 | | 1.18 | 5.8E+00 | 7881557 | NT | Homo sapiens DESC1 protein (DESC1), mRNA |
| 7215 | 19746 | 32801 | 0.87 | 5.7E+00 | AF302046.1 | NT | Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds |
| 7215 | 19746 | 32802 | 0.87 | 5.7E+00 | AF302046.1 | NT | Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7570 | 20087 | | 1.31 | 5.6E+00 | P75080 | SWISSPROT | DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLII) |
| 11349 | 23047 | 36059 | 2.68 | 5.0E+00 | Q55278 | SWISSPROT | LYCOPENE BETA CYCLASE |
| 6399 | 19002 | 31780 | 0.73 | 5.5E+00 | P47447 | SWISSPROT | HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HIRCA |
| 10858 | 23180 | | 1.54 | 5.5E+00 | AF175425.1 | NT | Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32 |
| 11348 | 23048 | 36058 | 3.79 | 5.5E+00 | P11980 | SWISSPROT | PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN) |
| 11578 | 24024 | | 2.08 | 5.5E+00 | AL161571.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67 |
| 7009 | 19507 | 32326 | 1.2 | 5.4E+00 | X02212.1 | NT | Chicken alpha-cardiac actin gene |
| 7009 | 19507 | 32327 | 1.2 | 5.4E+00 | X02212.1 | NT | Chicken alpha-cardiac actin gene |
| 7369 | 19895 | | 0.72 | 5.4E+00 | Q69435 | SWISSPROT | NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2) |
| | | | | | | | VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1G; LIPOVITELLIN LV-2] |
| 7811 | 20354 | | 1.58 | 5.4E+00 | Q91082 | SWISSPROT | REP1 PROTEIN |
| 8734 | 21273 | 34183 | 0.78 | 5.4E+00 | P40379 | SWISSPROT | REP1 PROTEIN |
| 8734 | 21273 | 34184 | 0.78 | 5.4E+00 | P40379 | SWISSPROT | REP1 PROTEIN |
| 9949 | 22444 | 35423 | 1.33 | 5.4E+00 | Q17094 | SWISSPROT | RHODOPSIN |
| 9949 | 22444 | 35424 | 1.33 | 5.4E+00 | Q17094 | SWISSPROT | RHODOPSIN |
| 4899 | 17474 | 29930 | 1.52 | 5.3E+00 | L43128.1 | NT | Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds |
| 6614 | 19211 | | 0.67 | 5.3E+00 | P41779 | SWISSPROT | HOMEOBOX PROTEIN CEH-20 |
| 8024 | 20568 | | 3.71 | 5.3E+00 | P54098 | SWISSPROT | DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT) |
| 8914 | 21452 | | 0.62 | 5.3E+00 | AB034890.1 | NT | Homo sapiens HERPUD1 gene for stress protein Herp, complete cds |
| 5655 | 18262 | | 1.04 | 5.2E+00 | BE184840.1 | EST_HUMAN | QV4-HT0691-270400-186-009 HT0691 Homo sapiens cDNA |
| 10274 | 22769 | | 0.78 | 5.2E+00 | AF248070.1 | NT | Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds |
| 11074 | 23586 | | 2.1 | 5.2E+00 | Q10136 | SWISSPROT | HYPOPHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I |
| 8892 | 21430 | 34354 | 0.88 | 5.1E+00 | O16005 | SWISSPROT | RHODOPSIN |
| 9739 | 22237 | 35217 | 0.87 | 5.1E+00 | P08182 | SWISSPROT | COLICIN N IMMUNITY PROTEIN (MICROGICIN N IMMUNITY PROTEIN) |
| 6430 | 19033 | 31817 | 0.85 | 5.0E+00 | BF310443.1 | EST_HUMAN | 601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114.5 |
| 10086 | 22591 | | 0.69 | 5.0E+00 | BF308561.1 | EST_HUMAN | 601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509.5 |
| 10327 | 22821 | 35817 | 3.37 | 5.0E+00 | AF162445.2 | NT | Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds |
| 11170 | 23677 | 36723 | 13.54 | 5.0E+00 | Z83860.1 | NT | Mycobacterium tuberculosis H37Rv complete genome; segment 103/162 |
| | | | | | | | |
| 10131 | 22828 | | 0.71 | 4.9E+00 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 4135 | 16727 | | 12.06 | 4.8E+00 | AF185255.1 | NT | Eunice australis histone H3 (H3) gene, partial cds |
| 8095 | 20636 | 33547 | 0.65 | 4.8E+00 | BF367809.1 | EST_HUMAN | RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA |
| 8478 | 21017 | | 4.95 | 4.8E+00 | AW750087.1 | EST_HUMAN | PMO-BT0547-310100-002-504 BT0547 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 311 | 12966 | 25454 | 1.88 | 4.7E+00 | BF240552.1 | EST_HUMAN | 601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4088718 5' |
| 312 | 12966 | 25454 | 1.88 | 4.7E+00 | BF240552.1 | EST_HUMAN | 601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4088718 5' |
| 3312 | 15923 | 28398 | 1.08 | 4.7E+00 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 8124 | 21659 | 34801 | 1.09 | 4.6E+00 | BE846437.1 | EST_HUMAN | 7e88g10.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:332088 3' similar to TR:O76140 O76140 |
| 8124 | 21659 | 34802 | 1.09 | 4.6E+00 | BE846437.1 | EST_HUMAN | KIAA0845 PROTEIN; contains element PTR5 repetitive element; KIAA0845 PROTEIN; contains element PTR5 repetitive element; Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 10280 | 22785 | | 0.77 | 4.6E+00 | AF240786.1 | NT | Archaeoglobus fulgidus section 63 of 172 of the complete genome |
| 11474 | 23924 | 36994 | 1.99 | 4.5E+00 | AE001044.1 | NT | 602123238F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4280218 5' |
| 11588 | 24039 | 37108 | 1.07 | 4.5E+00 | BF088841.1 | EST_HUMAN | 602072585F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5' |
| 3078 | 15681 | 28164 | 1.53 | 4.4E+00 | BF530883.1 | EST_HUMAN | 602072585F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5' |
| 3078 | 15681 | 28165 | 1.53 | 4.4E+00 | BF530883.1 | EST_HUMAN | Murine l gene for MHC class II (a) associated invariant chain |
| 6349 | 18854 | | 1.8 | 4.4E+00 | X13414.1 | NT | Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR |
| 6288 | 18874 | | 0.82 | 4.3E+00 | AF058679.1 | NT | Plasmodium falciparum R28R+ var 1 gene, exon 1 |
| 7484 | 19886 | 32851 | 2.36 | 4.3E+00 | Y13402.1 | NT | Trepone pallidum section 38 of 87 of the complete genome |
| 7611 | 20124 | 33001 | 0.84 | 4.3E+00 | AE001222.1 | NT | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |
| 10741 | 23286 | 36282 | 8.82 | 4.3E+00 | AF240786.1 | NT | MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP) |
| 5708 | 18334 | | 3.21 | 4.2E+00 | P16444 | SWISSPROT | LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN) |
| 5780 | 18405 | 31121 | 1.46 | 4.2E+00 | P51828 | SWISSPROT | EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) |
| 6888 | 19603 | 32435 | 1.86 | 4.2E+00 | P13983 | SWISSPROT | EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) |
| 6889 | 19603 | 32436 | 1.86 | 4.2E+00 | P13983 | SWISSPROT | EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) |
| 8880 | 21428 | 34353 | 4.95 | 4.2E+00 | AI808013.1 | EST_HUMAN | w87603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360682 3' |
| 9832 | 22330 | 35312 | 2.07 | 4.2E+00 | P31368 | SWISSPROT | NUBBIN PROTEIN (TWININ PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1) |
| 7168 | 18688 | 32545 | 0.81 | 4.1E+00 | BE253688.1 | EST_HUMAN | 60110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5' |
| 7264 | 19702 | 32848 | 1.7 | 4.1E+00 | BF247839.1 | EST_HUMAN | 601858030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4088758 5' |
| 7657 | 20169 | 33056 | 8.1 | 4.1E+00 | O23810 | SWISSPROT | YY1 PROTEIN PRECURSOR |
| 7759 | 20267 | 33163 | 4.03 | 4.1E+00 | P28894 | SWISSPROT | GENE 68 PROTEIN |
| 7759 | 20267 | 33164 | 4.03 | 4.1E+00 | P28894 | SWISSPROT | GENE 68 PROTEIN |
| 7857 | 20308 | 33306 | 2.78 | 4.1E+00 | U57503.1 | NT | Pan troglodytes novel repetitive solo LTR element in the RNU2 locus |
| 9459 | 21885 | 34839 | 0.63 | 4.1E+00 | P11253 | SWISSPROT | SOS RIBOSOMAL PROTEIN L4 |
| 9590 | 22080 | 35054 | 2.26 | 4.1E+00 | BF682425.1 | EST_HUMAN | 602247838F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333208 5' |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10208 | 22703 | | 0.5 | 4.1E+00 | P48414 | SWISSPROT | CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1) |
| 10469 | 22983 | 36003 | 0.62 | 4.1E+00 | O84242 | SWISSPROT | 3-OXOXOACYL-JACYL-CARRIER-PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) |
| 10765 | 23289 | | 2.97 | 4.1E+00 | P09716 | SWISSPROT | HYPOTHETICAL PROTEIN HVLFI |
| 10851 | 23372 | | 13.84 | 4.1E+00 | BE885880.1 | EST_HUMAN | 801507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909031 5' |
| 3599 | 16203 | | 0.82 | 4.0E+00 | P36228 | SWISSPROT | GLC7-INTERACTING PROTEIN 1 |
| 5650 | 18515 | 32336 | 0.74 | 4.0E+00 | O62653 | SWISSPROT | SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE] |
| 5650 | 18515 | 32337 | 0.74 | 4.0E+00 | O62653 | SWISSPROT | SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE] |
| 7017 | 18515 | 32336 | 0.95 | 4.0E+00 | O62653 | SWISSPROT | SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE] |
| 7017 | 18515 | 32337 | 0.95 | 4.0E+00 | O62653 | SWISSPROT | SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE] |
| 7240 | 19769 | 32625 | 1.34 | 4.0E+00 | O33010 | SWISSPROT | CELL DIVISION PROTEIN FTSY HOMOLOG |
| 10070 | 22565 | 35560 | 0.8 | 4.0E+00 | AE002132.1 | NT | Ureaplasma urealyticum section 33 of 59 of the complete genome |
| 10158 | 22653 | 35647 | 0.49 | 4.0E+00 | Q00511 | SWISSPROT | URICASE (URATE OXIDASE) |
| 10158 | 22653 | 35648 | 0.49 | 4.0E+00 | Q00511 | SWISSPROT | URICASE (URATE OXIDASE) |
| 11423 | 23874 | 36937 | 3.99 | 4.0E+00 | P07584 | SWISSPROT | GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)] |
| 11423 | 23874 | 36938 | 3.99 | 4.0E+00 | P07584 | SWISSPROT | GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)] |
| 3550 | 16154 | 28636 | 4.78 | 3.9E+00 | X64518.1 | NT | N. tabacum chitinase gene 50 for class I chitinase C |
| 4413 | 18998 | | 0.74 | 3.9E+00 | AF055468.1 | NT | Mus musculus seminal vesicle secretory protein 88 (MSVSP88) gene, promoter region |
| 5839 | 18483 | 31188 | 3.08 | 3.9E+00 | BE814357.1 | EST_HUMAN | MFO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA |
| 5839 | 18483 | 31187 | 3.08 | 3.9E+00 | BE814357.1 | EST_HUMAN | MFO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA |
| 6746 | 18339 | 32145 | 0.71 | 3.9E+00 | AF288209.1 | NT | Dicystotellium discoidium non-L TR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (gag) genes, complete cds |
| 6762 | 18383 | 32188 | 0.72 | 3.9E+00 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 6855 | 18532 | 32357 | 4.12 | 3.9E+00 | P36289 | SWISSPROT | HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION |
| 7398 | 18823 | 32787 | 6.09 | 3.9E+00 | M23807.1 | NT | Human MHC class II lymphocyte antigen (DPw-beta-1) gene, exon 2 |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO.: | Exon SEQ ID NO.: | ORF SEQ ID NO.: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|-------------------------|------------------------|--------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8259 | 20800 | 33718 | 2.15 | 3.9E+00 | X65885.1 | NT | X.laensis mRNA for M4 muscarinic receptor |
| 11289 | 23007 | 36014 | 3.27 | 3.9E+00 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 11291 | 23743 | 36800 | 1.62 | 3.9E+00 | AA681489.1 | EST_HUMAN | nr18a12.s1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416 |
| 2658 | 15217 | | 1.1 | 3.8E+00 | AE001562.1 | NT | METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN); Helicobacter pylori, strain J99 section 123 of 132 of the complete genome |
| 6525 | 19125 | 31918 | 0.78 | 3.8E+00 | Q57830 | SWISSPROT | HYPOTHETICAL PROTEIN MJ0385 |
| 8371 | 20811 | 33631 | 1.06 | 3.8E+00 | DA4725.1 | EST_HUMAN | HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148 |
| 9710 | 22208 | | 0.55 | 3.8E+00 | AJ390981.1 | NT | Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7884 |
| 4082 | 16887 | 28144 | 13.56 | 3.7E+00 | AL161539.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39 |
| 7218 | 19749 | | 0.79 | 3.7E+00 | AL445065.1 | NT | Thermoplasma acidophilum complete genome; segment 3/5 |
| | | | | | | | Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA |
| 8842 | 21181 | | 0.53 | 3.7E+00 | 4503950 | NT | Mus musculus laminin beta 2 gene, exons 17-33, and complete cds |
| 9105 | 21641 | 34581 | 0.68 | 3.7E+00 | U43541.1 | NT | 602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5' |
| 11308 | 23801 | 36861 | 3.11 | 3.7E+00 | BF689278.1 | EST_HUMAN | 602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5' |
| 11308 | 23801 | 36862 | 3.11 | 3.7E+00 | BF689278.1 | EST_HUMAN | Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds |
| 11767 | 24158 | | 1.28 | 3.7E+00 | AB013748.3 | NT | AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5' |
| 619 | 13248 | 25719 | 2.6 | 3.6E+00 | AV761055.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2 |
| 4917 | 17482 | | 0.99 | 3.6E+00 | AL161472.2 | NT | HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08 |
| 8487 | 21028 | 33942 | 0.76 | 3.6E+00 | D12367.1 | EST_HUMAN | HUM000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08 |
| 8487 | 21028 | 33943 | 0.76 | 3.6E+00 | D12367.1 | EST_HUMAN | Pseudomonas aeruginosa PA01, section 8 of 528 of the complete genome |
| 8579 | 21118 | 34038 | 4.02 | 3.6E+00 | AE004447.1 | NT | Pseudomonas aeruginosa PA01, section 8 of 528 of the complete genome |
| 8578 | 21118 | 34038 | 4.02 | 3.6E+00 | AE004447.1 | NT | Escherichia coli glycerophosphate dehydrogenase (gipD) gene, partial cds; and the translation start site has been verified (gipE), the translation start site has been verified (gipG), and repressor protein (gipR) genes, complete cds |
| 10733 | 23259 | | 4.32 | 3.6E+00 | M86795.1 | NT | Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds |
| 3284 | 15895 | 28373 | 1.06 | 3.5E+00 | AF221538.1 | NT | Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds |
| 6151 | 18784 | | 1.06 | 3.5E+00 | L42888.1 | NT | Y940c08.l1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5' |
| 6360 | 18864 | 31742 | 0.82 | 3.5E+00 | R19745.1 | EST_HUMAN | THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS) |
| 8421 | 20861 | | 0.55 | 3.5E+00 | P24567 | SWISSPROT | zp88b04.s1 Stragene HeLa cell c3 937218 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element; |
| 8982 | 21500 | 34421 | 0.88 | 3.5E+00 | AA190898.1 | EST_HUMAN | zp88b04.s1 Stragene HeLa cell c3 937218 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element; |
| 8982 | 21500 | 34422 | 0.88 | 3.5E+00 | AA190898.1 | EST_HUMAN | contains Alu repetitive element/contains element MSR1 repetitive element; |
| 9414 | 21823 | 34872 | 1.12 | 3.5E+00 | AL161563.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53 |

Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1559 | 14151 | 26893 | 4.49 | 3.4E+00 | AF254577.1 | NT | Brassica napus RPB5d mRNA, complete cds |
| 2812 | 15174 | 27742 | 1.02 | 3.4E+00 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 7397 | 19922 | 32708 | 2.85 | 3.4E+00 | P04052 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT |
| 7690 | 20188 | 33098 | 0.88 | 3.4E+00 | P04052 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT |
| 8811 | 21150 | | 0.89 | 3.4E+00 | U85408.1 | NT | Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNU1) gene, complete cds |
| 9003 | 21540 | 34470 | 0.7 | 3.4E+00 | AJ228042.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3 |
| 9040 | 21577 | 34508 | 0.5 | 3.4E+00 | AJ250567.1 | NT | Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6 |
| 10165 | 22660 | 35655 | 3.61 | 3.4E+00 | AF013167.1 | NT | Saccharomyces cerevisiae MSS1 gene, complete cds |
| 11408 | 23857 | 36822 | 1.98 | 3.4E+00 | L77670.1 | NT | Homo sapiens DGeorge syndrome critical region, centromeric end |
| 6218 | 18828 | 31601 | 0.9 | 3.3E+00 | Q06668 | SWISSPROT | PUTATIVE IRON ALCOHOL DEHYDROGENASE |
| 6218 | 18828 | 31602 | 0.9 | 3.3E+00 | Q06668 | SWISSPROT | PUTATIVE IRON ALCOHOL DEHYDROGENASE |
| 7834 | 20376 | 33281 | 0.88 | 3.3E+00 | AF111168.2 | NT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| 10361 | 22655 | 35847 | 0.87 | 3.3E+00 | AP001511.1 | NT | Bacillus halodurans genomic DNA, section 5/14 |
| 10361 | 22655 | 35848 | 0.87 | 3.3E+00 | AP001511.1 | NT | Bacillus halodurans genomic DNA, section 5/14 |
| 528 | 13158 | 25640 | 1.72 | 3.2E+00 | X98422.1 | NT | D. rerio zp-50 POU gene |
| 4088 | 13158 | 25640 | 0.7 | 3.2E+00 | X98422.1 | NT | D. rerio zp-50 POU gene |
| 4835 | 17413 | 26898 | 1.24 | 3.2E+00 | 4502404 | NT | Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA |
| 5757 | 16383 | 31065 | 1.34 | 3.2E+00 | P54924 | SWISSPROT | SQUALENE-HOPENE CYCLASE |
| 5757 | 16383 | 31068 | 1.34 | 3.2E+00 | P54924 | SWISSPROT | SQUALENE-HOPENE CYCLASE |
| 5787 | 18412 | 31128 | 2.45 | 3.2E+00 | P12783 | SWISSPROT | PHOSPHOGLYCERATE KINASE, CYTOSOLIC |
| 5787 | 18412 | 31129 | 2.45 | 3.2E+00 | P12783 | SWISSPROT | PHOSPHOGLYCERATE KINASE, CYTOSOLIC |
| 6448 | 19049 | 31834 | 1.86 | 3.2E+00 | P18931 | SWISSPROT | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 |
| 6448 | 19049 | 31835 | 1.86 | 3.2E+00 | P18931 | SWISSPROT | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 |
| 7601 | 20114 | 32891 | 0.84 | 3.2E+00 | P04275 | SWISSPROT | VON WILLEBRAND FACTOR PRECURSOR (VWF) |
| 7760 | 20258 | 33154 | 2.22 | 3.2E+00 | Y13655.1 | NT | Chlamydomonas reinhardtii chloroplast DNA for psb9, ycf4, ycf3, psb18 genes |
| 7750 | 20258 | 33155 | 2.22 | 3.2E+00 | Y13655.1 | NT | Chlamydomonas reinhardtii chloroplast DNA for psb9, ycf4, ycf3, psb18 genes |
| 8980 | 21498 | | 4.84 | 3.2E+00 | P13081 | SWISSPROT | PERIPLASMIC (NIFE) HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN) |
| 9449 | 21975 | 34927 | 1.52 | 3.2E+00 | M30383.1 | NT | S. cerevisiae theonine deaminase (ILV1) gene, complete cds |
| 10047 | 22542 | 35539 | 1.91 | 3.2E+00 | AB016081.2 | NT | Oryzias latipes OIG08 gene for guanylyl cyclase C, complete cds |
| 11727 | 24133 | | 4.08 | 3.2E+00 | L33838.1 | NT | Sus scrofa choline acetyltransferase gene, promoter region |
| 6035 | 18954 | 31398 | 2.24 | 3.1E+00 | Q10135 | SWISSPROT | HYPOTHEICAL 142.6 KD PROTEIN C25E2.02 IN CHROMOSOME I |
| 7421 | 19945 | 32810 | 0.97 | 3.1E+00 | P52178 | SWISSPROT | TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID, PRECURSOR (C1P1) |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|---|
| 7711 | 20220 | | 1.09 | 3.1E+00 | AF003225.1 | NT | Bacillus subtilis peptidase (pelE) gene, complete cds |
| 8538 | 21077 | 33995 | 4.27 | 3.1E+00 | P49894 | SWISSPROT | TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5DEIODINASE) (DIOI) (TYPE 1 DI) (SDI) |
| 8538 | 21077 | 33996 | 4.27 | 3.1E+00 | P49894 | SWISSPROT | TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5DEIODINASE) (DIOI) (TYPE 1 DI) (SDI) |
| 9183 | 21760 | | 3.77 | 3.1E+00 | Q14957 | SWISSPROT | GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C) |
| 9249 | 21775 | 34728 | 0.52 | 3.1E+00 | Q01149 | SWISSPROT | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR |
| 9810 | 22308 | 35282 | 0.75 | 3.1E+00 | 7524759 | NT | Chlorella vulgaris chloroplast, complete genome |
| 9899 | 22396 | | 0.96 | 3.1E+00 | Q10125 | SWISSPROT | HYPOTHETICAL 58.3 KD PROTEIN F5C09.5 IN CHROMOSOME III |
| 10239 | 22734 | 35728 | 4.7 | 3.1E+00 | P49385 | SWISSPROT | DEOXYHYPUSINE SYNTHASE (DHS) |
| 11338 | 23036 | | 2.91 | 3.1E+00 | P33515 | SWISSPROT | GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)] |
| 11355 | 23809 | | 7.48 | 3.1E+00 | S58880.1 | NT | retinotic acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PC07-MZ1, mRNA, 2871 nt] |
| 12490 | 24619 | | 1.38 | 3.1E+00 | U77688.1 | NT | Brassica rapa pollen coat protein homolog (BAN103) gene, complete cds |
| 5541 | 18173 | 30588 | 1.68 | 3.0E+00 | X53096.1 | NT | S.aureus genes encoding Sae981 DNA methyltransferase and Sae981 restriction endonuclease |
| 6673 | 18268 | 32073 | 0.72 | 3.0E+00 | X56037.1 | NT | Corynebacterium glutamicum frtC gene for threonine synthase (EC 4.2.99.2) |
| 6673 | 18268 | 32074 | 0.72 | 3.0E+00 | X56037.1 | NT | Corynebacterium glutamicum frtC gene for threonine synthase (EC 4.2.99.2) |
| 7209 | 19740 | | 10.44 | 3.0E+00 | P18408 | SWISSPROT | CYR61 PROTEIN PRECURSOR (3CH61) |
| 7247 | 19778 | | 0.77 | 3.0E+00 | Q13201 | SWISSPROT | ENDOTHELIAL CELL MULTIMERIN PRECURSOR |
| 8638 | 21377 | | 1.33 | 3.0E+00 | X67838.1 | NT | B.napus DNA for myrosinase |
| 10195 | 22890 | 35883 | 0.53 | 3.0E+00 | Q58805 | SWISSPROT | S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYL TRANSFERASE) (ADOMET SYNTHETASE) |
| 10527 | 23094 | 36075 | 1.62 | 3.0E+00 | Q16181 | SWISSPROT | CDC10 PROTEIN HOMOLOG |
| 10888 | 23409 | 36428 | 7.04 | 3.0E+00 | P51842 | SWISSPROT | RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F) |
| 10888 | 23409 | 36427 | 7.04 | 3.0E+00 | P51842 | SWISSPROT | RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F) |
| 2055 | 14636 | 27207 | 2.32 | 2.9E+00 | AE002225.2 | NT | Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome |
| 6224 | 18833 | | 0.68 | 2.9E+00 | AB026033.1 | NT | Bonaparitia pediculus mitochondrial DNA for 16S ribosomal RNA |
| 6989 | 19487 | 32308 | 3.74 | 2.9E+00 | Z36878.1 | NT | F.pringlei gdc-pA gene for P-protein of the glycine cleavage system |
| 7262 | 19790 | 32844 | 4.37 | 2.9E+00 | O14514 | SWISSPROT | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7262 | 19780 | 32645 | 4.37 | 2.9E+00 | O14514 | SWISSPROT | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR |
| 7479 | 20001 | 32668 | 6.04 | 2.9E+00 | P46589 | SWISSPROT | ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN) |
| 7809 | 20352 | 33280 | 0.67 | 2.9E+00 | P05844 | SWISSPROT | STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3] |
| 7809 | 20352 | 33281 | 0.67 | 2.9E+00 | P05844 | SWISSPROT | STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3] |
| 8041 | 20583 | 33490 | 0.89 | 2.9E+00 | BF344171.1 | EST_HUMAN | 602017413F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4153058 5' |
| 1504 | 14098 | 26834 | 4.87 | 2.8E+00 | AF186398.1 | NT | Bufo marinus malarase K (malik) gene, partial cds; chloroplast gene for chloroplast product |
| 1675 | 14287 | | 3.45 | 2.8E+00 | AL161552.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52 |
| 7348 | 18874 | 32740 | 4.88 | 2.8E+00 | 8383724 | NT | Mus musculus endomucin (LOC53423), mRNA |
| 8531 | 22031 | | 0.57 | 2.8E+00 | BE565182.1 | EST_HUMAN | 601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5' |
| 10589 | 19874 | 32740 | 1.68 | 2.8E+00 | 8383724 | NT | Mus musculus endomucin (LOC53423), mRNA |
| 251 | 12911 | 26394 | 9.31 | 2.7E+00 | 6676306 | NT | Mus musculus per-hexamer repeat gene 3 (Phar3), mRNA |
| 251 | 12911 | 26395 | 9.31 | 2.7E+00 | 6676306 | NT | Mus musculus per-hexamer repeat gene 3 (Phar3), mRNA |
| 5740 | 18368 | 31073 | 1.2 | 2.7E+00 | L14005.1 | NT | Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2 |
| 8088 | 20628 | | 0.8 | 2.7E+00 | U15947.1 | NT | Ipomoea purpurea chalcone synthase (CHS8) gene including complete 5'UTR and complete cds |
| 8868 | 21438 | | 1.68 | 2.7E+00 | AL116458.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 8353 | 20282 | 33181 | 0.63 | 2.7E+00 | AW088191.1 | EST_HUMAN | xc88612x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733 |
| 10394 | 22688 | | 1.48 | 2.7E+00 | BE063527.1 | EST_HUMAN | THYMOSIN BETA-4 (HUMAN); |
| 4781 | 17382 | 29812 | 4.97 | 2.6E+00 | AF068749.1 | NT | CMA-BT0281-03189-087-H04 BT0281 Homo sapiens cDNA |
| 5736 | 18382 | 31068 | 1.94 | 2.6E+00 | 6755601 | NT | Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds |
| 5736 | 18382 | 31068 | 1.94 | 2.6E+00 | 6755601 | NT | Mus musculus SRY-box containing gene 13 (Sax13), mRNA |
| 5882 | 18812 | | 2.42 | 2.6E+00 | Y17062.1 | NT | Mus musculus SRY-box containing gene 13 (Sax13), mRNA |
| 7689 | 20188 | | 5.98 | 2.6E+00 | AF235602.1 | NT | Mycobacterium fortuitum furA II gene |
| 8003 | 20545 | 33447 | 1.08 | 2.6E+00 | AJ132180.1 | NT | Mus musculus SH-2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds |
| 8003 | 20545 | 33448 | 1.08 | 2.6E+00 | AJ132180.1 | NT | fabo bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-83 |
| 9676 | 22078 | 35038 | 3.02 | 2.6E+00 | AL161540.2 | NT | fabo bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-83 |
| 10257 | 22752 | | 1.51 | 2.6E+00 | 9055193 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40 |
| 10907 | 23428 | 36443 | 1.69 | 2.6E+00 | AF143675.1 | NT | Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA |
| 12300 | 24988 | | 2.78 | 2.6E+00 | 11418220 | NT | Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds |
| 1513 | 14105 | 26840 | 2.29 | 2.5E+00 | AJ271844.1 | NT | Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA |
| 1513 | 14105 | 26841 | 2.29 | 2.5E+00 | AJ271844.1 | NT | Aspergillus nidulans recQ gene for DNA helicase, exons 1-4 |
| 1513 | 14105 | 26841 | 2.29 | 2.5E+00 | AJ271844.1 | NT | Aspergillus nidulans recQ gene for DNA helicase, exons 1-4 |

Table 4

Single Exon Probes Expressed In Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5681 | 18601 | 31334 | 1.71 | 2.5E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 5681 | 18601 | 31335 | 1.71 | 2.5E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 6588 | 18601 | 31334 | 1.39 | 2.5E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 6586 | 18601 | 31335 | 1.39 | 2.5E+00 | P13485 | SWISSPROT | TEICHOIC ACID BIOSYNTHESIS PROTEIN F |
| 6628 | 19418 | 32734 | 0.73 | 2.5E+00 | D30052.1 | NT | Vibrio cholerae cbaA gene and cbaB gene for cholera toxins, complete cds |
| 7736 | 20244 | 33135 | 1.05 | 2.5E+00 | AW949158.1 | EST_HUMAN | QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA |
| 9032 | 21568 | 34498 | 1.75 | 2.5E+00 | D50307.1 | NT | Rice DNA for aldolase C-1, complete cds |
| 9766 | 27264 | 35247 | 0.88 | 2.5E+00 | BE287798.1 | EST_HUMAN | 601175779F1 NH1_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5' |
| 11724 | 24131 | | 1.68 | 2.5E+00 | AF289885.1 | NT | Mus musculus EIF-4H gene, partial cds; LMK1 gene, complete cds; and ELN gene, partial cds |
| 3047 | 15663 | 28144 | 0.9 | 2.4E+00 | M24282.1 | NT | Chicken alpha-3 collagen type VI mRNA, 3' and |
| 5033 | 17607 | 30052 | 6.78 | 2.4E+00 | 4503352 | NT | Homo sapiens double C2-like domains, alpha (DOC2A) mRNA |
| 6161 | 18774 | 31536 | 4.02 | 2.4E+00 | P02843 | SWISSPROT | VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) |
| 8082 | 20624 | 33536 | 1.99 | 2.4E+00 | P26842 | SWISSPROT | CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14) |
| 8082 | 20624 | 33537 | 1.99 | 2.4E+00 | P26842 | SWISSPROT | CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14) |
| 8153 | 20694 | | 2.33 | 2.4E+00 | AE001486.1 | NT | Helicobacter pylori, strain J99 section 47 of 132 of the complete genome |
| 8585 | 21124 | | 1.62 | 2.4E+00 | AW875128.1 | EST_HUMAN | RC2.PT0004-031299-011-005 PT0004 Homo sapiens cDNA |
| 8762 | 21301 | 34222 | 8.16 | 2.4E+00 | P24081 | SWISSPROT | ENDOCHITININASE B PRECURSOR (CHIN-B) |
| 8951 | 22446 | 35427 | 2.59 | 2.4E+00 | P13673 | SWISSPROT | SKIN GRANULE PROTEIN PRECURSOR |
| 8951 | 22446 | 35428 | 2.59 | 2.4E+00 | P13673 | SWISSPROT | SKIN GRANULE PROTEIN PRECURSOR |
| 10017 | 22512 | 35504 | 1.62 | 2.4E+00 | X02511.1 | NT | H.sapiens CTGF gene and promoter region |
| 10141 | 22636 | | 7.38 | 2.4E+00 | P09099 | SWISSPROT | XYLULOSE KINASE (XYLUKINASE) |
| 10225 | 22720 | 35710 | 1.63 | 2.4E+00 | BE326702.1 | EST_HUMAN | hr63108.x1 NCI_OGAP_KiH11 Homo sapiens cDNA clone IMAGE:3133187 3' |
| 10225 | 22720 | 35711 | 1.63 | 2.4E+00 | BE326702.1 | EST_HUMAN | hr63108.x1 NCI_OGAP_KiH11 Homo sapiens cDNA clone IMAGE:3133187 3' |
| 10483 | 22977 | 35988 | 1.27 | 2.4E+00 | Q51481 | SWISSPROT | DENITRIFICATION REGULATORY PROTEIN NIRQ |
| 10958 | 23473 | 36498 | 1.69 | 2.4E+00 | Y14070.1 | NT | Bacillus subtilis chromosomal DNA, region 75 degrees: gtpPKD operon and downstream |
| 11237 | 23768 | 36826 | 2.27 | 2.4E+00 | AF159953.2 | NT | Fragaria x anemassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds |
| 1298 | 13890 | 26413 | 11.15 | 2.3E+00 | Z46724.1 | NT | G.domesticus artificial single chain antibody gene (L3) |
| 4189 | 16786 | | 1.65 | 2.3E+00 | AJ401081.1 | NT | Bos taurus parval cyto gene for cytochrome b |
| 6000 | 18620 | | 0.91 | 2.3E+00 | N86245.1 | EST_HUMAN | J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to |
| 7477 | 18699 | 32864 | 2.54 | 2.3E+00 | 6878554 | NT | PROLYLCARBOXYPEPTIDASE |
| 7593 | 25120 | | 4.61 | 2.3E+00 | P07169 | SWISSPROT | Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA |
| 7756 | 20284 | 33159 | 1.09 | 2.3E+00 | X60285.1 | NT | MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) |
| | | | | | | | M.musci dnak and chak genes homologues coding for Dnak and Dnal |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9038 | 21575 | 34505 | 0.53 | 2.3E+00 | 5835317 | NT | Polyporus anatispiris mitochondrion, complete genome |
| 9097 | 21833 | 34572 | 1.79 | 2.3E+00 | Q11127 | SWISSPROT | ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) |
| 10681 | 21213 | 34224 | 2 | 2.3E+00 | Q07076 | SWISSPROT | (FUCOSYLTRANSFERASE 4) (FUCT-IV) |
| 11612 | 24055 | 37119 | 2.82 | 2.3E+00 | BF541987.1 | EST_HUMAN | ANNEXIN VII (SYNEXIN) |
| 11612 | 24055 | 37120 | 2.82 | 2.3E+00 | BF541987.1 | EST_HUMAN | 602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5' |
| 11850 | 24278 | 31020 | 7.31 | 2.3E+00 | BE885237.1 | EST_HUMAN | 602089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5' |
| 4089 | 16885 | 29143 | 91.07 | 2.2E+00 | AF020528.1 | NT | 601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918843 5' |
| 4403 | 16888 | 29432 | 4.5 | 2.2E+00 | D87071.1 | NT | Magnaporthe oryzae Class IV chitin synthase (chs4) gene, complete cds |
| 4403 | 16888 | 29433 | 4.5 | 2.2E+00 | D87071.1 | NT | Rat gene for regucalcin, exon1 (non-coding exon) |
| | | | | | | | Rat gene for regucalcin, exon1 (non-coding exon) |
| | | | | | | | SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>) |
| 5545 | 18177 | 30581 | 12.27 | 2.2E+00 | O88307 | SWISSPROT | SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>) |
| 5545 | 18177 | 30582 | 12.27 | 2.2E+00 | O88307 | SWISSPROT | SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>) |
| 6018 | 18635 | 31373 | 0.85 | 2.2E+00 | BE827220.1 | EST_HUMAN | RC3-CT0254-300800-022-406 CT0254 Homo sapiens cDNA |
| 6018 | 18635 | 31374 | 0.85 | 2.2E+00 | BE827220.1 | EST_HUMAN | RC3-CT0254-300800-022-406 CT0254 Homo sapiens cDNA |
| 6212 | 18822 | 31583 | 9.1 | 2.2E+00 | BE250383.1 | EST_HUMAN | 600843401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3' |
| 6485 | 18098 | 31880 | 4.32 | 2.2E+00 | Q00335 | SWISSPROT | MINOR VIRION STRUCTURAL PROTEIN MJ-2 |
| 6709 | 19503 | 32107 | 3.04 | 2.2E+00 | P51459 | SWISSPROT | INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A) |
| 7037 | 18057 | | 3.58 | 2.2E+00 | AA594574.1 | EST_HUMAN | n195b02.a1 NC1_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1058378 3' |
| 7358 | 18884 | 32747 | 0.9 | 2.2E+00 | AA137027.1 | EST_HUMAN | z187704.f1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:586143 5' |
| 7602 | 20115 | 32882 | 25.23 | 2.2E+00 | AA46012.1 | EST_HUMAN | z05g10.f1 Soares_tad_fetus_Nb27IF8_9w Homo sapiens cDNA clone IMAGE:785634 5' |
| 8046 | 20588 | 33494 | 0.65 | 2.2E+00 | BE301560.1 | EST_HUMAN | bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb-D45838 Mouse mRNA for nuclear pore-targeting-component of (MOUSE); |
| 8046 | 20588 | 33495 | 0.65 | 2.2E+00 | BE301560.1 | EST_HUMAN | bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb-D45838 Mouse mRNA for nuclear pore-targeting-component of (MOUSE); |
| 9265 | 21791 | | 12.17 | 2.2E+00 | BE741678.1 | EST_HUMAN | mRNA for nuclear pore-targeting-component of (MOUSE); |
| 9488 | 24783 | | 2.57 | 2.2E+00 | Q04708 | SWISSPROT | 601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5' |
| 9868 | 22481 | 35443 | 1.98 | 2.2E+00 | AI290373.1 | EST_HUMAN | TRANSPONSON TY1 PROTEIN A |
| | | | | | | | qnt68b03.x1 Soares_placenta_8to9weeks_2NbhIP8a0W Homo sapiens cDNA clone IMAGE:1883965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN); |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9898 | 22461 | 35444 | 1.96 | 2.2E+00 | A120073.1 | EST_HUMAN | qm88003.x1 Soares_plecanta_860weeks_2NhrIP81c9W Homo sapiens cDNA clone IMAGE:1883985 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN); |
| 10008 | 22503 | 35494 | 3.7 | 2.2E+00 | BF248782.1 | EST_HUMAN | 601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5' |
| 10353 | 22847 | 35941 | 2.89 | 2.2E+00 | AF163416.1 | NT | Homo sapiens ovarian granulosa cell 13.0 kDa protein HGR74 homolog mRNA, complete cds |
| 11316 | 23014 | 36023 | 4.01 | 2.2E+00 | P07911 | SWISSPROT | UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP) |
| 11482 | 23832 | 37003 | 4.23 | 2.2E+00 | P10407 | SWISSPROT | EARLY E1A 28 KD PROTEIN |
| 585 | 15419 | 25689 | 0.28 | 2.1E+00 | AF132612.2 | NT | Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region |
| 3648 | 16251 | | 0.85 | 2.1E+00 | AW446368.1 | EST_HUMAN | UHH-B13-ak-e-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3' |
| 6281 | 18889 | | 0.85 | 2.1E+00 | P76357 | SWISSPROT | HYPOTHETICAL PROTEIN MG302 HOMOLOG |
| 6889 | 19633 | 32471 | 3.38 | 2.1E+00 | O70159 | SWISSPROT | ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A) |
| 7110 | 19450 | 32268 | 5.13 | 2.1E+00 | N26575.1 | EST_HUMAN | Y08a10.s1 Soares_melanocyte_2NhrIM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654 |
| 8434 | 20974 | | 2.27 | 2.1E+00 | AU123630.1 | EST_HUMAN | TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN); |
| 10454 | 22948 | | 0.58 | 2.1E+00 | Y10284.1 | NT | AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5' |
| 1238 | 13838 | 26352 | 1.3 | 2.0E+00 | AF180527.1 | NT | H. sapiens TRAF1 gene, putative promoter region |
| 1238 | 13836 | 26353 | 1.3 | 2.0E+00 | AF180527.1 | NT | Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds |
| 1380 | 13973 | 26501 | 0.92 | 2.0E+00 | AF204927.1 | NT | Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds |
| 1619 | 14212 | | 2.89 | 2.0E+00 | P25582 | SWISSPROT | Oryctolagus cuniculus Net-K+-ATPase beta 1 subunit mRNA, complete cds |
| 2184 | 14770 | 27343 | 3.88 | 2.0E+00 | Z78279.1 | NT | PUTATIVE RRNA METHYLTRANSFERASE SPB1 |
| 2184 | 14770 | 27344 | 3.88 | 2.0E+00 | Z78279.1 | NT | R.norvegicus mRNA for collagen alpha1 type I |
| 4178 | 16787 | 28215 | 1.9 | 2.0E+00 | AW684486.1 | EST_HUMAN | R.norvegicus mRNA for collagen alpha1 type I |
| 4178 | 16787 | 28216 | 1.9 | 2.0E+00 | AW684486.1 | EST_HUMAN | h13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677 |
| 7552 | 20071 | | 0.77 | 2.0E+00 | P07568 | SWISSPROT | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); |
| 7867 | 20509 | 33415 | 3.56 | 2.0E+00 | AB0008876.1 | NT | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); |
| 7867 | 20509 | 33416 | 3.56 | 2.0E+00 | AB0008876.1 | NT | STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2] |
| 7867 | 20509 | 33417 | 3.56 | 2.0E+00 | AB0008876.1 | NT | Escherichia coli 0157 DNA, map position at 46 min., complete cds |
| 8853 | 21392 | 34314 | 3.62 | 2.0E+00 | F31500.1 | EST_HUMAN | Escherichia coli 0157 DNA, map position at 46 min., complete cds |
| 12295 | 24946 | 30822 | 7.77 | 2.0E+00 | | NT | Escherichia coli 0157 DNA, map position at 46 min., complete cds |
| 5784 | 18409 | 31124 | 6.88 | 1.9E+00 | 5834843 | NT | HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08 |
| 5784 | 18409 | 31125 | 6.88 | 1.9E+00 | 6754388 | NT | Gallus gallus mitochondrion, complete genome |
| 6249 | 18858 | 31630 | 1.2 | 1.9E+00 | BE868695.1 | EST_HUMAN | Mus musculus inositol 1,4,5-trisphosphate receptor 1 (htr1), mRNA |
| | | | | | | | Mus musculus inositol 1,4,5-trisphosphate receptor 1 (htr1), mRNA |
| | | | | | | | 601679036F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5' |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6760 | 19353 | | 1.02 | 1.8E+00 | AW845689.1 | EST_HUMAN | MR0-CT0063-071069-002-q02 CT0063 Homo sapiens cDNA |
| 6845 | 19435 | | 2.31 | 1.8E+00 | Q63627 | SWISSPROT | CTD-BINDING SR-LIKE PROTEIN RA4 |
| 8396 | 20638 | 33859 | 2.16 | 1.8E+00 | P02467 | SWISSPROT | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR |
| 8396 | 20638 | 33859 | 2.16 | 1.8E+00 | P02467 | SWISSPROT | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR |
| 8593 | 21132 | | 2.45 | 1.8E+00 | BF360208.1 | EST_HUMAN | CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA |
| 8825 | 21384 | | 1.35 | 1.8E+00 | Q51781 | SWISSPROT | ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD) |
| | | | | | | | ab94e04.s1 Streptococcus sp. (837210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Adu repetitive element; contains element L1 L1 repetitive element ; |
| 9648 | 22048 | 35009 | 0.6 | 1.8E+00 | AA689125.1 | EST_HUMAN | Homo sapiens gag-pro-pod precursor protein gene, partial cds |
| 10459 | 22950 | 35959 | 0.52 | 1.8E+00 | AF248269.1 | NT | PROTEIN B8 PRECURSOR |
| 3128 | 15742 | 28211 | 1.88 | 1.8E+00 | P21004 | SWISSPROT | Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds |
| 3154 | 15788 | 28234 | 2.42 | 1.8E+00 | U04356.1 | NT | Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds |
| 3154 | 15788 | 28235 | 2.42 | 1.8E+00 | U04356.1 | NT | HEDGEHOG RECEPTOR (PATCHED PROTEIN) |
| 6027 | 18946 | | 2.02 | 1.8E+00 | P18502 | SWISSPROT | 601887854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4177394 5' |
| 6253 | 18962 | 31634 | 2.02 | 1.8E+00 | BF311989.1 | EST_HUMAN | 602139470F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298272 5' |
| 6532 | 19132 | | 1.53 | 1.8E+00 | BF683327.1 | EST_HUMAN | 601883488F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5' |
| 6838 | 19428 | 32244 | 1.35 | 1.8E+00 | BF305652.1 | EST_HUMAN | MAJOR ANTIGEN |
| 7119 | 19459 | 32274 | 1.08 | 1.8E+00 | P21249 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; |
| 8060 | 20602 | 33512 | 0.81 | 1.8E+00 | P11369 | SWISSPROT | ENDONUCLEASE] |
| 8060 | 20602 | 33513 | 0.81 | 1.8E+00 | P11369 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; |
| 8788 | 21327 | 34252 | 2.12 | 1.8E+00 | Q43281 | SWISSPROT | ENDONUCLEASE] |
| 9102 | 21638 | 34577 | 0.63 | 1.8E+00 | R31042.1 | EST_HUMAN | EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS) |
| 9186 | 21703 | 34845 | 0.8 | 1.8E+00 | AW880004.1 | EST_HUMAN | Yh72a08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5' |
| 9763 | 22261 | 35244 | 0.87 | 1.8E+00 | P27050 | SWISSPROT | QV0-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA |
| 10163 | 22878 | | 3.78 | 1.8E+00 | AF111849.1 | NT | CHITINASE D PRECURSOR |
| 10447 | 22941 | | 0.85 | 1.8E+00 | P44325 | SWISSPROT | Homo sapiens PRO5530 mRNA, complete cds |
| | | | | | | | CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA) |
| 12076 | 24915 | | 6.85 | 1.8E+00 | AF314254.1 | NT | Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein |
| 12163 | 24403 | | 4.96 | 1.8E+00 | 9508404 | NT | Rattus norvegicus Actin-related protein complex 1b (Apc1b), mRNA |
| 12476 | 24815 | 30790 | 1.38 | 1.8E+00 | BF212412.1 | EST_HUMAN | 601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1147 | 13750 | 20259 | 2.08 | 1.7E+00 | Q60114 | SWISSPROT | LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE) |
| 2311 | 14883 | 27458 | 2.37 | 1.7E+00 | AL183280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 2411 | 14878 | 27554 | 1.29 | 1.7E+00 | AI141087.1 | EST_HUMAN | aa43h05.x1 Soares_NHHPu_S1 Homo sapiens cDNA clone IMAGE:1878137 3' |
| 4558 | 17141 | 29580 | 0.74 | 1.7E+00 | Q60114 | SWISSPROT | LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE) |
| 5787 | 18422 | 31137 | 1.65 | 1.7E+00 | BE063546.1 | EST_HUMAN | CM0-BT0282-171289-127-c05 BT0282 Homo sapiens cDNA |
| 5787 | 18422 | 31138 | 1.65 | 1.7E+00 | BE063546.1 | EST_HUMAN | CM0-BT0282-171289-127-c05 BT0282 Homo sapiens cDNA |
| 6168 | 18780 | 31545 | 3.35 | 1.7E+00 | Q81TR8 | SWISSPROT | COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I) |
| 7270 | 19768 | 32654 | 1.33 | 1.7E+00 | Q03703 | SWISSPROT | HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION |
| 7270 | 19798 | 32655 | 1.33 | 1.7E+00 | Q03703 | SWISSPROT | HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION |
| 7308 | 19834 | 32693 | 1.63 | 1.7E+00 | P20393 | SWISSPROT | ORPHAN NUCLEAR RECEPTOR NR1D1 (V-ERBA RELATED PROTEIN EAR-1) (REV-ERBA-ALPHA) |
| 7786 | 20339 | 33247 | 0.96 | 1.7E+00 | AF021335.1 | NT | Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters |
| 7876 | 20518 | 33425 | 1.34 | 1.7E+00 | 6755715 | NT | Mus musculus T-cell acute lymphocytic leukemia 1 (Tall), mRNA |
| 8008 | 20548 | 33452 | 0.57 | 1.7E+00 | BF530830.1 | EST_HUMAN | 602071817F-1 NCJ_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4214689 5' |
| 8478 | 21018 | 33933 | 0.61 | 1.7E+00 | AF245613.1 | NT | Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds |
| 8502 | 21101 | 34086 | 2.08 | 1.7E+00 | BF308000.1 | EST_HUMAN | 601894256F-1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5' |
| 8638 | 21177 | 34087 | 0.49 | 1.7E+00 | X69063.1 | NT | M. musculus Ank-1 mRNA for erythroid ankyrin |
| 8638 | 21177 | 34087 | 0.49 | 1.7E+00 | X69063.1 | NT | M. musculus Ank-1 mRNA for erythroid ankyrin |
| 9076 | 24782 | 34545 | 2.25 | 1.7E+00 | Q60479 | SWISSPROT | HOMEOBOX PROTEIN DLX-3 |
| 9076 | 24782 | 34546 | 2.25 | 1.7E+00 | Q60479 | SWISSPROT | HOMEOBOX PROTEIN DLX-3 |
| 9524 | 22024 | 36885 | 1.65 | 1.7E+00 | AF161380.1 | NT | Homo sapiens HSPC282 mRNA, partial cds |
| 11467 | 23917 | 36885 | 2.16 | 1.7E+00 | W22424.1 | EST_HUMAN | 67B7 Human retina cDNA Tsp508I-cleaved sublibrary Homo sapiens cDNA not directional |
| 12030 | 24320 | 30963 | 1.52 | 1.7E+00 | AI678443.1 | EST_HUMAN | tu82d07.x1 NCJ_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257548 3' similar to contains MSR1.11 |
| 12558 | 24658 | 30873 | 1.79 | 1.7E+00 | AI198573.1 | EST_HUMAN | MSR1 repetitive element ; |
| 2078 | 14858 | 27228 | 21.82 | 1.6E+00 | AF196339.1 | NT | qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.11 L1 |
| 2087 | 14888 | 27238 | 4.3 | 1.6E+00 | AF077374.1 | NT | repetitive element ; |
| 2083 | 14673 | 27243 | 1.04 | 1.6E+00 | Y11944.1 | NT | Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds |
| 2323 | 14894 | | 1.13 | 1.6E+00 | X98373.1 | NT | Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds |
| 2888 | 15804 | 28084 | 1.5 | 1.6E+00 | W58426.1 | EST_HUMAN | Mus musculus ST6GalNAcII gene, exon 2 |
| - 4104 | 16898 | | 7.23 | 1.6E+00 | BF570077.1 | EST_HUMAN | Mus musculus ST6GalNAcII gene, exon 2 |
| | | | | | | | B. napus gene encoding endo-polygalacturonase |
| | | | | | | | ztd25f01.r1 Soares_fetal_heart_NHHP19W Homo sapiens cDNA clone IMAGE:341689 5' similar to |
| | | | | | | | gb:D29805 N-ACETYL-LACTOSAMINE SYNTHASE (HUMAN); |
| | | | | | | | 602186085T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3' |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4444 | 17030 | 28470 | 1.11 | 1.6E+00 | AF155827.1 | NT | Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds |
| 4444 | 17030 | 28471 | 1.11 | 1.6E+00 | AF155827.1 | NT | Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds |
| 5145 | 17715 | 30145 | 0.6 | 1.6E+00 | AF075394.1 | NT | Urbauthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 5145 | 17715 | 30148 | 0.6 | 1.6E+00 | AF075394.1 | NT | Urbauthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 5243 | 17807 | 30228 | 2.2 | 1.6E+00 | Y11344.1 | NT | Mus musculus ST6GalNAcIII gene, exon 2 |
| 5243 | 17807 | 30229 | 2.2 | 1.6E+00 | Y11344.1 | NT | Mus musculus ST6GalNAcIII gene, exon 2 |
| 5993 | 18813 | 31347 | 1.95 | 1.6E+00 | L04808.1 | NT | Brachydanio rerio MHC class II DA-beta-2701 gene, 3' end |
| 6072 | 18889 | 31434 | 0.82 | 1.6E+00 | AF005631.1 | NT | Homo sapiens transglutaminase type I (Tgase) gene, promoter region |
| 6596 | 19180 | 31988 | 0.83 | 1.6E+00 | BF390703.1 | EST_HUMAN | IL2-JT0073-060800-145-E02 UT0073 Homo sapiens cDNA |
| 6811 | 19402 | 32218 | 1.07 | 1.6E+00 | AW294681.1 | EST_HUMAN | UHH-B12-afv-b-04-0-J1.s1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727511 3' |
| 7293 | 19821 | 32680 | 2.32 | 1.6E+00 | BE5997267.1 | EST_HUMAN | RCO-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA |
| 7973 | 20319 | | 1.09 | 1.6E+00 | Q46378 | SWISSPROT | VIRULENCE FACTOR MVIN HOMOLOG |
| 8320 | 20881 | 33786 | 3.24 | 1.6E+00 | AJ287131.1 | NT | Mus musculus SIL, MAP 17, CYP a, SCL & CYP b genes |
| 8831 | 21370 | 34294 | 0.95 | 1.6E+00 | 11437222 | NT | Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA |
| 8831 | 21370 | 34295 | 0.95 | 1.6E+00 | 11437222 | NT | Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA |
| 9381 | 24790 | 33221 | 3.18 | 1.6E+00 | X52046.1 | NT | M.musculus COL3A1 gene for collagen alpha-1 |
| 9381 | 24790 | 33222 | 3.18 | 1.6E+00 | X52046.1 | NT | M.musculus COL3A1 gene for collagen alpha-1 |
| 9649 | 22148 | 35119 | 1.34 | 1.6E+00 | T41280.1 | EST_HUMAN | ph658_184TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph658_184TV |
| 10052 | 22547 | 35541 | 0.52 | 1.6E+00 | AF121361.1 | NT | Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase lal (LAL), and zinc finger protein (DNZ1) genes, complete cds |
| 10088 | 22583 | 35575 | 0.92 | 1.6E+00 | AW835644.1 | EST_HUMAN | QV4-LT0018-080200-100-d07 LT0018 Homo sapiens cDNA |
| 10088 | 22583 | 35576 | 0.92 | 1.6E+00 | AW835644.1 | EST_HUMAN | QV4-LT0018-080200-100-d07 LT0018 Homo sapiens cDNA |
| 10248 | 22741 | 35731 | 0.49 | 1.6E+00 | AF037352.1 | NT | Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters |
| 10650 | 23182 | 36198 | 1.59 | 1.6E+00 | P54817 | SWISSPROT | CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE) : CAPSID ASSEMBLY PROTEIN] |
| 10688 | 23216 | 36228 | 1.56 | 1.6E+00 | P54817 | SWISSPROT | CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE) : CAPSID ASSEMBLY PROTEIN] |
| 10723 | 18889 | 31434 | 6.41 | 1.6E+00 | AF005631.1 | NT | Homo sapiens transglutaminase type I (Tgase) gene, promoter region |
| 11552 | 24000 | 37072 | 2.82 | 1.6E+00 | AF104913.1 | NT | Homo sapiens unknown mRNA |
| 35 | 12714 | 25173 | 4.02 | 1.5E+00 | U53449.1 | NT | Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds |
| 252 | 12912 | 25396 | 2.17 | 1.5E+00 | AE002201.2 | NT | Chlamydomonas reinhardtii AR39, section 32 of 94 of the complete genome |
| 649 | 13272 | | 1.98 | 1.5E+00 | 6752961 | NT | Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagardisin) (Adam15), mRNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1960 | 14544 | 27101 | 2.55 | 1.5E+00 | AF275265.1 | NT | Mus musculus receptor protein tyrosine phosphatase-rho (Ptp-rho) gene, exons 10 and 11 and partial cds |
| 2454 | 15021 | 27592 | 2.13 | 1.5E+00 | AJ131402.1 | NT | Potato virus A RNA complete genome, isolate U |
| 2558 | 15120 | 27690 | 1.83 | 1.5E+00 | 6878360 | NT | Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA |
| 3172 | 15021 | 27592 | 1.54 | 1.5E+00 | AJ131402.1 | NT | Potato virus A RNA complete genome, isolate U |
| 3421 | 16029 | 28510 | 0.7 | 1.5E+00 | AE001945.1 | NT | Deinococcus radiodurans R1 section 82 of 228 of the complete chromosome 1 |
| 5903 | 18525 | 31250 | 0.94 | 1.5E+00 | A1855301.1 | EST_HUMAN | h12110.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1.; |
| 5903 | 18525 | 31251 | 0.94 | 1.5E+00 | A1855301.1 | EST_HUMAN | h12110.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1.; |
| 6538 | 19137 | 31830 | 2.68 | 1.5E+00 | R17879.1 | EST_HUMAN | y010602.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31683 5' |
| 7182 | 19714 | | 1.37 | 1.5E+00 | BE785358.1 | EST_HUMAN | 601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5' |
| 7214 | 19745 | 32599 | 20.84 | 1.5E+00 | P47179 | SWISSPROT | HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR |
| 7214 | 19745 | 32600 | 20.84 | 1.5E+00 | P47179 | SWISSPROT | HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR |
| 7383 | 18909 | 32774 | 1.02 | 1.5E+00 | AA989259.1 | EST_HUMAN | ak28110.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3' |
| 8065 | 20807 | 33519 | 0.85 | 1.5E+00 | BE987448.1 | EST_HUMAN | 601509588F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5' |
| 8578 | 21117 | 34037 | 1.1 | 1.5E+00 | K02138.1 | NT | Mouse germline IgM chain gene, mu-delta region |
| 8946 | 21484 | | 0.53 | 1.5E+00 | AB038518.1 | NT | Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds |
| 9061 | 21598 | 34528 | 0.54 | 1.5E+00 | BF217818.1 | EST_HUMAN | 601882662F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4085135 5' |
| 9404 | 21913 | 34862 | 0.9 | 1.5E+00 | R81928.1 | EST_HUMAN | y03h01.r1 Soares placenta Nb2b-HP Homo sapiens cDNA clone IMAGE:147697 5' |
| 9553 | 22053 | 35018 | 1.12 | 1.5E+00 | AW375697.1 | EST_HUMAN | QV3-CT0192-281099-008-d09 CT0192 Homo sapiens cDNA |
| 9774 | 22272 | 35257 | 5.97 | 1.5E+00 | BF378754.1 | EST_HUMAN | RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA |
| 9865 | 22480 | | 1.47 | 1.5E+00 | BF337044.1 | EST_HUMAN | 602035771F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183865 5' |
| 10098 | 22593 | 35585 | 2.85 | 1.5E+00 | AA017889.1 | EST_HUMAN | z638g08.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381308 5' |
| 10098 | 22593 | 35588 | 2.85 | 1.5E+00 | AA017889.1 | EST_HUMAN | z638g08.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381308 5' |
| 11277 | 23790 | 36785 | 4.1 | 1.5E+00 | AL134197.1 | EST_HUMAN | DKFZp547P243_s1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547P243 3' |
| 11418 | 23887 | | 8.57 | 1.5E+00 | X07390.1 | NT | Malva mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene |
| 12022 | 25010 | 30015 | 1.59 | 1.5E+00 | D63480.1 | NT | Human mRNA for KIAA0148 gene, partial cds |
| 12255 | 24465 | | 4.99 | 1.5E+00 | AL445065.1 | NT | Thermoplasma acidophilum complete genome, segment 3/5 |
| 32 | 12711 | 25169 | 1.8 | 1.4E+00 | 7681685 | NT | Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA |
| 32 | 12711 | 25170 | 1.8 | 1.4E+00 | 7681685 | NT | Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA |
| 1774 | 14384 | 26809 | 1.32 | 1.4E+00 | H10859.1 | EST_HUMAN | y057e03.r1 Soares adult brain N2b-5f-B55Y Homo sapiens cDNA clone IMAGE:172540 5' |
| 2316 | 14888 | | 0.98 | 1.4E+00 | AF053357.1 | NT | Helicobacter pylori glutamine synthetase (gluA) gene, complete cds |
| 2372 | 14942 | | 7.8 | 1.4E+00 | U67922.1 | NT | Ovis aries prion protein gene, complete cds |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2693 | 15250 | 27820 | 1.45 | 1.4E+00 | X74483.1 | NT | Human papillomavirus type 7 genomic DNA |
| 2802 | 15354 | 27822 | 2.79 | 1.4E+00 | AF084584.2 | NT | Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds |
| 2802 | 15354 | 27823 | 2.79 | 1.4E+00 | AF084584.2 | NT | Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds |
| 3376 | 15685 | | 0.68 | 1.4E+00 | 5453733 | NT | Homo sapiens Mad4 homolog (MAD4) mRNA |
| 4342 | 16929 | 28369 | 1.14 | 1.4E+00 | AW900455.1 | EST_HUMAN | CMV-NN1005-140300-286-H06 NN1005 Homo sapiens cDNA |
| 4342 | 16929 | 28370 | 1.14 | 1.4E+00 | AW900455.1 | EST_HUMAN | CMV-NN1005-140300-286-H06 NN1005 Homo sapiens cDNA |
| 4685 | 17267 | | 1.78 | 1.4E+00 | BF681547.1 | EST_HUMAN | 602156887F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287558 5' |
| 5575 | 18208 | 30657 | 1.78 | 1.4E+00 | AW054978.1 | EST_HUMAN | wt45g07.x1 NC1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3' |
| 5719 | 18345 | | 5.04 | 1.4E+00 | AB032883.1 | NT | Homo sapiens mRNA for KIAA1157 protein, partial cds |
| 6425 | 19028 | 31811 | 2.73 | 1.4E+00 | Q13472 | SWISSPROT | DNA TOPOISOMERASE III ALPHA |
| 6437 | 25118 | | 4.4 | 1.4E+00 | AB020712.1 | NT | Homo sapiens mRNA for KIAA0805 protein, complete cds |
| 6544 | 19143 | 31936 | 2.32 | 1.4E+00 | Q92777 | SWISSPROT | SYNAPSIN II |
| 6544 | 19143 | 31937 | 2.32 | 1.4E+00 | Q92777 | SWISSPROT | SYNAPSIN II |
| 6583 | 19181 | 31981 | 0.67 | 1.4E+00 | 11066333 | NT | Mus musculus WW domain binding protein 11 (Wbp11-pending), mRNA |
| 6811 | 19570 | 32398 | 0.77 | 1.4E+00 | AW883057.1 | EST_HUMAN | CM3-NN0008-300300-132-b12 NN0008 Homo sapiens cDNA |
| 7330 | 19857 | 32720 | 2.31 | 1.4E+00 | AJ133269.1 | NT | Homo sapiens catenin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2) |
| 7343 | 19870 | 32735 | 1.1 | 1.4E+00 | AW467700.1 | EST_HUMAN | ha23f05.x1 NC1_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918873 3' similar to contains Alu repetitive element |
| 8277 | 20818 | | 0.68 | 1.4E+00 | P07683 | SWISSPROT | GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE)(1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) |
| 8728 | 21268 | | 4.01 | 1.4E+00 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region, segment 1/2 |
| 9023 | 21560 | 34487 | 2.13 | 1.4E+00 | R20459.1 | EST_HUMAN | y939f12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5' |
| 9125 | 21680 | 34603 | 3.72 | 1.4E+00 | BE084887.1 | EST_HUMAN | RC1-BT0313-301289-012-f05 BT0313 Homo sapiens cDNA |
| 9158 | 21693 | 34637 | 0.58 | 1.4E+00 | AF134944.1 | NT | Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds |
| 10109 | 22804 | 35594 | 0.77 | 1.4E+00 | BF575545.1 | EST_HUMAN | 602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5' |
| 10160 | 22845 | 35637 | 0.67 | 1.4E+00 | BE145374.1 | EST_HUMAN | IL5-HT0188-281089-008-C04 HT0188 Homo sapiens cDNA |
| 10150 | 22845 | 35638 | 0.67 | 1.4E+00 | BE145374.1 | EST_HUMAN | IL5-HT0188-281089-008-C04 HT0188 Homo sapiens cDNA |
| 10418 | 22912 | 35912 | 1.11 | 1.4E+00 | D63441.1 | NT | Pandorina colimani chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds |
| 10418 | 22912 | 35913 | 1.11 | 1.4E+00 | D63441.1 | NT | Pandorina colimani chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds |
| 10848 | 23463 | 36485 | 2.16 | 1.4E+00 | AA195528.1 | EST_HUMAN | zr36e09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:685512 5' similar to contains element MER22 repetitive element |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11104 | 23614 | 36854 | 6.28 | 1.4E+00 | AB006982.1 | NT | Homo sapiens APECEB mRNA for AIRE-1, complete cds |
| 11283 | 23736 | 36781 | 3.92 | 1.4E+00 | BE982107.2 | EST_HUMAN | 601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3' |
| 11283 | 23736 | 36782 | 3.92 | 1.4E+00 | BE982107.2 | EST_HUMAN | 601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3' |
| 11304 | 23797 | 36855 | 3.19 | 1.4E+00 | U30780.1 | NT | Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds |
| 11304 | 23797 | 36858 | 3.19 | 1.4E+00 | U30780.1 | NT | Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds |
| 11865 | 24935 | | 2.43 | 1.4E+00 | AL161500.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12 |
| 12287 | 25108 | | 2.38 | 1.4E+00 | 11645838 | NT | Homo sapiens cutaneous T-cell lymphoma tumor antigen sa70-2 (SE70-2), mRNA |
| 598 | 13225 | | 1.38 | 1.3E+00 | Z79640.1 | NT | M.mucosa gene encoding 4-Dihydroxymethyl-trispartate dehydrogenase |
| 935 | 13548 | 26065 | 2.33 | 1.3E+00 | AJ271192.1 | NT | Cartharius sp. partial 25S rRNA gene, isolate Tibet |
| 1168 | 13770 | | 22.19 | 1.3E+00 | Y19213.1 | NT | Homo sapiens putative psbHbA pseudogene for hair keratin, exons 2 to 7 |
| 1340 | 13935 | 26456 | 13.67 | 1.3E+00 | 4507898 | NT | Homo sapiens zinc finger protein 157 (ZFP157) mRNA |
| 1340 | 13935 | 26457 | 13.67 | 1.3E+00 | 4507898 | NT | Homo sapiens zinc finger protein 157 (ZFP157) mRNA |
| 1400 | 13994 | | 1.05 | 1.3E+00 | U81730.2 | NT | Cox lacryme-jobi dihydrodipicolinate synthase (dispa) gene, complete cds |
| 1653 | 14245 | | 2.35 | 1.3E+00 | AE002338.2 | NT | Chlamydia muridarum, section 68 of 85 of the complete genome |
| 2285 | 14859 | | 1.1 | 1.3E+00 | AB030447.1 | NT | Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds |
| 2586 | 15149 | | 0.97 | 1.3E+00 | BE986735.2 | EST_HUMAN | 601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3' |
| 2666 | 15581 | 28080 | 0.98 | 1.3E+00 | 6755621 | NT | Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA |
| 3657 | 16260 | 28732 | 0.91 | 1.3E+00 | AF016494.1 | NT | Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c> |
| 4713 | 15581 | 28080 | 1.31 | 1.3E+00 | 6755621 | NT | Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA |
| 5184 | 17749 | 30178 | 0.92 | 1.3E+00 | AJ252087.1 | NT | Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1 |
| 5184 | 17749 | 30178 | 0.92 | 1.3E+00 | AJ252087.1 | NT | Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1 |
| 5705 | 18331 | 30835 | 1.06 | 1.3E+00 | P19732 | SWISSPROT | PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT) |
| 6169 | 18781 | 31546 | 7.47 | 1.3E+00 | AW362834.1 | EST_HUMAN | PMO-CT0288-291189-004-f08 CT0289 Homo sapiens cDNA |
| 6169 | 18781 | 31547 | 7.47 | 1.3E+00 | AW362834.1 | EST_HUMAN | PMO-CT0288-291189-004-f08 CT0289 Homo sapiens cDNA |
| 6549 | 19147 | 31943 | 1.24 | 1.3E+00 | M33498.1 | NT | D.melanogaster no-on-transient A gene product, complete cds |
| 6847 | 19437 | | 0.71 | 1.3E+00 | Q00156 | SWISSPROT | HYPOTHETICAL GENE 64 PROTEIN |
| 6926 | 19595 | 32415 | 0.85 | 1.3E+00 | M13918.2 | NT | Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds |
| 7033 | 19587 | 32394 | 1.01 | 1.3E+00 | BE538819.1 | EST_HUMAN | 601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7157 | 19889 | 32533 | 0.79 | 1.3E+00 | BE243571.1 | EST_HUMAN | TCBAP-ID0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TC8A Homo sapiens cDNA clone TCBAP0959 |
| 7481 | 20003 | 32868 | 3.97 | 1.3E+00 | P24540 | SWISSPROT | ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE) |
| 8239 | 20780 | 33701 | 2.08 | 1.3E+00 | AJ008912.1 | NT | Sus scrofa pig gene |
| 8384 | 20824 | 33844 | 2.54 | 1.3E+00 | BE963379.2 | EST_HUMAN | 601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868195 3' |
| 8486 | 21035 | 33856 | 0.89 | 1.3E+00 | BE974280.1 | EST_HUMAN | 601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3' |
| 8844 | 21183 | | 1.57 | 1.3E+00 | 8910247 | NT | Homo sapiens GL004 protein (GL004), mRNA |
| 8725 | 21284 | 34184 | 0.88 | 1.3E+00 | AI927829.1 | EST_HUMAN | wc85a07.x1 NCI CGAP_KJ411 Homo sapiens cDNA clone IMAGE:2462100 3' |
| 8073 | 21610 | 34540 | 0.48 | 1.3E+00 | H42881.1 | EST_HUMAN | y088c03.s1 Soares breast 3NtH18t Homo sapiens cDNA clone IMAGE:183078 3' |
| 9073 | 21610 | 34541 | 0.48 | 1.3E+00 | H42881.1 | EST_HUMAN | y088c03.s1 Soares breast 3NtH18t Homo sapiens cDNA clone IMAGE:183078 3' |
| 9434 | 21980 | | 4.54 | 1.3E+00 | AF042084.1 | NT | Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds |
| 9443 | 21989 | 34917 | 2.12 | 1.3E+00 | X72019.1 | NT | S. alba phr-1 mRNA for photolyase |
| 9443 | 21989 | 34918 | 2.12 | 1.3E+00 | X72019.1 | NT | S. alba phr-1 mRNA for photolyase |
| 9542 | 22042 | 35003 | 1.1 | 1.3E+00 | AF050250.1 | NT | Homo sapiens lipoygenase (ALOX12B) mRNA, complete cds |
| 9588 | 22088 | 35052 | 1.62 | 1.3E+00 | O00754 | SWISSPROT | LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN) |
| 9685 | 22184 | 35137 | 1.21 | 1.3E+00 | AI927829.1 | EST_HUMAN | wc85a07.x1 NCI CGAP_KJ411 Homo sapiens cDNA clone IMAGE:2462100 3' |
| 9740 | 22238 | 35218 | 0.83 | 1.3E+00 | AJ223982.1 | NT | Lactococcus lactis cremoris NCDO-11v1 chromosomal inversion junction DNA |
| 9740 | 22238 | 35219 | 0.83 | 1.3E+00 | AJ223982.1 | NT | Lactococcus lactis cremoris NCDO-11v1 chromosomal inversion junction DNA |
| 9780 | 22278 | 35263 | 3.85 | 1.3E+00 | BE963379.2 | EST_HUMAN | 601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868195 3' |
| 10114 | 22609 | 35600 | 1.25 | 1.3E+00 | AE004392.1 | NT | Vibrio cholerae chromosome II, section 49 of 83 of the complete chromosome |
| 10130 | 22625 | 35615 | 2.41 | 1.3E+00 | M28953.1 | NT | Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds |
| 10476 | 22970 | | 0.85 | 1.3E+00 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 10504 | 22988 | | 0.52 | 1.3E+00 | 8923637 | NT | Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA |
| 10507 | 23001 | 36008 | 0.48 | 1.3E+00 | H42881.1 | EST_HUMAN | y088c03.s1 Soares breast 3NtH18t Homo sapiens cDNA clone IMAGE:183078 3' |
| 10507 | 23001 | 36009 | 0.48 | 1.3E+00 | H42881.1 | EST_HUMAN | y088c03.s1 Soares breast 3NtH18t Homo sapiens cDNA clone IMAGE:183078 3' |
| 10573 | 23108 | | 4.68 | 1.3E+00 | Q14117 | SWISSPROT | DIHYDROXYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP) |
| 10785 | 23309 | 36318 | 2.3 | 1.3E+00 | P25298 | SWISSPROT | MRNA 3'-END PROCESSING PROTEIN RNA15 |
| 10807 | 23330 | 36342 | 2.17 | 1.3E+00 | Z16892.2 | NT | Mus musculus desmin gene |
| 11216 | 23718 | | 1.87 | 1.3E+00 | AW274791.1 | EST_HUMAN | XP00603.x1 NCI CGAP_HJN9 Homo sapiens cDNA clone IMAGE:2739868 3' |
| 11414 | 23865 | 36928 | 3.09 | 1.3E+00 | D42042.1 | NT | Human mRNA for KIAA0085 gene, partial cds |
| 11488 | 23937 | 37007 | 3.09 | 1.3E+00 | Z98682.1 | NT | Bacillus subtilis genomic DNA 23.6kB fragment |
| 12011 | 24312 | | 3.63 | 1.3E+00 | AF187873.1 | NT | Caixa porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12182 | 24423 | 30949 | 3.47 | 1.3E+00 | BF348043.1 | EST_HUMAN | 602023185F1 NCJ CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4168462 5' |
| 12204 | 24828 | | 1.78 | 1.3E+00 | P33464 | SWISSPROT | E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN) |
| 12303 | 24500 | | 2.08 | 1.3E+00 | AF187035.1 | NT | Stamira lilium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product |
| 12673 | 24904 | | 1.25 | 1.3E+00 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 678 | 13302 | 25784 | 9.75 | 1.2E+00 | AA678246.1 | EST_HUMAN | 2122008.at Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3' |
| 858 | 13472 | 25883 | 1.04 | 1.2E+00 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 858 | 13472 | 25884 | 1.04 | 1.2E+00 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 858 | 13472 | 25885 | 1.04 | 1.2E+00 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 911 | 13524 | | 1.9 | 1.2E+00 | 8924234 | NT | Homo sapiens hypothetical protein PRO3077 (PRO3077). mRNA |
| 1203 | 13803 | 26316 | 4.87 | 1.2E+00 | AF080245.2 | NT | Eleis claffera sesquiterpene synthase mRNA, complete cds |
| 1247 | 13844 | 26361 | 1.3 | 1.2E+00 | AJ252242.1 | NT | pea seed-borne mosaic virus complete genome |
| 1247 | 13844 | 26362 | 1.3 | 1.2E+00 | AJ252242.1 | NT | pea seed-borne mosaic virus complete genome |
| 2054 | 14635 | 27308 | 53.59 | 1.2E+00 | AF140631.1 | NT | Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds |
| 2417 | 14985 | 27559 | 1.53 | 1.2E+00 | AF156486.1 | NT | Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds |
| 3144 | 16758 | 28224 | 1.16 | 1.2E+00 | AB020681.1 | NT | Homo sapiens mRNA for KIAA0874 protein, partial cds |
| 3201 | 15813 | 28287 | 7.17 | 1.2E+00 | AL161563.2 | NT | Homo sapiens thaliana DNA chromosome 4, contig fragment No. 63 |
| 3201 | 15813 | 28288 | 7.17 | 1.2E+00 | AL161563.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63 |
| 3325 | 15935 | | 3.43 | 1.2E+00 | P54910 | SWISSPROT | CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR |
| 3399 | 16007 | 28489 | 0.57 | 1.2E+00 | AF188740.1 | NT | Homo sapiens LHX3 gene, intron 2 |
| 3774 | 16374 | 28839 | 8.66 | 1.2E+00 | U75902.1 | NT | Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds |
| 4058 | 16855 | 29121 | 1.87 | 1.2E+00 | BF373570.1 | EST_HUMAN | MRO-F10175-050800-203-g09_1 FT0175 Homo sapiens cDNA |
| 4388 | 16907 | 28489 | 1.12 | 1.2E+00 | AF188740.1 | NT | Homo sapiens LHX3 gene, intron 2 |
| 4570 | 17153 | | 2.09 | 1.2E+00 | M87000.1 | NT | Rattus rattus cardiac AE3 gene, exons 1-23 |
| 4621 | 17204 | 28853 | 1.08 | 1.2E+00 | AL161509.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21 |
| 4659 | 17241 | 28895 | 1.5 | 1.2E+00 | AF158405.1 | NT | Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds |
| 4680 | 17272 | | 9.41 | 1.2E+00 | Y08200.1 | NT | T. pinnastrum chloroplast rbcL gene, partial |
| 4791 | 18008 | | 0.77 | 1.2E+00 | M81778.1 | NT | G. gallus T-cadherin mRNA, complete cds |
| 5628 | 18258 | 30728 | 1.08 | 1.2E+00 | U20760.1 | NT | Human extracellular calcium-sensing receptor mRNA, complete cds |
| 5743 | 18389 | 31077 | 2.27 | 1.2E+00 | AW813276.1 | EST_HUMAN | MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA |
| 6034 | 18653 | 31395 | 0.72 | 1.2E+00 | AF016052.1 | NT | Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds |
| 6300 | 18908 | 31679 | 2.17 | 1.2E+00 | X74885.1 | NT | D. hydei ey1 repeat cluster DNA, fragment D |
| 6361 | 18965 | 31743 | 3.98 | 1.2E+00 | BE003113.1 | EST_HUMAN | QV4-BN0090-270400-190-403 BN0090 Homo sapiens cDNA |
| 6433 | 19036 | 31822 | 1.43 | 1.2E+00 | X88084.1 | NT | C. glutamicum pta gene and ackA gene |
| 6433 | 19036 | 31823 | 1.43 | 1.2E+00 | X88084.1 | NT | C. glutamicum pta gene and ackA gene |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6475 | 18078 | 31859 | 34.98 | 1.2E+00 | AA756254.1 | EST_HUMAN | sh84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3' |
| 6828 | 18225 | 32030 | 2.26 | 1.2E+00 | AW813278.1 | EST_HUMAN | MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA |
| 6895 | 19493 | 32314 | 1.18 | 1.2E+00 | AB028010.1 | NT | Homo sapiens mRNA for KIAA1087 protein, partial cds |
| 7007 | 19505 | 32324 | 2.8 | 1.2E+00 | AJ002141.1 | NT | Mus musculus DSPP gene |
| 7300 | 19828 | | 0.8 | 1.2E+00 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 7417 | 24782 | 32808 | 1.59 | 1.2E+00 | AV734585.1 | EST_HUMAN | AV734585 cda Homo sapiens cDNA clone cdaAFH03 5' |
| 7849 | 20158 | 33045 | 2.84 | 1.2E+00 | X74207.1 | NT | L.lactis pyrD and pyrF genes |
| 8504 | 21043 | 33984 | 3.05 | 1.2E+00 | AB033030.1 | NT | Homo sapiens mRNA for KIAA1204 protein, partial cds |
| | | | | | | | ALPHA ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE) |
| 8597 | 21138 | 34051 | 0.69 | 1.2E+00 | P38427 | SWISSPROT | Homo sapiens CGI-30 protein (LOC51611), mRNA |
| 8809 | 21348 | | 0.53 | 1.2E+00 | 7708271 | NT | MR2-CT0222-201089-001-e07 CT0222 Homo sapiens cDNA |
| 8955 | 21493 | 34416 | 2.03 | 1.2E+00 | AW377210.1 | EST_HUMAN | IR communis gene for pyrophosphate-dependent phosphofructokinase beta subunit |
| 9319 | 21833 | 34783 | 2.92 | 1.2E+00 | Z32850.1 | NT | |
| 9523 | 22023 | 34981 | 1.96 | 1.2E+00 | D11745.1 | EST_HUMAN | HUMHMD1A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01 |
| 9844 | 22342 | 35324 | 3.47 | 1.2E+00 | X56832.1 | NT | H. sapiens ENO3 gene for muscle specific endase |
| 10229 | 22724 | | 0.67 | 1.2E+00 | AB008686.1 | NT | Homo sapiens kiofno gene, exon 1 |
| 11224 | 23755 | 36813 | 2.19 | 1.2E+00 | AW817817.1 | EST_HUMAN | PM0-ST0284-161189-001-d01 ST0284 Homo sapiens cDNA |
| 11262 | 23780 | | 6.64 | 1.2E+00 | BE160761.1 | EST_HUMAN | PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA |
| 11331 | 23029 | 36038 | 3.76 | 1.2E+00 | U50147.1 | NT | Rattus norvegicus synapse-associated protein 102 mRNA, complete cds |
| 11976 | 24907 | 30712 | 32.4 | 1.2E+00 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 11998 | 24304 | | 2.11 | 1.2E+00 | AP001515.1 | NT | Bacillus halodurans genomic DNA, section 8/14 |
| 489 | 13122 | 25608 | 1.19 | 1.1E+00 | D66980.1 | NT | Human mRNA for KIAA0227 gene, partial cds |
| 1786 | 14389 | 26934 | 1.48 | 1.1E+00 | AW695383.1 | EST_HUMAN | QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA |
| 2617 | 15179 | 27748 | 1.09 | 1.1E+00 | AF087124.1 | NT | Wheat yellow mosaic virus RNA1 270 kDa precursor protein gene, complete cds |
| 3373 | 15981 | 28458 | 9.32 | 1.1E+00 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 3373 | 15981 | 28459 | 9.32 | 1.1E+00 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 3533 | 16138 | 28620 | 0.84 | 1.1E+00 | | NT | Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA |
| | | | | | 8822641 | NT | wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW_P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ; |
| 3639 | 16242 | 28718 | 1.08 | 1.1E+00 | AB083880.1 | EST_HUMAN | Xyella fastidiosa, section 32 of 229 of the complete genome |
| 3781 | 16381 | 28845 | 1.41 | 1.1E+00 | AE003986.1 | NT | Xyella fastidiosa, section 32 of 229 of the complete genome |
| 3781 | 16381 | 28846 | 1.41 | 1.1E+00 | AE003986.1 | NT | Xyella fastidiosa, section 32 of 229 of the complete genome |
| 3889 | 16488 | | 0.61 | 1.1E+00 | X85374.1 | NT | H. parahaeemolyticus hphIM(A), hphIM(C), hphIR and menB genes |
| 4016 | 16814 | 29087 | 0.67 | 1.1E+00 | 8822641 | NT | Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4093 | 16988 | 29145 | 0.65 | 1.1E+00 | 6755205 | NT | Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA |
| 4295 | 16981 | | 7.81 | 1.1E+00 | 5835331 | NT | R. uniconis complete mitochondrial genome |
| 5131 | 17703 | 30137 | 3.54 | 1.1E+00 | U18488.1 | NT | African swine fever virus, complete genome |
| 5132 | 17704 | 30138 | 0.96 | 1.1E+00 | AJ271740.1 | NT | Drosophila melanogaster D-Titin gene, exons 1-37 |
| 5201 | 17768 | 30180 | 1 | 1.1E+00 | U34740.1 | NT | Emeticella nidulans starigmatocystin biosynthetic gene cluster: (stcA), (stcB), (stcC), (stcE), (stcF), (stcI), (stcJ), (stcK), (stcL), (stcO), (stcQ), (stcS), (stcT), (stcU), (stcV) and (stcW) genes, complete cds |
| 5230 | 17794 | 30213 | 0.96 | 1.1E+00 | X78425.1 | NT | E. faecalis pbp5 gene |
| 5409 | 17866 | | 1.04 | 1.1E+00 | AE003868.1 | NT | Xylella fastidiosa, section 15 of 229 of the complete genome |
| 5510 | 18143 | 30555 | 1.52 | 1.1E+00 | 6978530 | NT | Rattus norvegicus Aquaporin 4 (Aqp4), mRNA |
| 5798 | 18423 | 31139 | 18.98 | 1.1E+00 | BE980184.1 | EST_HUMAN | 601652778F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3' |
| 5815 | 18439 | 31161 | 3.23 | 1.1E+00 | A1138582.1 | EST_HUMAN | q85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738260 3' |
| 6242 | 18851 | 31821 | 1.25 | 1.1E+00 | 11419739 | NT | Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA |
| 6420 | 19023 | 31807 | 0.71 | 1.1E+00 | AF197881.1 | NT | Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product |
| 6539 | 19138 | 31931 | 0.71 | 1.1E+00 | R06037.1 | EST_HUMAN | ye89e03.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124824 5' |
| 6617 | 19408 | 32225 | 0.7 | 1.1E+00 | AJ404004.1 | NT | Mus musculus mRNA for ER protein 68 (EP68 gene) |
| 7338 | 19885 | 32729 | 0.78 | 1.1E+00 | X55081.1 | NT | Maize mRNA for endase (2-phospho-D-glycerate hydrolase) |
| 7501 | 20023 | 32898 | 2.08 | 1.1E+00 | Z72338.1 | NT | Herpes simplex virus type 1 (strain KOS) UL41 gene |
| 7501 | 20023 | 32887 | 2.08 | 1.1E+00 | Z72338.1 | NT | Herpes simplex virus type 1 (strain KOS) UL41 gene |
| 7521 | 20041 | 32810 | 9.72 | 1.1E+00 | AL161588.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84 |
| 7580 | 24787 | 32973 | 0.99 | 1.1E+00 | 11967860 | NT | Mus musculus silent mating type information regulation 2 (S.cerevisiae, homolog)-like (Sir2), mRNA |
| 8074 | 20616 | 33530 | 2.8 | 1.1E+00 | BF683896.1 | EST_HUMAN | 602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246828 5' |
| 8163 | 20704 | 33620 | 0.76 | 1.1E+00 | A1478339.1 | EST_HUMAN | tm39h1.x1 NCI_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2180549 3' |
| 8672 | 21211 | 34150 | 0.75 | 1.1E+00 | AB003088.1 | NT | Acetabularia caliculus mitochondrial COX-like gene |
| 8749 | 21288 | 34208 | 0.78 | 1.1E+00 | S90750.1 | NT | VH=anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt] |
| 8958 | 20297 | | 0.88 | 1.1E+00 | BE384678.1 | EST_HUMAN | 601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5' |
| 9546 | 22048 | 35007 | 0.68 | 1.1E+00 | AJ245772.1 | NT | Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene) |
| 9599 | 22099 | | 0.81 | 1.1E+00 | Y12227.1 | NT | Arabidopsis thaliana DNA, 24 kb surrounding PFL locus |
| 9687 | 22186 | 35160 | 0.84 | 1.1E+00 | L76301.1 | NT | Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9747 | 22245 | 35228 | 1.59 | 1.1E+00 | AB023151.1 | NT | Homo sapiens mRNA for KIAA0634 protein, partial cds |
| 9850 | 22348 | 35330 | 4.82 | 1.1E+00 | AL161515.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 9809 | 22408 | 35381 | 19.39 | 1.1E+00 | 8754021 | NT | Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA |
| 10395 | 22889 | 35983 | 1 | 1.1E+00 | P73789 | SWISSPROT | DNA MISMATCH REPAIR PROTEIN MUTS |
| 10530 | 23067 | 36079 | 2.93 | 1.1E+00 | 11067364 | NT | Homo sapiens KIAA0628 gene product (KIAA0628), mRNA |
| 10586 | 23121 | | 4.06 | 1.1E+00 | AF068942.1 | NT | Klebsiella pneumoniae cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 10878 | 18028 | | 5.28 | 1.1E+00 | 8922973 | NT | Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA |
| 10883 | 23497 | 36528 | 3.78 | 1.1E+00 | AF012882.1 | NT | Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds |
| 10983 | 23497 | 36527 | 3.78 | 1.1E+00 | AF012882.1 | NT | Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds |
| 11234 | 23765 | 36822 | 6.02 | 1.1E+00 | AI809698.1 | EST_HUMAN | w78611.x1 Source_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3' |
| 11946 | 24275 | | 1.82 | 1.1E+00 | P07860 | SWISSPROT | LOW TEMPERATURE ESSENTIAL PROTEIN |
| 12051 | 24335 | 30897 | 2.25 | 1.1E+00 | AF216898.1 | NT | Taenia solium immunogenic protein Ts76 mRNA, partial cds |
| 12184 | 24803 | | 1.64 | 1.1E+00 | AF234169.1 | NT | Dictyostelium discoideum isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds |
| 103 | 12779 | | 3.22 | 1.0E+00 | U23808.1 | NT | Xenopus laevis rhodopsin gene, complete cds |
| 118 | 12789 | 25271 | 3.48 | 1.0E+00 | D88425.1 | NT | Canis caryacus mRNA for serine/threonine kinase, complete cds |
| 443 | 13078 | | 2.14 | 1.0E+00 | AB021884.1 | NT | Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA |
| 602 | 13231 | 25704 | 1.53 | 1.0E+00 | AJ251860.1 | NT | Girardinia litorea mRNA for homeodomain transcription factor (so gene) |
| 705 | 13328 | 25813 | 7.12 | 1.0E+00 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 707 | 13328 | | 0.89 | 1.0E+00 | AF125884.1 | NT | Aedes aegypti much-like protein MUC1 mRNA, complete cds |
| 1429 | 15441 | | 1.73 | 1.0E+00 | X80416.1 | NT | V. carteri Algal-CAM mRNA |
| 1794 | 14394 | 26929 | 0.91 | 1.0E+00 | AB006531.1 | NT | Plasmodium falciparum virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds |
| 2528 | 15080 | 27682 | 1.2 | 1.0E+00 | P48355 | SWISSPROT | DNA GYRASE SUBUNIT B |
| 2528 | 15080 | 27683 | 1.2 | 1.0E+00 | P48355 | SWISSPROT | DNA GYRASE SUBUNIT B |
| 2800 | 15517 | 27886 | 4.47 | 1.0E+00 | P24008 | SWISSPROT | 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) |
| 2800 | 15517 | 27987 | 4.47 | 1.0E+00 | P24008 | SWISSPROT | 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) |
| 2884 | 15610 | | 0.83 | 1.0E+00 | O14226 | SWISSPROT | HYPOTHETICAL 67.9 KD PROTEIN CBF12.08C IN CHROMOSOME 1 |
| 3232 | 15844 | 28324 | 0.91 | 1.0E+00 | AA628453.1 | EST_HUMAN | af28608.s1 Source_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:CA2D8.3 CE04204 ;contains element MER22 MER22 repetitive element ; |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3659 | 12779 | | 0.78 | 1.0E+00 | U23808.1 | NT | Xenopus laevis rhodopsin gene, complete cds |
| 3744 | 16345 | 28813 | 1.55 | 1.0E+00 | AJ223818.1 | NT | Agaricus bisporus mRNA for tyrosinase |
| 4144 | 16736 | 28189 | 1.5 | 1.0E+00 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 4362 | 16949 | | 0.64 | 1.0E+00 | 8822245 | NT | Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA |
| 5165 | 17734 | | 17.2 | 1.0E+00 | D10852.1 | NT | Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds |
| 5339 | 17900 | | 0.6 | 1.0E+00 | AF200817.1 | NT | Pilot whale morbillivirus phosphoprotein (P) gene, partial cds |
| 5432 | 18010 | 30394 | 1 | 1.0E+00 | AB038022.1 | NT | Oncorhynchus mykiss sII1 mRNA for rhamnose binding lectin STL1, complete cds |
| 5486 | 18120 | 30527 | 2.56 | 1.0E+00 | Z97022.1 | NT | Hordeum vulgare gene encoding cysteine proteinase |
| 6013 | 18633 | 31368 | 4.54 | 1.0E+00 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 6013 | 18633 | 31369 | 4.54 | 1.0E+00 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 6111 | 18727 | 31480 | 1.22 | 1.0E+00 | Z97341.2 | NT | Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6 |
| 6263 | 18871 | 31641 | 4.41 | 1.0E+00 | P04501 | SWISSPROT | FIBER PROTEIN |
| 6269 | 18877 | 31645 | 1.56 | 1.0E+00 | AW452782.1 | EST_HUMAN | UHL-B13-alk-4-09-Q-U1.s1 NCI_CGAP Sub5 Homo sapiens cDNA clone IMAGE:3068969 3' |
| 6615 | 19212 | 32018 | 1.79 | 1.0E+00 | U75902.1 | NT | Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds |
| 6662 | 19258 | 32062 | 0.83 | 1.0E+00 | AF104669.1 | NT | Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5 |
| 6742 | 19336 | | 1.5 | 1.0E+00 | P46508 | SWISSPROT | SRB-11 PROTEIN |
| 6874 | 19608 | 32442 | 1.27 | 1.0E+00 | Y1204.1 | NT | V. carteri gene encoding volvoxpsin |
| 7192 | 19724 | 32573 | 1.22 | 1.0E+00 | S52770.1 | NT | Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt] |
| 7493 | 20016 | | 8.58 | 1.0E+00 | P20273 | SWISSPROT | B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) |
| 7697 | 20208 | 33093 | 1.36 | 1.0E+00 | AF192531.1 | NT | Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds |
| 7710 | 20219 | 33107 | 7.92 | 1.0E+00 | AA775191.1 | EST_HUMAN | ac79808.s1 Stratiotes lung (#837210) Homo sapiens cDNA clone IMAGE:868781 3' |
| 7902 | 20444 | 33349 | 1.49 | 1.0E+00 | BE688267.1 | EST_HUMAN | 601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5' |
| 7902 | 20444 | 33350 | 1.49 | 1.0E+00 | BE688267.1 | EST_HUMAN | 601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5' |
| 8094 | 17734 | | 1.28 | 1.0E+00 | D10852.1 | NT | Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds |
| 8291 | 20632 | 33763 | 2.1 | 1.0E+00 | Q02207 | SWISSPROT | PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE] |

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8291 | 20832 | 33754 | 2.1 | 1.0E+00 | Q02207 | SWISSPROT | PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE] |
| 8413 | 20853 | | 0.85 | 1.0E+00 | P51784 | SWISSPROT | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11) |
| 8447 | 20887 | 33902 | 0.48 | 1.0E+00 | Q9Y5T5 | SWISSPROT | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M) |
| 8447 | 20887 | 33903 | 0.48 | 1.0E+00 | Q9Y5T5 | SWISSPROT | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN-PROCESSING PROTEASE UBP-M) |
| 8475 | 24791 | | 2.17 | 1.0E+00 | BE147331.1 | EST_HUMAN | RC1-HT02228-18:1089-011-406 HT02229 Homo sapiens cDNA |
| 8513 | 21052 | 33974 | 1.06 | 1.0E+00 | U42720.2 | NT | Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, > |
| 8659 | 21198 | 34116 | 1.07 | 1.0E+00 | M39427.1 | NT | Human immunodeficiency virus type 1 (HIV-1), isolate SF33, |
| 9195 | 21712 | 34855 | 2.05 | 1.0E+00 | BE807592.1 | EST_HUMAN | 601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5' |
| 9402 | 21911 | 34860 | 1.34 | 1.0E+00 | 6753429 | NT | Mus musculus chloride channel calcium activated 1 (Clca1), mRNA |
| 9402 | 21911 | 34861 | 1.34 | 1.0E+00 | 6753429 | NT | Mus musculus chloride channel calcium activated 1 (Clca1), mRNA |
| 9428 | 22028 | 34987 | 2.06 | 1.0E+00 | AV088554.1 | EST_HUMAN | AV689564 GK Homo sapiens cDNA clone GKCCYA11 5' |
| 9534 | 22034 | 34993 | 1.33 | 1.0E+00 | U44952.1 | NT | Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds |
| 9634 | 22034 | 34994 | 1.33 | 1.0E+00 | U44952.1 | NT | Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds |
| 9767 | 22265 | 35248 | 0.5 | 1.0E+00 | X15468.1 | NT | Human Coronavirus gene for membrane protein |
| 9767 | 22265 | 35249 | 0.5 | 1.0E+00 | X15468.1 | NT | Human Coronavirus gene for membrane protein |
| 10021 | 22516 | 35510 | 0.62 | 1.0E+00 | 5174562 | NT | Homo sapiens MHC binding factor, beta (MHC8FB) mRNA |
| 10021 | 22516 | 35511 | 0.62 | 1.0E+00 | 5174562 | NT | Homo sapiens MHC binding factor, beta (MHC8FB) mRNA |
| 10105 | 22800 | 35592 | 0.75 | 1.0E+00 | A1077920.1 | EST_HUMAN | 015407.s1 Soares_senescent_fibroblasts_NHHSF Homo sapiens cDNA clone IMAGE:1665901 3' |
| 10230 | 22725 | 35716 | 4.17 | 1.0E+00 | AV758825.1 | EST_HUMAN | AV758825 BM Homo sapiens cDNA clone BMFAW C04 5' |
| 10372 | 22868 | 35959 | 18.78 | 1.0E+00 | AA004982.1 | EST_HUMAN | zh84a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5' |
| 10372 | 22868 | 35960 | 18.78 | 1.0E+00 | AA004982.1 | EST_HUMAN | zh84a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5' |
| 10404 | 22898 | 35993 | 0.93 | 1.0E+00 | L11910.1 | NT | Human retinoblastoma susceptibility gene exons 1-27, complete cds |
| 10563 | 23374 | 36393 | 1.87 | 1.0E+00 | S90825.1 | NT | PBR1=proline-rich protein (intron 3) [human, Genomic, 898 nt] |
| 11587 | 18120 | 30527 | 1.57 | 1.0E+00 | Z97022.1 | NT | Hordeum vulgare gene encoding cysteine proteinase |
| 11837 | 24201 | | 4.85 | 1.0E+00 | P15306 | SWISSPROT | THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12171 | 24410 | | 3.08 | 1.0E+00 | AW978184.1 | EST_HUMAN | EST388283 IMAGE resequences, MAGN Homo sapiens cDNA |
| 1618 | 14209 | 26742 | 0.97 | 9.8E-01 | AF245455.1 | NT | Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds |
| 1618 | 14209 | 26743 | 0.97 | 9.8E-01 | AF245455.1 | NT | Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds |
| 2684 | 15222 | 27784 | 1.17 | 9.8E-01 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 3665 | 16267 | | 0.94 | 9.8E-01 | AF174585.1 | NT | Apple mosaic virus RNA 2 putative polymerase gene, complete cds |
| 5816 | 18440 | 31162 | 14.59 | 9.8E-01 | P49857 | SWISSPROT | SERINE/THREONINE PROTEIN KINASE MINIBRAIN |
| 6029 | 18648 | 31389 | 0.83 | 9.8E-01 | Q09632 | SWISSPROT | PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II |
| 9185 | 21702 | | 1.39 | 9.8E-01 | U66667.1 | NT | Lycopodium obscurum putative Mit1 copy 1 nematode-resistance gene |
| 9474 | 21873 | | 2.61 | 9.8E-01 | Q28642 | SWISSPROT | B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR) |
| 10583 | 23128 | 36142 | 1.68 | 9.8E-01 | AJ005029.1 | NT | Danio rerio mRNA for Epi-like receptor tyrosine kinase rtk8 |
| 549 | 13160 | 25658 | 1.77 | 9.8E-01 | P22567 | SWISSPROT | AMINO-ACID ACETYLTRANSFERASE (N-ACETYL-GLUTAMATE SYNTHASE) (AGS) (NAGS) |
| 2338 | 14907 | | 0.89 | 9.8E-01 | AJ003108.1 | NT | Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome |
| 2827 | 15379 | | 2.05 | 9.8E-01 | AF174844.1 | NT | Xenopus laevis rac GTPase mRNA, complete cds |
| 3869 | 18467 | 28630 | 0.95 | 9.8E-01 | O67551 | SWISSPROT | PROBABLE ENDONUCLEASE IV (ENDONUCLEONUCLEASE IV) |
| 3872 | 18470 | 28633 | 0.61 | 9.8E-01 | BE967439.2 | EST_HUMAN | 601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3638461 3' |
| 3872 | 18470 | 28634 | 0.61 | 9.8E-01 | BE967439.2 | EST_HUMAN | 601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3638461 3' |
| 7250 | 19779 | 32634 | 4.86 | 9.8E-01 | AJ302158.1 | NT | Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983 |
| 7250 | 19779 | 32635 | 4.86 | 9.8E-01 | AJ302158.1 | NT | Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983 |
| 7641 | 20153 | 33038 | 1.13 | 9.8E-01 | BF034016.1 | EST_HUMAN | 601456337F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3860049 5' |
| 7641 | 20153 | 33039 | 1.13 | 9.8E-01 | BF034016.1 | EST_HUMAN | 601456337F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3860049 5' |
| 8653 | 21192 | 34110 | 0.77 | 9.8E-01 | P38652 | SWISSPROT | PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM) |
| 10334 | 22828 | | 0.56 | 9.8E-01 | AA825565.1 | EST_HUMAN | cd55d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3' |
| 10874 | 23395 | 36410 | 4.86 | 9.8E-01 | BE258705.1 | EST_HUMAN | 601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5' |
| 10874 | 23395 | 36411 | 4.86 | 9.8E-01 | BE258705.1 | EST_HUMAN | 601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5' |
| 11587 | 24040 | 37108 | 1.78 | 9.8E-01 | AI680876.1 | EST_HUMAN | b42610.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2272242 3' |
| 12058 | 24341 | | 1.39 | 9.8E-01 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT1), CDM protein (CDM), adrenoleukodystrophy protein > |
| 7212 | 19743 | 32597 | 2.51 | 9.7E-01 | U26716.1 | NT | Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds |
| 8440 | 20980 | 33895 | 1.7 | 9.7E-01 | AF149112.1 | NT | Triticum aestivum shiwa rusi resistance protein Yr10 (Yr10) gene, complete cds |
| 8446 | 20986 | 33901 | 1.28 | 9.7E-01 | AB0544.1 | NT | Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res) |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11048 | 23562 | | 5.23 | 9.7E-01 | BF511208.1 | EST_HUMAN | UI-H-B14-act-e-07-Q-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3' |
| 12638 | 24728 | | 2.82 | 9.7E-01 | AL114281.1 | NT | Borhylls chinensis strain T4 cDNA library under conditions of nitrogen deprivation |
| 4531 | 17115 | 29559 | 0.58 | 9.6E-01 | AF197825.1 | NT | Bromus inermis putative cytosolic phosphoglucosyltransferase (pgm1) mRNA, complete cds |
| 4531 | 17115 | 29560 | 0.58 | 9.6E-01 | AF197825.1 | NT | Bromus inermis putative cytosolic phosphoglucosyltransferase (pgm1) mRNA, complete cds |
| 4557 | 17140 | 29588 | 1.71 | 9.6E-01 | AW788674.1 | EST_HUMAN | PM2-UM0053-240300-005-112 UM0053 Homo sapiens cDNA |
| 5928 | 18550 | 31278 | 3.9 | 9.6E-01 | Z70558.1 | NT | Parvovirus B19 DNA, patient C, genome position 2448-2804 |
| 5928 | 18550 | 31277 | 3.9 | 9.6E-01 | Z70558.1 | NT | Parvovirus B19 DNA, patient C, genome position 2448-2804 |
| 8331 | 20872 | | 1.23 | 9.6E-01 | X95275.1 | NT | P. falciparum complete gene map of plastid-like DNA (IR-A) |
| 8785 | 21324 | 34248 | 0.47 | 9.6E-01 | L81138.1 | NT | Rattus norvegicus (strain R21) Rps27 gene, complete cds |
| 9020 | 21557 | 34485 | 0.62 | 9.6E-01 | AF228843.1 | NT | Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene |
| 10668 | 23481 | 38507 | 1.81 | 9.6E-01 | AF041427.1 | NT | Homo sapiens ribosomal protein s4 Y isoform gene, complete cds |
| 11395 | 23847 | 38812 | 5.18 | 9.6E-01 | AV752805.1 | EST_HUMAN | AV752805 NPD Homo sapiens cDNA clone NPD8AG06 5' |
| 11395 | 23847 | 38813 | 5.18 | 9.6E-01 | AV752805.1 | EST_HUMAN | AV752805 NPD Homo sapiens cDNA clone NPD8AG06 5' |
| 11733 | 24138 | | 2.36 | 9.6E-01 | 11421722 | NT | Homo sapiens centrosomal protein 2 (CEP2), mRNA |
| 12388 | 24983 | 30609 | 2.8 | 9.6E-01 | U91423.1 | NT | Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 2515 | 15079 | 27851 | 1.02 | 9.5E-01 | 7705591 | NT | Homo sapiens CGI-125 protein (LOC31003), mRNA |
| 2891 | 15248 | 27817 | 1.2 | 9.5E-01 | Q02834 | SWISSPROT | ENDOGLUCANASE I PRECURSOR (EGI) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE I) |
| 3850 | 16448 | 28809 | 1.89 | 9.5E-01 | BE902340.1 | EST_HUMAN | 601675638F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5' |
| 3850 | 16448 | 28910 | 1.89 | 9.5E-01 | BE902340.1 | EST_HUMAN | 601675638F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5' |
| 8831 | 21469 | 34387 | 0.83 | 9.5E-01 | AH90162.1 | EST_HUMAN | qd57d07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3' |
| 9034 | 21571 | 34500 | 1.07 | 9.5E-01 | AW861102.1 | EST_HUMAN | RC1-CT0285-241199-011-b02 CT0285 Homo sapiens cDNA |
| 11123 | 23631 | 38874 | 1.71 | 9.5E-01 | BF218771.1 | EST_HUMAN | 601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5' |
| 11326 | 23024 | 38033 | 1.69 | 9.5E-01 | AW263789.1 | EST_HUMAN | UI-H-B12-act-f-03-Q-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3' |
| 3235 | 15947 | | 1.8 | 9.4E-01 | AF165990.1 | NT | Bartonella claridgeiae RNA polymerase beta subunit (pob) gene, partial cds |
| 3254 | 15888 | | 2.47 | 9.4E-01 | AF080585.1 | NT | Pimpla brachycarpa zinc finger protein (ZFP1) mRNA, complete cds |
| 8789 | 21338 | 34265 | 0.88 | 9.4E-01 | M90724.1 | NT | Human Fe-gamma-receptor (FCGR2A) gene, exon 4 |
| 1789 | 14358 | | 0.85 | 9.3E-01 | AF242382.1 | NT | Homo sapiens phytyl-CoA hydroxylase (PHYH) gene, exon 5 |
| 2682 | 15220 | 27782 | 1.09 | 9.3E-01 | BE071172.1 | EST_HUMAN | RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA |
| 4107 | 16701 | 29154 | 0.92 | 9.3E-01 | M20219.1 | NT | Bovine papillomavirus type 2, complete genome |
| 4107 | 16701 | 29155 | 0.92 | 9.3E-01 | M20219.1 | NT | Bovine papillomavirus type 2, complete genome |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5778 | 18403 | 31119 | 1.41 | 9.3E-01 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 5858 | 18481 | 31204 | 3.69 | 9.3E-01 | L36189.1 | NT | Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds |
| 8011 | 20553 | 33456 | 1.62 | 9.3E-01 | AA847040.1 | EST_HUMAN | oe08b03.s1 NC1 CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1365357 |
| 8748 | 21267 | | 1.13 | 9.3E-01 | AF081981.1 | NT | Xenopus laevis CCCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds |
| 8867 | 21406 | 34330 | 1.01 | 9.3E-01 | AL161634.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34 |
| 12508 | 24628 | 30893 | 1.87 | 9.3E-01 | 1140288 | NT | Homo sapiens Insitol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA |
| 12515 | 24634 | | 2 | 9.3E-01 | AF271207.1 | NT | Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds |
| 3278 | 15867 | 28369 | 3.99 | 9.2E-01 | BE622702.1 | EST_HUMAN | 601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3816184 3' |
| 5004 | 17577 | | 0.62 | 9.2E-01 | BF128973.1 | EST_HUMAN | 601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5' |
| 5894 | 18516 | | 1.41 | 9.2E-01 | 7106410 | NT | Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA |
| 6140 | 18764 | 31512 | 4.4 | 9.2E-01 | BF037588.1 | EST_HUMAN | 601461153F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3884061 5' |
| 9578 | 22078 | 35042 | 1.31 | 9.2E-01 | AL161565.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65 |
| 9683 | 22162 | 35135 | 1.15 | 9.2E-01 | 6671677 | NT | Mus musculus carbonic anhydrase 4 (Car4), mRNA |
| 10168 | 22661 | 35656 | 3.47 | 9.2E-01 | 11430863 | NT | Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA |
| 10314 | 22808 | 35900 | 1.99 | 9.2E-01 | BF583251.1 | EST_HUMAN | 7c58e08.x1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW-NU5M_TRYBB |
| 10526 | 23063 | 36074 | 1.75 | 9.2E-01 | BE503811.1 | EST_HUMAN | P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5: |
| 11568 | 24016 | 37085 | 2.27 | 9.2E-01 | BF132402.1 | EST_HUMAN | 601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5' |
| | | | | | | | 601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5' |
| 1668 | 14259 | 28783 | 4.89 | 9.1E-01 | T86875.1 | EST_HUMAN | yeS2101.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains |
| 2169 | 14746 | | 2.38 | 9.1E-01 | 8923056 | NT | Alu repetitive element |
| | | | | | | | Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA |
| 3239 | 15851 | 28331 | 0.93 | 9.1E-01 | T28418.1 | EST_HUMAN | AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5' |
| 3239 | 15851 | 28332 | 0.93 | 9.1E-01 | T28418.1 | EST_HUMAN | AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5' |
| 6315 | 18922 | 31699 | 1.42 | 9.1E-01 | L36033.1 | NT | Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds |
| 6630 | 19226 | 32031 | 2.82 | 9.1E-01 | G61704 | SWISSPROT | INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3) |
| 7577 | 20093 | 32970 | 15.96 | 9.1E-01 | AA806623.1 | EST_HUMAN | db71g08.s1 NC1 CGAP_G081 Homo sapiens cDNA clone IMAGE:1336862 3' |
| 7718 | 20227 | 33115 | 3.12 | 9.1E-01 | U72895.1 | NT | Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds |
| 12093 | 24978 | | 33.14 | 9.1E-01 | AF050113.1 | NT | Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds |
| 3241 | 15853 | 28335 | 0.81 | 9.0E-01 | 7681625 | NT | Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA |
| 3401 | 18010 | | 0.64 | 9.0E-01 | AL161515.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 4498 | 17054 | 28498 | 1.44 | 9.0E-01 | AF089810.1 | NT | Homo sapiens neuron III-alpha gene, partial cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7424 | 19048 | 32814 | 0.78 | 9.0E-01 | L42547.1 | NT | Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds |
| 7460 | 19074 | | 1.84 | 9.0E-01 | D38621.1 | NT | Xenopus laevis gene for aldolase, complete cds |
| 9271 | 21797 | 34748 | 0.54 | 9.0E-01 | AF089781.1 | NT | Danio rerio semaphorin Z1a mRNA, complete cds |
| 9744 | 22242 | 35223 | 0.47 | 9.0E-01 | U39702.1 | NT | Mycoplasma genitalium section 24 of 51 of the complete genome |
| | | | | | | | Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitotic-specific chromosome segregation protein SMC1 IV/ncog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit> |
| 5875 | 18497 | 31222 | 2.49 | 8.9E-01 | AF026188.1 | NT | Rabbit MHC fragment RLA-OF DNA |
| 6308 | 18989 | | 1.27 | 8.9E-01 | X60988.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 8152 | 20693 | | 0.47 | 8.9E-01 | AF260225.1 | NT | Oithona nana cytochrome-c oxidase subunit I (cod) gene, partial cds; mitochondrial gene for mitochondrial product |
| 8385 | 20905 | 33824 | 1.04 | 8.9E-01 | AF258687.1 | NT | Xyella fastidiosa, section 90 of 229 of the complete genome |
| 11618 | 24058 | 37122 | 2.59 | 8.9E-01 | AE003944.1 | NT | Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome |
| 11827 | 24262 | | 5.33 | 8.9E-01 | AE002186.2 | NT | PUTATIVE F420-DEPENDENT NADP REDUCTASE |
| 4840 | 17222 | 29678 | 2.1 | 8.8E-01 | O26350 | SWISSPROT | PUTATIVE F420-DEPENDENT NADP REDUCTASE |
| 5578 | 18207 | 30658 | 0.7 | 8.8E-01 | AF310617.1 | NT | Pseudorabies virus Ea glycoprotein M gene, complete cds |
| 10960 | 23475 | 36500 | 3.82 | 8.8E-01 | Z28337.1 | NT | M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1 |
| 11749 | 25087 | | 2.27 | 8.8E-01 | D80911.1 | NT | Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1710643 |
| 480 | 13123 | 25609 | 1.48 | 8.7E-01 | AF108953.2 | NT | Homo sapiens SOS1 (SOS1) gene, partial cds |
| 2448 | 15013 | 27585 | 1.13 | 8.7E-01 | 5901893 | NT | Homo sapiens AT-binding transcription factor 1 (ATBF-1), mRNA |
| 2898 | 15515 | 27884 | 5.67 | 8.7E-01 | AA595883.1 | EST_HUMAN | nr03f11.s1 NCJ CGAP Py4.1 Homo sapiens cDNA clone IMAGE:1076877 |
| 4845 | 17423 | 29875 | 0.61 | 8.7E-01 | AF158539.1 | NT | Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9 |
| 4845 | 17423 | 29876 | 0.61 | 8.7E-01 | AF158539.1 | NT | Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9 |
| | | | | | | | Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzonate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzonate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put- |
| 5151 | 17721 | | 3.08 | 8.7E-01 | AF121870.1 | NT | RCAN0057-120500-013-007 NN0057 Homo sapiens cDNA |
| 7883 | 20525 | 33431 | 0.66 | 8.7E-01 | AW897335.1 | EST_HUMAN | ch38a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3' |
| 8860 | 21399 | 34322 | 0.75 | 8.7E-01 | AI239458.1 | EST_HUMAN | ch38a06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3' |
| 8860 | 21399 | 34323 | 0.75 | 8.7E-01 | AI239458.1 | EST_HUMAN | Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome |
| 9853 | 22152 | 35122 | 1.7 | 8.7E-01 | AE004983.1 | NT | 802185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308908 3' |
| 10205 | 22700 | 35983 | 0.56 | 8.7E-01 | BF570169.1 | EST_HUMAN | 802185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308908 3' |
| 10205 | 22700 | 35984 | 0.56 | 8.7E-01 | BF570169.1 | EST_HUMAN | QV0-NN1021-100800-337-003 NN1021 Homo sapiens cDNA |
| 10711 | 23239 | 36254 | 5.79 | 8.7E-01 | BF3683970.1 | EST_HUMAN | 801823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3' |
| 11582 | 24028 | 37097 | 4.31 | 8.7E-01 | BF107694.1 | EST_HUMAN | 801823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3' |
| 11582 | 24028 | 37098 | 4.31 | 8.7E-01 | BF107694.1 | EST_HUMAN | 801823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12146 | 24861 | | 4.44 | 8.7E-01 | AV681898.1 | EST_HUMAN | AV681898 GLC Homo sapiens cDNA clone GLCGYG07 3' |
| 500 | 13132 | | 1.65 | 8.6E-01 | X17012.1 | NT | Rat IGFI gene for insulin-like growth factor II |
| 891 | 13505 | 26024 | 8.72 | 8.6E-01 | W68089.1 | EST_HUMAN | z44403.r1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:343518 5' |
| 2310 | 14882 | 27457 | 1.06 | 8.6E-01 | 4503210 | NT | Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA |
| 3681 | 16282 | 28750 | 0.78 | 8.6E-01 | AL161565.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65 |
| 3670 | 16468 | 28631 | 1.38 | 8.6E-01 | U49724.1 | NT | Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds |
| 6057 | 18674 | 31415 | 9.08 | 8.6E-01 | X60547.1 | NT | Chicken lipoprotein lipase gene |
| 6057 | 18674 | 31416 | 9.08 | 8.6E-01 | X60547.1 | NT | Chicken lipoprotein lipase gene |
| 6810 | 19401 | 32216 | 1.88 | 8.6E-01 | AF143732.1 | NT | Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds |
| 6810 | 19401 | 32217 | 1.88 | 8.6E-01 | AF143732.1 | NT | Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds |
| 7868 | 20410 | | 1.33 | 8.6E-01 | AP001518.1 | NT | Bacillus halodurans genomic DNA, section 12/14 |
| 7986 | 20528 | 33434 | 0.54 | 8.6E-01 | AF077837.1 | NT | Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds |
| 9603 | 22103 | | 0.48 | 8.6E-01 | AE000979.1 | NT | Archaeoglobus fulgidus section 128 of 172 of the complete genome |
| 12338 | 24812 | | 1.73 | 8.6E-01 | AL112162.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 6826 | 19416 | 32232 | 1.32 | 8.5E-01 | AF165214.1 | NT | Bacteriophage D3, complete genome |
| 7933 | 20053 | 32928 | 2.38 | 8.5E-01 | BE542812.1 | EST_HUMAN | 601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5' |
| 7932 | 20474 | 33383 | 0.51 | 8.5E-01 | AL161572.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68 |
| 8357 | 20897 | 33817 | 0.84 | 8.5E-01 | P06601 | SWISSPROT | SEGMENTATION PROTEIN PAIRED |
| 8357 | 20897 | 33818 | 0.84 | 8.5E-01 | P06601 | SWISSPROT | SEGMENTATION PROTEIN PAIRED |
| 8441 | 20961 | 33806 | 0.51 | 8.5E-01 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 10252 | 22747 | 35734 | 1.38 | 8.5E-01 | AB006798.1 | NT | Cyanidium caldarium gene for SigC, complete cds |
| 10252 | 22747 | 35735 | 1.38 | 8.5E-01 | AB006798.1 | NT | Cyanidium caldarium gene for SigC, complete cds |
| 12077 | 24978 | | 3.12 | 8.5E-01 | 11418543 | NT | Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA |
| 12084 | 24355 | | 7.82 | 8.5E-01 | 9507008 | NT | Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA |
| 4862 | 17440 | 29880 | 0.82 | 8.4E-01 | AF063975.2 | NT | Fowl adenovirus 8, complete genome |
| 5885 | 24747 | 30907 | 3.15 | 8.4E-01 | L78726.1 | NT | Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7 |
| 5885 | 24747 | 30908 | 3.15 | 8.4E-01 | L78726.1 | NT | Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7 |
| 9868 | 22365 | | 2.68 | 8.4E-01 | AJ248287.1 | NT | Pyrococcus abyssi complete genome; segment 5/6 |
| 771 | 13390 | 25889 | 2.48 | 8.3E-01 | M63437.1 | NT | Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds |
| 3129 | 15743 | 28212 | 3.26 | 8.3E-01 | AL161506.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18 |
| 3883 | 16481 | 28943 | 0.68 | 8.3E-01 | AB010879.1 | NT | Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds |
| 4084 | 18680 | 29140 | 3.24 | 8.3E-01 | Y19177.1 | NT | Streptomyces antibioticus polyketide biosynthetic gene cluster |
| 5473 | 16107 | 30426 | 2.15 | 8.3E-01 | AL161540.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40 |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9587 | 22087 | | 3.14 | 8.3E-01 | A1791852.1 | EST_HUMAN | nr011212.6 NCI_CGAP_Ccd Homo sapiens cDNA clone IMAGE:1076485 5' similar to contains THR.H1 THR repetitive element: |
| 10019 | 22514 | 35507 | 1.11 | 8.3E-01 | AF098070.1 | NT | Drosophila melanogaster Ls1 homolog mRNA, complete cds |
| 10119 | 22814 | 35604 | 3.5 | 8.3E-01 | AF108133.1 | NT | Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds |
| 10553 | 23089 | 36103 | 2.82 | 8.3E-01 | AE000903.1 | NT | Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome |
| 10571 | 23106 | | 2.52 | 8.3E-01 | 7212472 | NT | Phytophthora infestans mitochondrion, complete genome |
| 11183 | 23688 | 36735 | 2.45 | 8.3E-01 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphatase hydrolase (FHT) gene, exon 5 |
| 2098 | 14875 | 27244 | 3.23 | 8.2E-01 | AB000489.1 | NT | Rattus norvegicus mRNA for RPHO-1, complete cds |
| 2137 | 14715 | | 1.45 | 8.2E-01 | AF145589.1 | NT | Mus musculus trophinin (Tnn) gene, complete cds |
| 3089 | 16567 | 29036 | 1.12 | 8.2E-01 | AB014574.1 | NT | Homo sapiens mRNA for KIAA0674 protein, partial cds |
| 4209 | 16798 | 29246 | 0.61 | 8.2E-01 | Z72594.1 | NT | S. cerevisiae chromosome VII reading frame ORF YGLD82w |
| 4209 | 16798 | 29247 | 0.61 | 8.2E-01 | Z72594.1 | NT | S. cerevisiae chromosome VII reading frame ORF YGLD82w |
| 5270 | 17832 | 30758 | 1.08 | 8.2E-01 | AB000489.1 | NT | Rattus norvegicus mRNA for RPHO-1, complete cds |
| 5420 | 17977 | 30385 | 2.11 | 8.2E-01 | AB028957.1 | NT | Homo sapiens mRNA for KIAA1034 protein, partial cds |
| 6871 | 18605 | 32439 | 0.8 | 8.2E-01 | AJ010142.1 | NT | Acanthamoeba muscaria mRNA for SCIII25 protein |
| 6878 | 18554 | 32379 | 3.18 | 8.2E-01 | AW379433.1 | EST_HUMAN | CMA-HT0243-081189-037-401 HT0243 Homo sapiens cDNA |
| 7313 | 24779 | 32700 | 4.21 | 8.2E-01 | Z12128.1 | NT | S. cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial) |
| 9838 | 22433 | 35409 | 0.63 | 8.2E-01 | AB014530.1 | NT | Homo sapiens mRNA for KIAA0630 protein, partial cds |
| 9871 | 22468 | 35450 | 1.67 | 8.2E-01 | AF052659.1 | NT | Homo sapiens thiodoxin-related protein mRNA, complete cds |
| 10123 | 22818 | 35609 | 0.59 | 8.2E-01 | AF223988.1 | NT | Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1 |
| 10123 | 22818 | 35610 | 0.59 | 8.2E-01 | AF223988.1 | NT | Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1 |
| 10286 | 22781 | 35772 | 3.52 | 8.2E-01 | Q8J170 | SWISSPROT | MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN |
| 10286 | 22781 | 35773 | 3.52 | 8.2E-01 | Q8J170 | SWISSPROT | MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN |
| 11488 | 23947 | 37017 | 3.33 | 8.2E-01 | L10127.1 | NT | Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA |
| 11578 | 24022 | 37091 | 8.05 | 8.2E-01 | P10383 | SWISSPROT | OVARIAN TUMOR LOCUS PROTEIN |
| 11583 | 24029 | 37099 | 5.68 | 8.2E-01 | H87398.1 | EST_HUMAN | yr1402.1 Scores: placenta_BioWeeks_2N6HP869W Homo sapiens cDNA clone IMAGE:252185 5' similar to gb:M96072.6S RIBOSOMAL PROTEIN L7A (HUMAN); |
| 12102 | 24364 | 30870 | 1.86 | 8.2E-01 | AJ001261.1 | NT | Mus musculus mRNA for NIPSNAP2 protein |
| 2787 | 15340 | | 1.78 | 8.1E-01 | AF191839.1 | NT | Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds |
| 3504 | 16109 | 28585 | 2.99 | 8.1E-01 | AF055068.1 | NT | Homo sapiens MHC class 1 region |
| 3504 | 16109 | 28588 | 2.99 | 8.1E-01 | AF055068.1 | NT | Homo sapiens MHC class 1 region |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 5048 | 17619 | | 0.68 | 8.1E-01 | AF202834.1 | NT | Drosophila melanogaster Na/K-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds |
| 6457 | 19058 | 31843 | 0.88 | 8.1E-01 | U16780.1 | NT | Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds |
| 6735 | 19328 | 32134 | 2.54 | 8.1E-01 | Q13491 | SWISSPROT | NEURONAL MEMBRANE GLYCOPROTEIN M8-B |
| 6735 | 19328 | 32135 | 2.54 | 8.1E-01 | Q13491 | SWISSPROT | NEURONAL MEMBRANE GLYCOPROTEIN M8-B |
| | | | | | | | Drosophila melanogaster putative inorganic phosphatase cotransporter (Plocat) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds |
| 7852 | 20394 | 33298 | 0.84 | 8.1E-01 | AF022713.2 | NT | Drosophila melanogaster putative inorganic phosphatase cotransporter (Plocat) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds |
| 7852 | 20394 | 33299 | 0.84 | 8.1E-01 | AF022713.2 | NT | Drosophila melanogaster putative inorganic phosphatase cotransporter (Plocat) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds |
| 8545 | 21084 | 34006 | 0.92 | 8.1E-01 | AP001517.1 | NT | Bacillus halodurans genomic DNA, section 11/14 |
| 8545 | 21084 | 34007 | 0.92 | 8.1E-01 | AP001517.1 | NT | Bacillus halodurans genomic DNA, section 11/14 |
| | | | | | | | XP01M03.X1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2882469 3' similar to SW1.YAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN; contains MER22.b1 PTR5 repetitive element |
| 8705 | 21244 | 34167 | 1.08 | 8.1E-01 | AW242847.1 | EST_HUMAN | PROBABLE E4 PROTEIN |
| 10032 | 22527 | 35522 | 0.54 | 8.1E-01 | P08425 | SWISSPROT | RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA |
| 11356 | 23810 | 36869 | 2.87 | 8.1E-01 | BE938558.1 | EST_HUMAN | RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA |
| 11356 | 23810 | 36870 | 2.97 | 8.1E-01 | BE938558.1 | EST_HUMAN | RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA |
| 11811 | 24183 | 31031 | 3.32 | 8.1E-01 | AE001711.1 | NT | Thermotoga maritima section 23 of 138 of the complete genome |
| 188 | 12849 | | 4.98 | 8.0E-01 | AJ271510.1 | NT | Staphylococcus aureus partial pla gene for phosphatase acetyltransferase allele 15 |
| 310 | 12965 | 25453 | 7.95 | 8.0E-01 | AJ132772.1 | NT | Bos taurus tubb and rtf genes |
| 2080 | 14661 | | 1.47 | 8.0E-01 | BF530982.1 | EST_HUMAN | 602072473F1 NC1_CGAP_Erm87 Homo sapiens cDNA clone IMAGE:4215091 5' |
| 3113 | 15728 | 28199 | 1.24 | 8.0E-01 | AF127897.1 | NT | Salimiri boliviensis olfactory receptor (SBO27) gene, partial cds |
| 3354 | 15982 | 28439 | 1.13 | 8.0E-01 | AB006193.1 | NT | Mus musculus gene for olfactory glycoprotein, complete cds |
| 3766 | 16366 | | 1.05 | 8.0E-01 | AL102759.2 | NT | Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7 |
| 4630 | 17213 | 28804 | 5.65 | 8.0E-01 | X83739.2 | NT | G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit |
| 5117 | 17689 | 30127 | 1.09 | 8.0E-01 | 7657352 | NT | Mus musculus myosin D5 (MyoD5), mRNA |
| 7831 | 20473 | | 2.32 | 8.0E-01 | AW901488.1 | EST_HUMAN | RCO-NN1012-270300-021-H08 NN1012 Homo sapiens cDNA |
| 8462 | 21002 | 33919 | 1.17 | 8.0E-01 | Y11095.1 | NT | Rice stripe virus RNA 3 |
| 479 | 13112 | 25602 | 1.37 | 7.9E-01 | D11476.1 | NT | Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds |
| 744 | 13384 | | 1.05 | 7.9E-01 | AE002130.1 | NT | Ureaplasma urealyticum section 31 of 59 of the complete genome |
| 1648 | 14240 | | 28.9 | 7.9E-01 | AB040885.1 | NT | Homo sapiens mRNA for KIAA1462 protein, partial cds |
| 1695 | 14288 | | 1.11 | 7.9E-01 | U32739.1 | NT | Haemophilus influenzae Rd section 54 of 163 of the complete genome |
| 2303 | 14876 | 27452 | 8.76 | 7.9E-01 | AB004816.1 | NT | Oryctolagus cuniculus mRNA for mitsugumin29, complete cds |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2304 | 14877 | 27453 | 5.48 | 7.8E-01 | AF130459.1 | NT | Danio rerio Trp4-associated protein 1 (tap1A) mRNA, complete cds |
| 3567 | 16171 | 28653 | 2.33 | 7.9E-01 | AF228684.1 | NT | Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds |
| 4389 | 18975 | | 0.76 | 7.9E-01 | BE263612.1 | EST_HUMAN | 601182033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5' |
| 4717 | 17268 | 26743 | 1.04 | 7.9E-01 | 6753745 | NT | Mus musculus embigin (Emb), mRNA |
| 4717 | 17268 | 26744 | 1.04 | 7.9E-01 | 6753745 | NT | Mus musculus embigin (Emb), mRNA |
| 5315 | 17877 | | 5.8 | 7.9E-01 | M28930.1 | NT | Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17 |
| 6485 | 19088 | 31888 | 0.69 | 7.9E-01 | D38145.1 | NT | Human mRNA for prostacyclin synthase, complete cds |
| 8053 | 20595 | 33502 | 2.62 | 7.9E-01 | X90968.1 | NT | P. sativum GR gene |
| 9468 | 21891 | 34948 | 4.57 | 7.9E-01 | U01912.1 | NT | Giardia lamblia variant-specific surface protein G3M-B (vegG3M-B) mRNA, partial cds |
| 9982 | 22457 | 35440 | 4.27 | 7.9E-01 | P19719 | SWISSPROT | SMALL HYDROPHOBIC PROTEIN |
| 10003 | 22408 | 35487 | 0.75 | 7.9E-01 | AV700860.1 | EST_HUMAN | AV700860 GK Homo sapiens cDNA clone GKCDRE12 3' |
| 10405 | 22859 | 35894 | 0.71 | 7.9E-01 | AB000631.1 | NT | Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds |
| 10886 | 23407 | | 2.28 | 7.9E-01 | 7682471 | NT | Homo sapiens KIAA1072 protein (KIAA1072), mRNA |
| 11089 | 23801 | 38839 | 2.72 | 7.9E-01 | P16022 | SWISSPROT | NEURAL-CADHERIN PRECURSOR (N-CADHERIN) |
| 909 | 13522 | | 1.4 | 7.8E-01 | Z43785.1 | EST_HUMAN | HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04 |
| 2314 | 14888 | 27481 | 14 | 7.8E-01 | AW955667.1 | EST_HUMAN | EST371637 MAGE resequences, MAGF Homo sapiens cDNA |
| 4811 | 17389 | 28940 | 0.81 | 7.8E-01 | U87305.1 | NT | Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds |
| 5189 | 17754 | | 0.81 | 7.8E-01 | AW753353.1 | EST_HUMAN | RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA |
| 6219 | 18829 | 31803 | 2.33 | 7.8E-01 | AF115856.1 | NT | Sphenodon punctatus alpha enolase mRNA, partial cds |
| 6367 | 18971 | 31750 | 1.05 | 7.8E-01 | P05231 | SWISSPROT | INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR) |
| 6589 | 19188 | 31888 | 0.75 | 7.8E-01 | AL445068.1 | NT | Thermoplasma acidophilum complete genome; segment 4/6 |
| 8428 | 20888 | 33881 | 1.04 | 7.8E-01 | BF109827.1 | EST_HUMAN | 7154d05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3' |
| 8180 | 21695 | 34639 | 1.02 | 7.8E-01 | Y10159.1 | NT | D. discoideum racGAP gene |
| 9255 | 21781 | 34733 | 0.53 | 7.8E-01 | 4826873 | NT | Homo sapiens nucleoporin 214kD (CAN) (NUP214), mRNA |
| 10031 | 22528 | | 0.78 | 7.8E-01 | Q25452 | SWISSPROT | MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1) |
| 12071 | 24957 | | 2.33 | 7.8E-01 | L23260.1 | NT | Arabidopsis thaliana 1-aminino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds |
| 150 | 12813 | 25300 | 4.65 | 7.7E-01 | AF184345.1 | NT | Lycopodium hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds |
| 755 | 13374 | | 1.44 | 7.7E-01 | AF050157.1 | NT | Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Aa1pha) and major histocompatibility protein class II beta chain (Ib1beta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-lp |
| 2737 | 15292 | 27860 | 2.33 | 7.7E-01 | O33915 | SWISSPROT | CITRATE SYNTHASE |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3400 | 16009 | | 0.82 | 7.7E-01 | 8393408 | NT | Homo sapiens UDP-N-acetyl-alpha-D-galactose 4-epimerase N-acetylglucosaminyltransferase 7 (GALNAC-T7) (GALNAC-T7), mRNA |
| 3660 | 16262 | 28734 | 4.78 | 7.7E-01 | AF118085.1 | NT | Homo sapiens PRO1975 mRNA, complete cds |
| 4488 | 17071 | 28521 | 3.17 | 7.7E-01 | AF189488.1 | NT | Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds |
| 4488 | 17071 | 28522 | 3.17 | 7.7E-01 | AF189488.1 | NT | Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds |
| 5749 | 18375 | 31084 | 1.33 | 7.7E-01 | P16553 | SWISSPROT | RAFFINOSE INVERTASE (INVERTASE) |
| 5749 | 18375 | 31085 | 1.33 | 7.7E-01 | P16553 | SWISSPROT | RAFFINOSE INVERTASE (INVERTASE) |
| 6110 | 18726 | 31478 | 0.8 | 7.7E-01 | R08600.1 | EST_HUMAN | Y724502 s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3' |
| 9758 | 22256 | 35239 | 0.82 | 7.7E-01 | AB021134.1 | NT | Diaphria magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds |
| 11957 | 24280 | | 15.01 | 7.7E-01 | 11497621 | NT | Archaeoglobus fulgidus, complete genome |
| 4790 | 17370 | 29822 | 19.73 | 7.6E-01 | L27316.1 | NT | Oryctolagus cuniculus immunoglobulin VDJ region gene |
| 4790 | 17370 | 29823 | 19.73 | 7.6E-01 | L27316.1 | NT | Oryctolagus cuniculus immunoglobulin VDJ region gene |
| 6248 | 18857 | 31628 | 4.91 | 7.6E-01 | AF059510.1 | NT | Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds |
| 6248 | 18857 | 31628 | 4.91 | 7.6E-01 | AF059510.1 | NT | Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds |
| 6641 | 19237 | 32039 | 0.7 | 7.6E-01 | P37838 | SWISSPROT | MATING-TYPE PROTEIN A-ALPHA 24 |
| 6935 | 18043 | 30465 | 0.95 | 7.5E-01 | A1253399.1 | EST_HUMAN | seq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879 |
| 6935 | 18043 | 30488 | 0.95 | 7.5E-01 | A1253399.1 | EST_HUMAN | seq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879 |
| 7113 | 19453 | 32269 | 0.98 | 7.6E-01 | U72487.1 | NT | Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds |
| 8009 | 20551 | 33455 | 1.34 | 7.6E-01 | AF146793.2 | NT | Mus musculus neuromedin U precursor (Nmu) gene, partial cds; PHLIP (Tphp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds |
| 8068 | 20610 | 33522 | 1.76 | 7.6E-01 | 6857752 | NT | Mus musculus adinin (Adinl-pending), mRNA |
| 8068 | 20610 | 33523 | 1.76 | 7.6E-01 | 6857752 | NT | Mus musculus adinin (Adinl-pending), mRNA |
| 8267 | 20808 | 33727 | 0.55 | 7.6E-01 | Q01098 | SWISSPROT | GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C) |
| 8267 | 20808 | 33728 | 0.55 | 7.6E-01 | Q01098 | SWISSPROT | GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C) |
| 8897 | 21435 | 34359 | 0.91 | 7.6E-01 | 6753577 | NT | Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA |
| 9203 | 21720 | 34684 | 3.33 | 7.6E-01 | P30372 | SWISSPROT | MUSCARINIC ACETYLCHOLINE RECEPTOR M2 |
| 9203 | 21720 | 34695 | 3.33 | 7.6E-01 | P30372 | SWISSPROT | MUSCARINIC ACETYLCHOLINE RECEPTOR M2 |
| 11236 | 23767 | 36824 | 2.74 | 7.6E-01 | X86347.1 | NT | H. aspersa mRNA for neurofilament NF70 |
| 11236 | 23767 | 36825 | 2.74 | 7.6E-01 | X86347.1 | NT | H. aspersa mRNA for neurofilament NF70 |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11566 | 24004 | | 5.74 | 7.6E-01 | AL161592.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88 |
| 11711 | 24121 | | 6.31 | 7.6E-01 | AB020702.1 | NT | Homo sapiens mRNA for KIAA0895 protein, partial cds |
| 539 | 13170 | | 1.32 | 7.5E-01 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 610 | 13238 | 25712 | 1.13 | 7.5E-01 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5 |
| 7530 | 20050 | 32823 | 0.74 | 7.6E-01 | AF052730.1 | NT | Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds |
| 12027 | 24918 | | 5.26 | 7.5E-01 | AF169151.2 | NT | Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds |
| 12522 | 24638 | 30897 | 1.91 | 7.5E-01 | D00007.1 | NT | Synschoeculus sp. PCC6803 complete genome, 8/27, 1058467-1188885 |
| 1169 | 13771 | 26279 | 1.36 | 7.4E-01 | AI588148.1 | EST_HUMAN | Int14b08.x1 NCJ_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element ; |
| 3789 | 16369 | 28854 | 0.93 | 7.4E-01 | AF112538.1 | NT | Malva pusilla actin (Act1) mRNA, complete cds |
| 4400 | 16885 | 29430 | 7.7 | 7.4E-01 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 7785 | 20328 | 33234 | 1.03 | 7.4E-01 | AL161551.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51 |
| 7785 | 20328 | 33235 | 1.03 | 7.4E-01 | AL161551.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51 |
| 8568 | 21107 | 34026 | 0.93 | 7.4E-01 | BF346268.1 | EST_HUMAN | 602018456F1 NCJ_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4154340 5' |
| 8647 | 21186 | | 0.64 | 7.4E-01 | U87860.1 | NT | Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon |
| 9026 | 21563 | 34492 | 7.17 | 7.4E-01 | BE747503.1 | EST_HUMAN | 601573028F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5' |
| 9083 | 21619 | 34554 | 1.19 | 7.4E-01 | AA187886.1 | EST_HUMAN | zp67h01.s1 Strabegene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625287 3' similar to SW:TCPO_MOUSE P42832 T-COMPLEX PROTEIN 1, THETA SUBUNIT ; |
| 10301 | 22795 | 35786 | 0.59 | 7.4E-01 | 11424833 | NT | Homo sapiens NY-REN-45 antigen (LOC51133), mRNA |
| 11518 | 23964 | 37034 | 1.68 | 7.4E-01 | AB021490.2 | NT | Oryzias latipes gene for membrane guanylyl cyclase OGC1, complete cds |
| 11518 | 23964 | 37035 | 1.68 | 7.4E-01 | AB021490.2 | NT | Oryzias latipes gene for membrane guanylyl cyclase OGC1, complete cds |
| 11677 | 24096 | | 4.11 | 7.4E-01 | 6753217 | NT | Mus musculus complement component 1 inhibitor (C1inh), mRNA |
| 11784 | 24175 | | 1.28 | 7.4E-01 | AJ472841.1 | EST_HUMAN | Int13h01.x1 NCJ_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043385 3' |
| 4723 | 17304 | 28748 | 0.72 | 7.3E-01 | AE001168.1 | NT | Borrelia burgdorferi (section 62 of 70) of the complete genome |
| 4810 | 17388 | 28839 | 2.93 | 7.3E-01 | AF225421.1 | NT | Homo sapiens HT017 mRNA, complete cds |
| 5260 | 17823 | 30248 | 0.89 | 7.3E-01 | O43103 | SWISSPROT | FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE |
| 6720 | 16314 | 32116 | 5.86 | 7.3E-01 | L35772.1 | NT | Mus musculus antigen (CD72) gene |
| 6720 | 16314 | 32117 | 5.86 | 7.3E-01 | L35772.1 | NT | Mus musculus antigen (CD72) gene |
| 7151 | 24777 | 32525 | 0.82 | 7.3E-01 | AJ011418.1 | NT | Lycopodium obscurum mRNA for ubiquitin activating enzyme |
| 7549 | 20068 | 32842 | 7.77 | 7.3E-01 | M26511.1 | NT | V.alginolyticus sucrase (scrB) gene, complete cds |
| 7549 | 20068 | 32843 | 7.77 | 7.3E-01 | M26511.1 | NT | V.alginolyticus sucrase (scrB) gene, complete cds |
| 11307 | 23800 | 36859 | 3.86 | 7.3E-01 | AA678019.1 | EST_HUMAN | z125b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11307 | 23800 | 36880 | 3.86 | 7.3E-01 | AA678019.1 | EST_HUMAN | z25508.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431788 3' |
| 884 | 13479 | | 1.86 | 7.2E-01 | U29281.1 | NT | Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds |
| 2000 | 14582 | 27141 | 3.04 | 7.2E-01 | X79140.1 | NT | N. tabacum Nelf-4A13 mRNA |
| 2501 | 15065 | 27639 | 1.36 | 7.2E-01 | AB009605.1 | NT | Gallus gallus gene for melanocortin 2-receptor, complete cds |
| 3103 | 15718 | 28188 | 1.29 | 7.2E-01 | AF188100.1 | NT | Footpox virus, complete genome |
| 3500 | 16105 | 28580 | 2.97 | 7.2E-01 | AF065906.1 | NT | Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-I) allele, complete cds |
| 3040 | 16538 | 29005 | 1.81 | 7.2E-01 | BF338350.1 | EST_HUMAN | 602035589F1 NC1 CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5' |
| 4185 | 16775 | 29222 | 0.6 | 7.2E-01 | U02568.1 | NT | Diclyocaulus viviparus nematode polyprotein antigen precursor (Dva) mRNA, complete cds |
| 4884 | 17459 | 28911 | 2.54 | 7.2E-01 | D80314.1 | NT | L. mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7) |
| 5348 | 17908 | 30323 | 0.9 | 7.2E-01 | AF158800.2 | NT | Streptococcus thermophilus bacteriophage Sfi11, complete genome |
| 5386 | 17945 | 30358 | 0.69 | 7.2E-01 | AL181583.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63 |
| 7265 | 19783 | 32849 | 0.82 | 7.2E-01 | U68633.1 | NT | Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds |
| 8301 | 20931 | 33851 | 1.15 | 7.2E-01 | AF236061.1 | NT | Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds |
| 8893 | 21431 | | 0.53 | 7.2E-01 | AV749773.1 | EST_HUMAN | AV743773 CB Homo sapiens cDNA clone CBMAFD06 5' |
| 10243 | 22738 | 35729 | 2.14 | 7.2E-01 | BF670061.1 | EST_HUMAN | 602118381F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4275381 5' |
| 10618 | 23150 | 36182 | 5.23 | 7.2E-01 | U82623.1 | NT | Rattus norvegicus cytochrome mRNA, complete cds |
| 12037 | 18775 | 29222 | 1.86 | 7.2E-01 | U02568.1 | NT | Diclyocaulus viviparus nematode polyprotein antigen precursor (Dva) mRNA, complete cds |
| 12233 | 24449 | | 4.42 | 7.2E-01 | AF000063.1 | NT | Aeropyrum pernix genomic DNA, section 8/7 |
| 12266 | 24995 | | 1.67 | 7.2E-01 | Y10168.1 | NT | B. thuringiensis PK1 & cap genes, putative |
| 721 | 13341 | 25831 | 10.56 | 7.1E-01 | D21070.1 | NT | Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds |
| 3098 | 15713 | 28185 | 18.71 | 7.1E-01 | AJ270777.1 | NT | Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16 |
| 4287 | 16873 | 29321 | 4.11 | 7.1E-01 | 7305360 | NT | Mus musculus obogelin (Otog), mRNA |
| 4287 | 16873 | 29322 | 4.11 | 7.1E-01 | 7305360 | NT | Mus musculus obogelin (Otog), mRNA |
| 6103 | 18719 | 31471 | 1.81 | 7.1E-01 | BF681034.1 | EST_HUMAN | 602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5' |
| 6103 | 18719 | 31472 | 1.81 | 7.1E-01 | BF681034.1 | EST_HUMAN | 602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5' |
| 7029 | 19563 | 32360 | 6.04 | 7.1E-01 | U36232.1 | NT | Drosophila melanogaster 6-pyruvoyltryptophan synthase (pr) gene, complete cds |
| 8132 | 20673 | 33584 | 0.53 | 7.1E-01 | H54244.1 | EST_HUMAN | y98609.s1 Soares fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:202981 3' |
| 8671 | 21210 | 34128 | 0.78 | 7.1E-01 | BE074185.1 | EST_HUMAN | RC1-B10567-301289-011-009 BT0567 Homo sapiens cDNA |
| 8671 | 21210 | 34129 | 0.78 | 7.1E-01 | BE074185.1 | EST_HUMAN | RC1-B10567-301289-011-009 BT0567 Homo sapiens cDNA |
| 9769 | 22287 | 35252 | 1.48 | 7.1E-01 | BE004405.1 | EST_HUMAN | 601486330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5' |
| 10309 | 22803 | 35795 | 1.06 | 7.1E-01 | M12961.1 | NT | Human T-cell receptor gamma-chain J2 gene |
| 12012 | 24878 | | 2.58 | 7.1E-01 | AA421492.1 | EST_HUMAN | zu06h11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731109 3' |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1272 | 13988 | 26387 | 1.3 | 7.0E-01 | AB014514.1 | NT | Homo sapiens mRNA for KIAA0814 protein, partial cds |
| 1272 | 13988 | 26388 | 1.3 | 7.0E-01 | AB014514.1 | NT | Homo sapiens mRNA for KIAA0814 protein, partial cds |
| 2482 | 15057 | 27630 | 1.22 | 7.0E-01 | NC2412.1 | EST_HUMAN | yz73e07.s1 Soares_multiple_sclerobels_2NbrHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element |
| 2482 | 15057 | 27631 | 1.22 | 7.0E-01 | NC2412.1 | EST_HUMAN | yz73e07.s1 Soares_multiple_sclerobels_2NbrHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element |
| 5213 | 17778 | | 1.98 | 7.0E-01 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 5362 | 17922 | 30336 | 2.99 | 7.0E-01 | AE003921.1 | NT | Xylella fastidiosa, section 87 of 228 of the complete genome |
| 6107 | 18723 | | 1.03 | 7.0E-01 | AB021316.1 | NT | Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds |
| 8319 | 20800 | | 11.92 | 7.0E-01 | AE000253.1 | NT | Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome |
| 9240 | 21766 | 34714 | 0.61 | 7.0E-01 | U53988.1 | NT | Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, and mtlD genes, complete cds |
| 9240 | 21766 | 34715 | 0.61 | 7.0E-01 | U53988.1 | NT | Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, and mtlD genes, complete cds |
| 10699 | 23513 | 36546 | 1.99 | 7.0E-01 | AV763942.1 | EST_HUMAN | AV763942 MDS Homo sapiens cDNA clone MDSCH04 5' |
| 10699 | 23513 | 36547 | 1.98 | 7.0E-01 | AV763942.1 | EST_HUMAN | AV763942 MDS Homo sapiens cDNA clone MDSCH04 5' |
| 12584 | 24918 | 30715 | 1.35 | 7.0E-01 | 8630484 | NT | Bacteriophage N15 virion, complete genome |
| 1005 | 13616 | 26130 | 10.2 | 6.9E-01 | U69674.1 | NT | Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds |
| 1005 | 13616 | 26131 | 10.2 | 6.9E-01 | U69674.1 | NT | Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds |
| 1353 | 13948 | 28472 | 2.8 | 6.9E-01 | AA503530.1 | EST_HUMAN | nm28e09.s1 NCI_OGAP_Gas1 Homo sapiens cDNA clone IMAGE:1065176 3' |
| 3258 | 15868 | 28348 | 1.7 | 6.9E-01 | AE002271.2 | NT | Chlamydia muridarum, section 3 of 85 of the complete genome |
| 5654 | 18576 | 31310 | 0.8 | 6.9E-01 | AB035982.1 | NT | Branchiostoma belcheri BBN43 mRNA for nucleohand actin, complete cds |
| 6508 | 19108 | 31803 | 1.31 | 6.9E-01 | BE286188.1 | EST_HUMAN | 601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5' |
| 7821 | 20483 | 33369 | 3.4 | 6.9E-01 | AL161573.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69 |
| 7821 | 20483 | 33370 | 3.4 | 6.9E-01 | AL161573.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69 |
| 6098 | 21634 | | 0.83 | 6.9E-01 | AF118048.1 | NT | Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds |
| 9611 | 22111 | 35073 | 0.62 | 6.9E-01 | AF206319.1 | NT | Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds |
| 9611 | 22111 | 35074 | 0.62 | 6.9E-01 | AF206319.1 | NT | Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds |
| 10307 | 22801 | 35793 | 0.66 | 6.9E-01 | BF242687.1 | EST_HUMAN | 601880580F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4109419 5' |
| 11138 | 23646 | 36687 | 1.94 | 6.9E-01 | D89013.1 | NT | Homo sapiens DAN gene, complete cds |
| 11138 | 23646 | 36688 | 1.94 | 6.9E-01 | D89013.1 | NT | Homo sapiens DAN gene, complete cds |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11661 | 24870 | | 2.38 | 6.9E-01 | Q69558 | SWISSPROT | FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK |
| 12070 | 25003 | 30811 | 1.33 | 6.9E-01 | AJ888312.1 | EST_HUMAN | HEAD PROTEIN 1) (MFT-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14) |
| 992 | 13604 | 28118 | 1.28 | 6.9E-01 | AF017784.1 | NT | wn3102.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2447067 3' |
| 2898 | 15266 | | 1.25 | 6.9E-01 | D90917.1 | NT | Giardia intestinalis carbamate kinase gene, complete cds |
| 2858 | 14249 | 28783 | 1.62 | 6.9E-01 | AA854475.1 | EST_HUMAN | Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470 |
| 4872 | 17264 | 28706 | 1.45 | 6.9E-01 | J00782.1 | NT | aj75a06.a1 Soares parathyroid tumor_NHHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to |
| 8558 | 22058 | 35017 | 2.11 | 6.9E-01 | AB037766.1 | NT | gb:X58411_mn1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN); |
| 10281 | 22756 | | 0.48 | 6.9E-01 | AA687838.1 | EST_HUMAN | Rat(hooded) prolactin gene: exon III and flanks |
| 10965 | 23480 | 36505 | 2.86 | 6.9E-01 | AJ276875.1 | NT | Homo sapiens mRNA for KIAA1345 protein, partial cds |
| 10965 | 23480 | 36508 | 2.86 | 6.9E-01 | AJ276875.1 | NT | hnt13e07.a1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:X13546_mn1 |
| 10983 | 23507 | 36540 | 2.16 | 6.9E-01 | AF038939.1 | NT | Human HMG-17 gene for non-histone chromosomal protein (HUMAN); |
| 10983 | 23507 | 36541 | 2.16 | 6.9E-01 | AF038939.1 | NT | Stagonospora avenae bg1 gene for beta-glucosidase, exons 1-4 |
| 11178 | 23884 | 36730 | 2.2 | 6.9E-01 | AF184151.1 | NT | Stagonospora avenae bg1 gene for beta-glucosidase, exons 1-4 |
| 11475 | 23925 | 36995 | 1.77 | 6.9E-01 | AF110520.1 | NT | Mus musculus zinc finger protein (Peg3) mRNA, complete cds |
| 11475 | 23925 | 36996 | 1.77 | 6.9E-01 | AF110520.1 | NT | Mus musculus zinc finger protein (Peg3) mRNA, complete cds |
| 320 | 12074 | 25463 | 27.63 | 6.7E-01 | AF213884.1 | NT | Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds |
| 361 | 13010 | 25463 | 28.51 | 6.7E-01 | AF213884.1 | NT | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, |
| 1955 | 14539 | | 0.97 | 6.7E-01 | M12132.1 | NT | KIFC1, Fas-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and |
| 2192 | 14768 | 27340 | 1.85 | 6.7E-01 | AA451864.1 | EST_HUMAN | RPS18 genes, complete cds; Sacm21 gene, partial> |
| 2211 | 15460 | 27361 | 2.68 | 6.7E-01 | AF186073.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete |
| 3028 | 15942 | 28120 | 4.28 | 6.7E-01 | 6878580 | NT | cds |
| 4550 | 17133 | 28581 | 0.64 | 6.7E-01 | X74421.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete |
| | | | | | | | cds |
| | | | | | | | Quail fast skeletal muscle troponin I gene, complete cds |
| | | | | | | | zx12g12.s1 Soares total_fetus_Nb27IF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to |
| | | | | | | | contains element TAR1 repetitive element: |
| | | | | | | | Drosophila melanogaster Msl85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, |
| | | | | | | | alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced |
| | | | | | | | Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA |
| | | | | | | | S.tuberosum mRNA for glucose-6-phosphatase dehydrogenase |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5100 | 17672 | 30111 | 0.96 | 6.7E-01 | AW079110.1 | EST_HUMAN | xs95g12.x1 NCL CGAP_Co17 Homo sapiens cDNA clone IMAGE:2574598 3' |
| 5700 | 18328 | 30829 | 0.8 | 6.7E-01 | J04836.1 | NT | M.barkei ATPase alpha and beta subunit (atpA and atpB) genes, complete cds |
| 5700 | 18328 | 30830 | 0.8 | 6.7E-01 | J04836.1 | NT | M.barkei ATPase alpha and beta subunit (atpA and atpB) genes, complete cds |
| 6116 | 18732 | 31485 | 0.83 | 6.7E-01 | AE001488.1 | NT | Helicobacter pylori, strain J99 section 47 of 132 of the complete genome |
| 6465 | 19068 | 31851 | 1.55 | 6.7E-01 | 9635035 | NT | Gallid herpesvirus 2, complete genome |
| 6465 | 19068 | 31852 | 1.55 | 6.7E-01 | 9635035 | NT | Gallid herpesvirus 2, complete genome |
| 7358 | 19882 | | 4.12 | 6.7E-01 | AE004806.1 | NT | Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome |
| 7378 | 19904 | 32768 | 0.9 | 6.7E-01 | AE001488.1 | NT | Helicobacter pylori, strain J99 section 47 of 132 of the complete genome |
| 10049 | 22544 | | 0.87 | 6.7E-01 | M34046.1 | NT | Human placental protein 14 (PP14) gene, complete cds |
| 10832 | 23553 | 36368 | 2.52 | 6.7E-01 | BF354649.1 | EST_HUMAN | CM3-HT07088-010800-197-c03 HT07088 Homo sapiens cDNA |
| 11333 | 23031 | 36040 | 3.45 | 6.7E-01 | O14357 | SWISSPROT | N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1 |
| 2546 | 15110 | 27682 | 2.68 | 6.6E-01 | AF075240.1 | NT | Homo sapiens SLT1 protein (SLIL2) mRNA, partial cds |
| 2724 | 15279 | 27846 | 1.01 | 6.6E-01 | AF199330.1 | NT | Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds |
| 3536 | 16141 | 28623 | 1.35 | 6.6E-01 | 4606880 | NT | Homo sapiens same domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sarnaphorin) 5A (SEMA5A) mRNA |
| 3719 | 16320 | 28788 | 3.42 | 6.6E-01 | Y07698.1 | NT | C.albicans random DNA marker, 282bp |
| 4187 | 16777 | | | 6.6E-01 | U91326.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds |
| 5227 | 17791 | 30210 | 0.97 | 6.6E-01 | AI218230.1 | EST_HUMAN | q23a10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845488 3' similar to contains PTR5.b2 MER28 repetitive element: |
| 6474 | 18075 | 31858 | 4.22 | 6.6E-01 | 6680577 | NT | Mus musculus kinesin light chain 2 (Klc2), mRNA |
| 7675 | 20188 | 33074 | 3.61 | 6.6E-01 | AV660506.1 | EST_HUMAN | AV660506 GLC Homo sapiens cDNA clone GLCGID04 3' |
| 8501 | 21040 | 33981 | 0.64 | 6.6E-01 | AV704700.1 | EST_HUMAN | AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5' |
| 8582 | 22082 | | 1.73 | 6.6E-01 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 8915 | 22411 | | 0.68 | 6.6E-01 | AU118198.1 | EST_HUMAN | AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5' |
| 12118 | 24377 | 30973 | 1.27 | 6.6E-01 | AF110001.1 | NT | Homo sapiens guanylate cyclase activating protein 3 (GCAP3) gene, exon 4 and complete cds |
| 651 | 13274 | 25751 | 1.12 | 6.5E-01 | M75140.1 | NT | H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds |
| 651 | 13274 | 25752 | 1.12 | 6.5E-01 | M75140.1 | NT | H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds |
| 3480 | 16086 | 28560 | 5.04 | 6.5E-01 | AB041225.1 | NT | Mus musculus gene for Tob2, complete cds |
| 4110 | 16704 | 29157 | 1.1 | 6.5E-01 | 4504632 | NT | Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA |
| 4368 | 16856 | 28398 | 3.29 | 6.5E-01 | AJ272285.1 | NT | Homo sapiens SP2 gene for secreted phosphoprotein 24 precursor, exons 1-8 |
| 4699 | 17261 | 29728 | 1.28 | 6.5E-01 | D00584.1 | NT | Oryza sativa gene for prepro-glutelin, exons 1, 2, 3, 4, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5219 | 17784 | 30202 | 2.39 | 6.5E-01 | U28021.1 | NT | Phascolarctus ATPase gamma subunit mRNA, nuclear genes encoding mitochondrial protein, partial cds |
| 5336 | 17897 | 30312 | 1.02 | 6.5E-01 | Z70628.1 | NT | H.sapiens mRNA for immunoglobulin heavy chain variable region (9D4-A6, VH4, 4-59/DP-71) |
| 6825 | 19415 | 32231 | 1.26 | 6.5E-01 | D88348.1 | NT | Chicken mRNA for 115-kDa melanocortin matrix protein, complete cds |
| 7663 | 20176 | 33062 | 0.96 | 6.5E-01 | A1790882.1 | EST_HUMAN | wc46a02.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:2321642 3' |
| 9751 | 22249 | | 1.25 | 6.5E-01 | T78004.1 | EST_HUMAN | yc21b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108847 3' |
| 10238 | 22733 | 35725 | 2.49 | 6.5E-01 | AF119676.1 | NT | Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds |
| 10512 | 23050 | 36061 | 3.35 | 6.5E-01 | H87583.1 | EST_HUMAN | yw1706.r1 Soares placenta_8to9weeks_2NdrHP8b09W Homo sapiens cDNA clone IMAGE:252515 5' |
| 10566 | 23102 | 36116 | 4.35 | 6.5E-01 | AA601287.1 | EST_HUMAN | nc15c07.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3' |
| 10669 | 23201 | | 4.29 | 6.5E-01 | AU138078.1 | EST_HUMAN | AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5' |
| 11470 | 23920 | 36988 | 2.7 | 6.5E-01 | AF014115.1 | NT | Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds |
| 12067 | 24348 | | 8.24 | 6.5E-01 | BE485050.1 | EST_HUMAN | hiv74e10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3' |
| 12321 | 24817 | | 3.04 | 6.5E-01 | Z74145.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL097c |
| 273 | 12930 | 25417 | 9.34 | 6.4E-01 | U48948.1 | NT | Drosophila melanogaster 8kd dyenin light chain mRNA, complete cds |
| 3502 | 16107 | 28583 | 3.78 | 6.4E-01 | U48854.2 | NT | Mus musculus dyoglobulin 1 (DAG1) gene, exons 1 and 2 and complete cds |
| 3928 | 16528 | 28693 | 1.33 | 6.4E-01 | AB046827.1 | NT | Homo sapiens mRNA for KIAA1807 protein, partial cds |
| 4591 | 17174 | 29619 | 0.66 | 6.4E-01 | Y12498.1 | NT | M.musculus wtn gene |
| 4591 | 17174 | 29620 | 0.66 | 6.4E-01 | Y12498.1 | NT | M.musculus wtn gene |
| 5402 | 17960 | 30371 | 0.97 | 6.4E-01 | AE002551.2 | NT | Neisseria meningitidis serogroup B strain MC58 section 183 of 208 of the complete genome |
| 8549 | 21088 | 34010 | 1.76 | 6.4E-01 | AE001247.1 | NT | Treponema pallidum section 63 of 87 of the complete genome |
| 10001 | 22496 | 35486 | 8.26 | 6.4E-01 | U82828.1 | NT | Homo sapiens ataxia telangiectasia (ATM) gene, complete cds |
| 10015 | 22510 | 35501 | 1.16 | 6.4E-01 | BF670405.1 | EST_HUMAN | 602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291128 5' |
| 12188 | 24420 | | 29.97 | 6.4E-01 | AV759212.1 | EST_HUMAN | AV759212 MDS Homo sapiens cDNA clone MDSGCC09 5' |
| 459 | 13093 | 25587 | 3.75 | 6.3E-01 | P05228 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III) |
| 560 | 13191 | 25669 | 58.3 | 6.3E-01 | U32686.1 | NT | Haemophilus influenzae Rd section 4 of 163 of the complete genome |
| 2207 | 14763 | 27356 | 3.24 | 6.3E-01 | U81136.1 | NT | Shigella flexneri multi-antigen resistance locus |
| 2614 | 15176 | 27744 | 2.78 | 6.3E-01 | U75331.1 | NT | Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds |
| 2614 | 15176 | 27745 | 2.78 | 6.3E-01 | U75331.1 | NT | Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds |
| 3050 | 15668 | | 0.76 | 6.3E-01 | Y17275.1 | NT | Lycopodium obscurum p80a gene, complete CDS |
| 6214 | 18624 | 31595 | 0.78 | 6.3E-01 | BE083808.1 | EST_HUMAN | PMO-B10757-010500-002-a05 BT0757 Homo sapiens cDNA |
| 6712 | 19306 | 32110 | 1 | 6.3E-01 | L27798.1 | NT | Streptococcus dysgalactiae (msg) gene, complete cds |
| 6712 | 19306 | 32111 | 1 | 6.3E-01 | L27798.1 | NT | Streptococcus dysgalactiae (msg) gene, complete cds |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8458 | 20908 | | 3.32 | 6.3E-01 | BE02044.1 | EST_HUMAN | 601676888F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956351 5' |
| 8819 | 21358 | 34284 | 0.81 | 6.3E-01 | S62927.1 | NT | glycoprotein IIIa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt] |
| 9147 | 21682 | 34627 | 1.15 | 6.3E-01 | BF216884.1 | EST_HUMAN | 601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102598 5' |
| 9341 | 21855 | 34804 | 2.9 | 6.3E-01 | 6827521 | NT | Varicella virus, complete genome |
| 9341 | 21855 | 34805 | 2.9 | 6.3E-01 | 6827521 | NT | Varicella virus, complete genome |
| 9851 | 22349 | | 0.67 | 6.3E-01 | AE002329.2 | NT | Chlamydia muridarum, section 69 of 95 of the complete genome |
| 10324 | 22818 | 35814 | 1.52 | 6.3E-01 | Z73003.1 | NT | S. cerevisiae chromosome VII reading frame ORF YGR216w |
| 10421 | 22916 | 35916 | 0.87 | 6.3E-01 | AE000313.1 | NT | Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome |
| 10839 | 23456 | 36479 | 2.45 | 6.3E-01 | AA877715.1 | EST_HUMAN | tr00h08.at NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002816 002816 HLARK: |
| 11216 | 23719 | 36773 | 15.21 | 6.3E-01 | A1804160.1 | EST_HUMAN | CM-BT043-080298-046 BT043 Homo sapiens cDNA |
| 11302 | 23795 | 36853 | 1.94 | 6.3E-01 | P47003 | SWISSPROT | HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION |
| 11458 | 23908 | 36975 | 2.02 | 6.3E-01 | P36073 | SWISSPROT | HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION |
| 11789 | 25042 | 30505 | 30.63 | 6.3E-01 | 6810283 | NT | Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA |
| 11884 | 24219 | | 1.85 | 6.3E-01 | AF106227.1 | NT | Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds |
| 12082 | 24953 | | 3.2 | 6.3E-01 | X63528.1 | NT | C. limicola pscD gene |
| 5175 | 17742 | 30171 | 0.71 | 6.2E-01 | AF157898.1 | NT | Spermophilus suslicus isolate S47 cytochrome b (cyb) gene, complete cds; mitochondrial gene for mitochondrial product |
| 6030 | 18049 | 31390 | 2.03 | 6.2E-01 | Q10195 | SWISSPROT | HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1 |
| 7506 | 20028 | | 3.14 | 6.2E-01 | AF022253.1 | NT | Mus musculus calcium-sensing receptor related protein 4 (Carr-rs4) mRNA, partial cds |
| 7548 | 24786 | 32941 | 1.08 | 6.2E-01 | AL021127.2 | NT | Mus musculus chromosome X contigA; putative Magea8 gene, Celltractin, NAD(P) sterol dehydrogenase and Zinc finger protein 185 |
| 8243 | 20784 | 33703 | 5.85 | 6.2E-01 | H72255.1 | EST_HUMAN | ys01608.at Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3' |
| 8780 | 21329 | 34254 | 0.54 | 6.2E-01 | AF034411.1 | NT | Lycopodium obscurum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase dehydratase/aldimase:NADP oxidoreductase gene, complete cds |
| 9370 | 20308 | 33212 | 1.75 | 6.2E-01 | BE562687.1 | EST_HUMAN | 601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3660010 5' |
| 9429 | 21938 | | 2.35 | 6.2E-01 | M24461.1 | NT | Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds |
| 9880 | 22485 | 35472 | 5.85 | 6.2E-01 | AL161511.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23 |
| 10428 | 22923 | 35927 | 3.78 | 6.2E-01 | P27410 | SWISSPROT | NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN] |
| 10429 | 22923 | 35928 | 3.78 | 6.2E-01 | P27410 | SWISSPROT | NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN] |
| 2438 | 15005 | | 4.95 | 6.1E-01 | 6878076 | NT | Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA |
| 4632 | 17215 | 28688 | 1.05 | 6.1E-01 | 4557538 | NT | Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 6141 | 17712 | 30142 | 1.09 | 6.1E-01 | L20427.1 | NT | Rattus norvegicus dihydroxydiphenylbenzoate methyltransferase mRNA, complete cds |
| 5141 | 17712 | 30143 | 1.09 | 6.1E-01 | L20427.1 | NT | Rattus norvegicus dihydroxydiphenylbenzoate methyltransferase mRNA, complete cds |
| 5727 | 18353 | 31057 | 1.34 | 6.1E-01 | M59840.1 | NT | Caenorhabditis elegans N2 CehMyd (nhr-1) alternatively spliced genes, complete cds |
| 6951 | 19528 | 32351 | 3.55 | 6.1E-01 | M64733.1 | NT | Rat TRPM-2 gene, complete cds |
| 6951 | 19528 | 32352 | 3.55 | 6.1E-01 | M64733.1 | NT | Rat TRPM-2 gene, complete cds |
| 8175 | 20716 | 33632 | 3.57 | 6.1E-01 | AF035535.1 | NT | Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds |
| 8730 | 21289 | 34187 | 1.23 | 6.1E-01 | 11431065 | NT | Homo sapiens mitogen-activated protein kinase kinase 4 (MAP4K4), mRNA |
| 8730 | 21289 | 34188 | 1.23 | 6.1E-01 | 11431065 | NT | Homo sapiens mitogen-activated protein kinase kinase 4 (MAP4K4), mRNA |
| 8338 | 21850 | 34798 | 19.4 | 6.1E-01 | AF236117.1 | NT | Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds |
| 8338 | 21850 | 34799 | 19.4 | 6.1E-01 | AF236117.1 | NT | Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds |
| 9756 | 22254 | 35238 | 1.15 | 6.1E-01 | AE004462.1 | NT | Pseudomonas aeruginosa PA01, section 13 of 528 of the complete genome |
| 8958 | 22454 | 35436 | 1.8 | 6.1E-01 | AF119117.1 | NT | Homo sapiens dopamine transporter (SLC8A3) gene, complete cds |
| 10637 | 23358 | | 8.53 | 6.1E-01 | X74507.1 | NT | P. sativum mdh mRNA for chloroplast malate dehydrogenase (NADP++) |
| 11581 | 24027 | 37095 | 2.19 | 6.1E-01 | S83182.1 | NT | hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt] |
| 11581 | 24027 | 37098 | 2.19 | 6.1E-01 | S83182.1 | NT | hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt] |
| 12530 | 24643 | | 1.91 | 6.1E-01 | X95287.1 | NT | M.mazai orfA, orfB, and orfC of archaeal ABC-transporter system |
| 520 | 13152 | 25635 | 1.46 | 6.0E-01 | D87875.1 | NT | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 587 | 13217 | | 3.41 | 6.0E-01 | 5802888 | NT | Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLAS2), mRNA |
| 1496 | 13999 | 26528 | 1.93 | 6.0E-01 | AF066263.1 | NT | Human respiratory syncytial virus strain CH89-53b attachment protein (G) gene, complete cds |
| 3887 | 16485 | 28946 | 0.88 | 6.0E-01 | AJ233396.1 | NT | Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71 |
| 4267 | 18853 | | 1.16 | 6.0E-01 | AF058895.1 | NT | Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28 |
| 5485 | 18118 | 30528 | 1.93 | 6.0E-01 | P20288 | SWISSPROT | D(2) DOPAMINE RECEPTOR |
| 5631 | 18280 | 30732 | 2.28 | 6.0E-01 | AW139713.1 | EST_HUMAN | U1-HB1-eeb-a-10-0-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718819.3' |
| 6660 | 19256 | 32059 | 3.73 | 6.0E-01 | U38813.1 | NT | Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds |
| 6787 | 19380 | 32189 | 0.79 | 6.0E-01 | Q04912 | SWISSPROT | MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) |
| 7391 | 19816 | 32780 | 5.29 | 6.0E-01 | AJ277681.1 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, even 1 |
| 8066 | 20608 | 33520 | 4.72 | 6.0E-01 | P02835 | SWISSPROT | SEGMENTATION PROTEIN FUSHI TARAZU |
| 8066 | 20608 | 33521 | 4.72 | 6.0E-01 | P02835 | SWISSPROT | SEGMENTATION PROTEIN FUSHI TARAZU |
| 9737 | 22235 | 35214 | 2.22 | 6.0E-01 | AB008183.1 | NT | Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10174 | 22688 | | 1.61 | 6.0E-01 | Q01487 | SWISSPROT | PEROXISOMAL MEMBRANE PROTEIN PER8 (PEROXIN-3) |
| 10638 | 23453 | 38478 | 2.14 | 6.0E-01 | AJ131892.1 | NT | Gallus gallus mRNA for Hyperion protein, 419 kD isoform |
| 10638 | 23453 | 38477 | 2.14 | 6.0E-01 | AJ131892.1 | NT | Gallus gallus mRNA for Hyperion protein, 419 kD isoform |
| 11428 | 23877 | 38842 | 2.84 | 6.0E-01 | A420623.1 | EST_HUMAN | U0807.1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2086821 3' |
| 12158 | 24398 | 30878 | 1.82 | 6.0E-01 | 11421883 | NT | Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA |
| 12285 | 24475 | | 1.88 | 6.0E-01 | AA708087.1 | EST_HUMAN | XP8905.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA clone IMAGE:482778 3' |
| 12428 | 24879 | | 1.29 | 6.0E-01 | 5803138 | NT | Homo sapiens RNA binding motif protein 3 (RBM3), mRNA |
| 12469 | 24885 | 30709 | 2.49 | 6.0E-01 | 0055303 | NT | Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA |
| 12489 | 24810 | | 6.82 | 6.0E-01 | BE157817.1 | EST_HUMAN | RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA |
| 1038 | 13848 | 28160 | 1.08 | 5.9E-01 | U32701.1 | NT | Haemophilus influenzae Rd section 16 of 163 of the complete genome |
| 1447 | 14039 | 28568 | 1.08 | 5.9E-01 | 6880232 | NT | Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl), mRNA |
| 3308 | 15919 | 28395 | 5.12 | 5.9E-01 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C067 |
| 3308 | 15919 | 28396 | 5.12 | 5.9E-01 | AL163267.2 | NT | Homo sapiens chromosome 21 segment HS21C067 |
| 4304 | 16890 | | 4.32 | 5.9E-01 | AF162756.1 | NT | Rattus norvegicus ceroidin 2 mRNA, partial cds |
| 6591 | 19188 | 31981 | 1.48 | 5.9E-01 | AF065440.2 | NT | Homo sapiens low density lipoprotein receptor-related protein II (LRP-2) gene, exon 1 and partial cds |
| 7310 | 19838 | 32696 | 5.58 | 5.9E-01 | AB023486.1 | NT | Homo sapiens gene for histamine H2 receptor, promoter region and complete cds |
| 7841 | 20483 | 33395 | 0.57 | 5.9E-01 | D80911.1 | NT | Synschoecydis sp. POC8803 complete genome, 13/27, 1576593-1718843 |
| 9462 | 21987 | 34943 | 0.83 | 5.9E-01 | AF063204.2 | NT | Chlamydia trachomatis strain KUW/31/Cx major outer membrane protein (omp1) gene, complete cds |
| 9827 | 22325 | | 0.68 | 5.9E-01 | P08483 | SWISSPROT | E6 PROTEIN |
| 10091 | 22586 | 35579 | 1.15 | 5.9E-01 | P56284 | SWISSPROT | VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5) |
| 10551 | 23087 | 36102 | 3.24 | 5.9E-01 | Q9X015 | SWISSPROT | THYMIDYLATE KINASE (DTMP KINASE) |
| 10557 | 23083 | 36105 | 1.75 | 5.9E-01 | AF187944.1 | NT | Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds |
| 10840 | 23381 | 36378 | 3 | 5.9E-01 | AW837176.1 | EST_HUMAN | PM1-DT0041-190100-002-H03 DT0041 Homo sapiens cDNA |
| 11073 | 23585 | 36828 | 2.25 | 5.9E-01 | AF064608.1 | NT | Mus musculus strain SPRET/EI CD48 antigen (C48) gene, partial cds |
| 11810 | 24182 | 31030 | 1.92 | 5.9E-01 | L42320.1 | NT | Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region |
| 12053 | 24336 | | 2.88 | 5.9E-01 | AB017706.1 | NT | Aspergillus cryase pyrG gene for orobidine-5-phosphate decarboxylase, complete cds |
| 12280 | 24483 | | 7.56 | 5.9E-01 | P34828 | SWISSPROT | MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2] |
| 1852 | 14536 | 27082 | 1.8 | 5.8E-01 | P40472 | SWISSPROT | SIM1 PROTEIN |
| 4058 | 16853 | 28119 | 1.22 | 5.8E-01 | BF685738.1 | EST_HUMAN | 60185247AF1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4078131 5' |
| 4812 | 17106 | 28641 | 3.73 | 5.8E-01 | AB008077.1 | NT | Vigna radiata mRNA for proton pyrophosphatase, complete cds |
| 4814 | 17489 | | 1.18 | 5.8E-01 | AF110848.1 | NT | Megascelia scalaris sac-lethal homolog (Megsd) gene, partial cds, alternatively spliced products |
| 5577 | 18208 | | 0.75 | 5.8E-01 | AE002182.1 | NT | Ureaplasma urealyticum section 53 of 59 of the complete genome |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5722 | 18348 | 31051 | 2.52 | 5.8E-01 | Q10699 | SWISSPROT | POTENTIAL 5'-3' EXONUCLEASE |
| 6331 | 18937 | 31713 | 2.37 | 6.8E-01 | D78659.1 | EST_HUMAN | HUM500E088 Human placenta polyA+ (TFujizawa) Homo sapiens cDNA clone GEN-600E08 5' |
| 6454 | 19055 | 31840 | 0.71 | 5.8E-01 | D50601.1 | NT | Shigella sonnei DNA for 28 ORFs, complete cds |
| 6903 | 19637 | | 2.47 | 5.8E-01 | S65091.1 | NT | cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt] |
| 7628 | 20370 | | 2.57 | 5.8E-01 | H41571.1 | EST_HUMAN | yn81b03.s1 Soares adult brain N2651B55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to |
| 8031 | 20573 | 33477 | 0.66 | 5.8E-01 | A1280051.1 | EST_HUMAN | gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN); |
| 8031 | 20573 | 33478 | 0.66 | 5.8E-01 | A1280051.1 | EST_HUMAN | qf85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3' |
| 8131 | 20872 | 33582 | 2.34 | 5.8E-01 | P14328 | SWISSPROT | qf85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3' |
| 8131 | 20872 | 33583 | 2.34 | 5.8E-01 | P14328 | SWISSPROT | SPORE COAT PROTEIN SP08 |
| 8823 | 21362 | 34287 | 9.48 | 5.8E-01 | AJ270774.1 | NT | SPORE COAT PROTEIN SP08 |
| 8802 | 21440 | 34363 | 0.88 | 5.8E-01 | Q27368 | SWISSPROT | Homo sapiens partial TGF-4 gene for T-cell transcription factor-4, exons 6-11 |
| 8903 | 21441 | 34364 | 0.96 | 5.8E-01 | Q20471 | SWISSPROT | TRANSCRIPTION FACTOR E2F |
| 9514 | 22014 | | 0.89 | 5.8E-01 | BF031606.1 | EST_HUMAN | PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X |
| 10869 | 23380 | 36405 | 9.44 | 5.8E-01 | AJ243213.1 | NT | P01557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827288 5' |
| 10915 | 23434 | | 3.66 | 5.8E-01 | BF700082.1 | EST_HUMAN | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 11021 | 23535 | | 2.04 | 5.8E-01 | BF700082.1 | EST_HUMAN | 602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5' |
| 3078 | 15694 | | 0.86 | 5.7E-01 | 6766263 | NT | 602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5' |
| 3260 | 15872 | 26352 | 1.56 | 5.7E-01 | Q9W1J2 | SWISSPROT | Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVOT1) (MOVOT1) |
| 3552 | 16156 | | 2.63 | 5.7E-01 | AB033503.1 | NT | Populus euphratica peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds |
| 3973 | 16571 | 28041 | 3.08 | 5.7E-01 | AF011591.1 | NT | Homo sapiens T cell receptor beta chain (BV6S72-BJ1S1) mRNA, partial cds |
| 6498 | 19097 | 31881 | 3.67 | 5.7E-01 | BF035413.1 | EST_HUMAN | 601454982F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5' |
| 6812 | 19403 | 32219 | 0.72 | 5.7E-01 | AA194201.1 | EST_HUMAN | zr38c08.r1 Soares_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:685674 5' |
| 6945 | 18053 | 30478 | 1.26 | 5.7E-01 | AL111440.1 | NT | Bethyis chinensis strain T4 cDNA library under conditions of nitrogen deprivation |
| 7741 | 20249 | 33142 | 1.97 | 5.7E-01 | P00373 | SWISSPROT | PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR)(P5C REDUCTASE) |
| 7911 | 20453 | | 0.57 | 5.7E-01 | AJ251835.1 | NT | Mus musculus Kcrq1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts |
| 9715 | 22213 | 35186 | 1.17 | 5.7E-01 | AL161532.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32 |
| 9715 | 22213 | 35187 | 1.17 | 5.7E-01 | AL161532.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32 |
| 10468 | 22662 | 35973 | 0.86 | 5.7E-01 | BF540982.1 | EST_HUMAN | 602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068810 5' |
| 3410 | 16019 | 28498 | 1 | 5.6E-01 | AB018283.2 | NT | Homo sapiens mRNA for KIAA0740 protein, partial cds |
| 3410 | 16019 | 28499 | 1 | 5.6E-01 | AB018283.2 | NT | Homo sapiens mRNA for KIAA0740 protein, partial cds |
| 4324 | 16910 | 28351 | 0.89 | 5.6E-01 | D83135.1 | NT | Chicken TBP gene, second, complete cds |
| 8738 | 21277 | 34200 | 4.42 | 5.6E-01 | AV684703.1 | EST_HUMAN | AV/684703 GKc Homo sapiens cDNA clone GKCF5R05 5' |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8738 | 21277 | 34201 | 4.42 | 5.6E-01 | AV684703.1 | EST_HUMAN | AV684703 GKX Homo sapiens cDNA clone GKCF5F05 5' |
| 9297 | 21897 | 34844 | 1.11 | 6.6E-01 | AB038782.1 | NT | Homo sapiens MUC3A gene for intestinal mucin, partial cds |
| 11658 | 24085 | | 2.5 | 5.6E-01 | BE888280.1 | EST_HUMAN | 601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5' |
| 11779 | 24168 | 36775 | 1.28 | 5.6E-01 | AA493535.1 | EST_HUMAN | 1075g10.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:940874 similar to contains element PTR7 repetitive element: |
| 12156 | 18028 | 30490 | 3.31 | 5.6E-01 | AL161501.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13 |
| 12185 | 24419 | | 2.58 | 5.6E-01 | P50505 | SWISSPROT | HIGH AFFINITY POTASSIUM TRANSPORTER |
| 12619 | 24698 | | 3.11 | 5.6E-01 | BF573828.1 | EST_HUMAN | 602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5' |
| 1253 | 13650 | 26367 | 1.13 | 5.5E-01 | 8383912 | NT | Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA |
| 2725 | 15280 | 27847 | 13.6 | 5.5E-01 | P03341 | SWISSPROT | GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |
| 2725 | 15280 | 27848 | 13.6 | 5.5E-01 | P03341 | SWISSPROT | GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |
| 2843 | 15559 | 28033 | 0.69 | 5.5E-01 | 5902085 | NT | Homo sapiens superkiller virulence activity 2 (S. cerevisiae homolog)-like (SKV2L), mRNA |
| 3102 | 15717 | | 1.51 | 5.5E-01 | H46219.1 | EST_HUMAN | Y018a10.s1 Soares adult brain N2b5tHB55Y Homo sapiens cDNA clone IMAGE:178266 3' |
| 3271 | 15883 | 28365 | 2.68 | 5.5E-01 | AF227240.1 | NT | Rabbit oral papillomavirus, complete genome |
| 3755 | 16356 | 28825 | 0.97 | 5.5E-01 | P48755 | SWISSPROT | FOS-RELATED ANTIGEN-1 |
| 8386 | 20928 | 33846 | 0.68 | 5.5E-01 | A1791768.1 | EST_HUMAN | cr2b201.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5' |
| 9082 | 22161 | | 0.74 | 5.5E-01 | U88415.1 | NT | Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds |
| 10279 | 22774 | 35763 | 0.84 | 5.5E-01 | T05047.1 | EST_HUMAN | EST02835 Fetal brain, Strabagene (cat#836206) Homo sapiens cDNA clone HFBCCQ35 |
| 151 | 12814 | 25301 | 12.97 | 5.4E-01 | 7657268 | NT | Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 161 | 12814 | 25302 | 12.97 | 5.4E-01 | 7657268 | NT | Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA |
| 611 | 13239 | 25713 | 1.6 | 5.4E-01 | AF232008.1 | NT | Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes |
| 611 | 13239 | 25714 | 1.6 | 5.4E-01 | AF232008.1 | NT | Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes |
| 1314 | 13908 | 28428 | 2.58 | 5.4E-01 | AW896087.1 | EST_HUMAN | QV4NN0040-070400-160-c04 NN0040 Homo sapiens cDNA |
| 2154 | 14731 | | 3.6 | 5.4E-01 | AE002247.2 | NT | Chlamydia pneumoniae AR39, section 74 of 94 of the complete genome |
| 2298 | 14870 | 27446 | 2.18 | 5.4E-01 | AJ276682.1 | NT | Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene) |
| 3384 | 16582 | 28053 | 0.62 | 5.4E-01 | U07561.1 | NT | Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds |
| 6269 | 17822 | | 1.04 | 5.4E-01 | AW747872.1 | EST_HUMAN | QV0-BT0041-061088-033-c02 BT0041 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed In Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5388 | 13239 | 25713 | 0.59 | 5.4E-01 | AF232008.1 | NT | <i>Pseudomonas syringae</i> pv. tomato strain DC3000 AwE (awE), <i>HrpW</i> (hrpW), and <i>GstA</i> (gstA) genes, complete cds; and unknown genes |
| 5388 | 13239 | 25714 | 0.59 | 5.4E-01 | AF232008.1 | NT | <i>Pseudomonas syringae</i> pv. tomato strain DC3000 AwE (awE), <i>HrpW</i> (hrpW), and <i>GstA</i> (gstA) genes, complete cds; and unknown genes |
| 5838 | 18482 | 31185 | 0.81 | 5.4E-01 | AW842327.1 | EST_HUMAN | PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA |
| 6338 | 18944 | 31723 | 1.49 | 5.4E-01 | AB025017.1 | NT | <i>Rattus norvegicus</i> gene for TIS11, complete cds |
| 7084 | 18885 | 32504 | 1.1 | 5.4E-01 | BE98582.2 | EST_HUMAN | 607680278R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:38060890 3' |
| 7374 | 18900 | 32762 | 0.75 | 5.4E-01 | Z21619.1 | NT | <i>S. cerevisiae</i> RIB3 gene encoding DBP synthase |
| 7374 | 18900 | 32763 | 0.75 | 5.4E-01 | Z21619.1 | NT | <i>S. cerevisiae</i> RIB3 gene encoding DBP synthase |
| | | | | | | | MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE] |
| 7378 | 19902 | 32766 | 1.47 | 5.4E-01 | Q64428 | SWISSPROT | 602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5' |
| 9801 | 22398 | | 1.98 | 6.4E-01 | BF572636.1 | EST_HUMAN | NITRATE REDUCTASE [NADPH] (NIR) |
| 10957 | 23472 | 38497 | 3.25 | 5.4E-01 | P38858 | SWISSPROT | LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) |
| 11485 | 23934 | 37004 | 5.79 | 5.4E-01 | Q60875 | SWISSPROT | LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) |
| 11485 | 23934 | 37005 | 5.79 | 5.4E-01 | Q60875 | SWISSPROT | LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) |
| 11586 | 18944 | 31723 | 2.42 | 5.4E-01 | AB025017.1 | NT | <i>Rattus norvegicus</i> gene for TIS11, complete cds |
| 11725 | 24132 | | 2.52 | 5.4E-01 | A1858368.1 | EST_HUMAN | w437g04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN); |
| | | | | | | | Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, hepcase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes.? |
| 542 | 13173 | 25683 | 2.28 | 5.3E-01 | AF019413.1 | NT | Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA |
| 2811 | 15363 | 27831 | 6.51 | 5.3E-01 | 4506328 | NT | Homo sapiens secreted C-type lectin precursor (LSL CL) gene, complete cds |
| 2811 | 15363 | 27832 | 6.51 | 5.3E-01 | 4506328 | NT | Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA |
| 3280 | 15891 | 28370 | 3.13 | 5.3E-01 | AF087658.1 | NT | Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA |
| 4280 | 16876 | | 1.39 | 5.3E-01 | U39887.1 | NT | Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA |
| 5649 | 18277 | 30753 | 1.91 | 5.3E-01 | A1820821.1 | EST_HUMAN | Myoplasma genitalium section 9 of 51 of the complete genome |
| 5649 | 18277 | 30754 | 1.91 | 5.3E-01 | A1820821.1 | EST_HUMAN | z142h12.j6 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:740711 5' |
| 5742 | 18388 | 31075 | 0.87 | 5.3E-01 | AA193872.1 | EST_HUMAN | z142g09.f1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:688112 5' |
| 5742 | 18388 | 31076 | 0.87 | 5.3E-01 | AA193872.1 | EST_HUMAN | z142g09.f1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:688112 5' |
| | | | | | | | 7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 |
| 5827 | 18451 | 31174 | 1.84 | 5.3E-01 | BE645620.1 | EST_HUMAN | PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN); |
| 5827 | 18451 | 31175 | 1.84 | 5.3E-01 | BE645620.1 | EST_HUMAN | PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN); |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8835 | 21374 | | 1.83 | 5.3E-01 | L01950.2 | NT | Ribulose biphosphate carboxylase (rbcl.) gene, partial cds; chloroplast gene for chloroplast product |
| 8885 | 21423 | 34348 | 0.63 | 5.3E-01 | BF433956.1 | EST_HUMAN | 7q71c12.x1 NC1_CGAP_L124 Homo sapiens cDNA clone IMAGE:3 similar to contains element MER29 repetitive element: |
| 8885 | 21423 | 34349 | 0.63 | 5.3E-01 | BF433956.1 | EST_HUMAN | 7q71c12.x1 NC1_CGAP_L124 Homo sapiens cDNA clone IMAGE:3 similar to contains element MER29 repetitive element: |
| 10112 | 22807 | 35597 | 0.48 | 5.3E-01 | AB54210.1 | EST_HUMAN | w94b02.x1 NC1_CGAP_Met15 Homo sapiens cDNA clone IMAGE:2561275 3' similar to SW-COXa_HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR: |
| 11435 | 23885 | 36952 | 6.92 | 5.3E-01 | BE566281.1 | EST_HUMAN | 601339867F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3692168 5' |
| 11650 | 24881 | | 4.22 | 5.3E-01 | AA918053.1 | EST_HUMAN | cg30a05.s1 NC1_CGAP_Br7 Homo sapiens cDNA clone IMAGE:141378 3' similar to gb:J02811 APOLIPROTEIN D PRECURSOR (HUMAN); |
| 849 | 13465 | 25973 | 19.16 | 5.2E-01 | L20770.1 | NT | Drosophila melanogaster helix-loop-helix mRNA, complete cds |
| 1208 | 13808 | 28319 | 10.07 | 5.2E-01 | Q8WV30 | SWISSPROT | NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5) |
| 1233 | 13632 | 26348 | 2.91 | 5.2E-01 | AF224492.1 | NT | Homo sapiens phospholipid scramblase 1 gene, complete cds |
| 1830 | 14514 | | 4.11 | 5.2E-01 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 2191 | 14767 | 27339 | 2.97 | 5.2E-01 | AB018283.2 | NT | Homo sapiens mRNA for KIAA0740 protein, partial cds |
| 3163 | 15767 | 28233 | 1.67 | 5.2E-01 | U65942.1 | NT | Chlamydomonas abortus strain S203 POMF91A and POMF90A precursor, genes, complete cds |
| 3274 | 15888 | | 0.71 | 5.2E-01 | D73443.1 | NT | Azotobacter vinelandii lcd gene for isocitrate dehydrogenase, complete cds |
| 3452 | 16059 | | 1.74 | 5.2E-01 | AL116780.1 | NT | Bovine cDNA library under conditions of nitrogen deprivation |
| 3492 | 16097 | 28572 | 2.49 | 5.2E-01 | AA984165.1 | EST_HUMAN | am77g05.s1 Strabegene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3' |
| 3694 | 16285 | | 0.92 | 5.2E-01 | AF020269.1 | NT | Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds |
| 5161 | 17730 | | 0.87 | 5.2E-01 | 7106444 | NT | Mus musculus vanilloid receptor-like protein 1 (VHL), mRNA |
| 5314 | 17878 | | 0.89 | 5.2E-01 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 5834 | 18458 | 31179 | 0.97 | 5.2E-01 | AA284281.1 | EST_HUMAN | z044408.T7 Saccharomyces cerevisiae NthSF Homo sapiens cDNA clone IMAGE:325169 3' |
| 9046 | 24795 | 35115 | 1.19 | 5.2E-01 | X02218.1 | NT | Chicken duplicated genes for histone H2A, H4 and a histone H3 gene |
| 9046 | 24795 | 35116 | 1.19 | 5.2E-01 | X02218.1 | NT | Chicken duplicated genes for histone H2A, H4 and a histone H3 gene |
| 9845 | 22343 | 35325 | 0.64 | 5.2E-01 | AA194518.1 | EST_HUMAN | z050509.J1 Strabegene muscle 937209 Homo sapiens cDNA clone IMAGE:628793 5' |
| 9840 | 22435 | 35411 | 1.65 | 5.2E-01 | AF143952.2 | NT | Homo sapiens PELOTA (PELOTA) gene, complete cds |
| 12580 | 24682 | | 4.94 | 5.2E-01 | P18516 | SWISSPROT | RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA) |
| 645 | 13288 | 25748 | 2.13 | 5.1E-01 | M59509.1 | NT | Human adrenodoxin reductase gene, exons 3 to 12 |
| 676 | 13300 | 25781 | 3.88 | 5.1E-01 | AJ233944.1 | NT | Polypodium vitellinum (strain P1 vt1) 16S rRNA gene |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 676 | 13300 | 25782 | 3.98 | 5.1E-01 | AJ233944.1 | NT | Polyomavirus (strain PI wt1) 16S rRNA gene |
| 1682 | 14284 | | 0.88 | 5.1E-01 | X87885.1 | NT | R. norvegicus mRNA for mammalian fusca protein |
| 2069 | 14949 | | 11.33 | 5.1E-01 | BF683095.1 | EST_HUMAN | 602139319F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4288117 5' |
| 4151 | 16743 | 29197 | 4.61 | 5.1E-01 | A1858495.1 | EST_HUMAN | W39b12.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2427283 3' |
| 4268 | 16852 | 28300 | 3.03 | 5.1E-01 | P66380 | SWISSPROT | TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) |
| 5228 | 17763 | | 0.71 | 5.1E-01 | BE091798.1 | EST_HUMAN | IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA |
| 6422 | 19025 | | 0.79 | 5.1E-01 | AV712328.1 | EST_HUMAN | AV712328 DCA Homo sapiens cDNA clone DCAALU707 5' |
| 6897 | 19495 | 32316 | 1.42 | 5.1E-01 | R80873.1 | EST_HUMAN | y94e09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3' |
| 8507 | 21046 | 33068 | 0.73 | 5.1E-01 | AW806881.1 | EST_HUMAN | QV4-ST0023-160400-172-e01 ST0023 Homo sapiens cDNA |
| 8507 | 21046 | 33067 | 0.73 | 5.1E-01 | AW806881.1 | EST_HUMAN | QV4-ST0023-160400-172-e01 ST0023 Homo sapiens cDNA |
| 9602 | 22102 | 35065 | 4.6 | 5.1E-01 | J05412.1 | NT | Human regenerating protein (reg) gene, complete cds |
| 9605 | 22105 | 35068 | 3.4 | 5.1E-01 | W22302.1 | EST_HUMAN | 6581 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional |
| 10065 | 22580 | 35555 | 0.95 | 5.1E-01 | M94579.1 | NT | Human carboxyl ester lipase (CEL) gene, complete cds |
| 11874 | 24805 | | 2.04 | 5.1E-01 | BF030207.1 | EST_HUMAN | 60155883F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3826767 5' |
| 12128 | 24385 | | 2.01 | 5.1E-01 | BF439882.1 | EST_HUMAN | nuc-511f10.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3408218 3' similar to contains element |
| 2180 | 14757 | 27328 | 1.4 | 5.0E-01 | 4885552 | NT | TAR1 repetitive element ; |
| 2180 | 14757 | 27327 | 1.4 | 5.0E-01 | 4885552 | NT | Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA |
| 2189 | 14785 | 27335 | 5.46 | 5.0E-01 | AF008210.1 | NT | Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA |
| 2189 | 14785 | 27336 | 5.46 | 5.0E-01 | AF008210.1 | NT | Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHIFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene> |
| 3740 | 16341 | 28809 | 5.58 | 5.0E-01 | AE001785.1 | NT | Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHIFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene> |
| 3811 | 16410 | 28875 | 0.85 | 5.0E-01 | U55574.1 | NT | Thermococcus maritima section 97 of 136 of the complete genome |
| 3942 | 16540 | 29008 | 3.11 | 5.0E-01 | AB033010.1 | NT | Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds |
| 8497 | 21007 | | 1.78 | 5.0E-01 | M92304.1 | NT | Homo sapiens mRNA for KIAA1184 protein, partial cds |
| 8604 | 21143 | 34057 | 0.64 | 5.0E-01 | BF107848.1 | EST_HUMAN | Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds |
| 8379 | 20318 | 33219 | 3.1 | 5.0E-01 | BF317212.1 | EST_HUMAN | 60182350R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3' |
| 9543 | 22043 | 35004 | 1.34 | 5.0E-01 | P35573 | SWISSPROT | 601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136832 5' |
| | | | | | | | GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE] (DEXTRIN 8-ALPHA-D-GLUCOSIDASE)] |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9543 | 22043 | 35005 | 1.34 | 5.0E-01 | P35573 | SWISSPROT | GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHIER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] |
| 10291 | 22788 | | 1.04 | 5.0E-01 | BE88218.1 | EST_HUMAN | 601445024F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3849438 5' |
| 11815 | 24187 | | 3.45 | 5.0E-01 | AF029215.1 | NT | Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds |
| 12554 | 24856 | | 2.38 | 5.0E-01 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 12569 | 24868 | | 4.27 | 5.0E-01 | O13861 | SWISSPROT | NUCLEAR ENVELOPE PROTEIN CUT11 |
| 822 | 13439 | 26948 | 2.31 | 4.9E-01 | BF571482.1 | EST_HUMAN | 602076849F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4243860 5' |
| 1689 | 14282 | 26827 | 1.6 | 4.9E-01 | AJ243955.1 | NT | Xenopus laevis mRNA for c-Jun protein, 1978 BP |
| 1949 | 14533 | 27089 | 1.35 | 4.9E-01 | U40869.1 | NT | Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds |
| 5602 | 18231 | 30881 | 1.32 | 4.9E-01 | Q81554 | SWISSPROT | FIBRILLIN 1 PRECURSOR |
| 6187 | 18797 | 31585 | 2.35 | 4.9E-01 | AF020831.1 | NT | Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10 |
| 6187 | 18797 | 31568 | 2.35 | 4.9E-01 | AF020831.1 | NT | Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10 |
| 7475 | 18997 | 32882 | 1.9 | 4.9E-01 | AB040051.1 | NT | Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds |
| 8920 | 21458 | | 1.49 | 4.9E-01 | BF209791.1 | EST_HUMAN | 601874984F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4102503 5' |
| 9115 | 21851 | 34582 | 0.86 | 4.8E-01 | AW339805.1 | EST_HUMAN | h90c02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2807288 3' similar to TR:095714 |
| 9220 | 25126 | | 2.2 | 4.8E-01 | 10948883 | NT | O95714 HERC2 ; |
| 10220 | 22715 | 35708 | 0.74 | 4.8E-01 | AF053880.1 | NT | Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA |
| 11704 | 24117 | | 2.48 | 4.8E-01 | AF178912.1 | NT | Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds |
| 12548 | 25081 | | 5.73 | 4.8E-01 | AA813562.1 | EST_HUMAN | Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds |
| 12555 | 24957 | 30872 | 1.74 | 4.8E-01 | AL163301.2 | NT | h922811.s1 NCI_CGAP_C010 Homo sapiens cDNA clone IMAGE:1144652 3' |
| 12630 | 24708 | | 1.36 | 4.8E-01 | 11431438 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 3591 | 16195 | | 1.05 | 4.8E-01 | AA012842.1 | EST_HUMAN | Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA |
| 4782 | 17011 | | 0.62 | 4.8E-01 | 4504850 | NT | cd32a09.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1525144 3' |
| 5688 | 18324 | 30827 | 8.6 | 4.8E-01 | J02387.1 | NT | Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products |
| 6790 | 18381 | | 4.22 | 4.8E-01 | AA655878.1 | EST_HUMAN | Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds |
| 7357 | 18853 | | 1.85 | 4.8E-01 | 5031650 | NT | nu85f09.s1 NCI_CGAP_AM1 Homo sapiens cDNA clone IMAGE:1217513 |
| 7682 | 20174 | 33061 | 0.87 | 4.8E-01 | AL163209.2 | NT | Homo sapiens reproduction 8 (D8S2288E) mRNA |
| 7738 | 20246 | 33138 | 3.72 | 4.8E-01 | AL161492.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 7738 | 20246 | 33139 | 3.72 | 4.8E-01 | AL161492.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4 |
| | | | | | | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4 |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7848 | 20388 | 33281 | 1.38 | 4.8E-01 | A1820744.1 | EST_HUMAN | y77110.y6 Soares breast 2NH1Bst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element |
| 9169 | 21746 | | 1.13 | 4.8E-01 | BE155148.1 | EST_HUMAN | MER6 repetitive element: |
| 9821 | 22417 | | 0.58 | 4.8E-01 | BF568833.1 | EST_HUMAN | PM1-HT0350-201288-004-b04 HT0350 Homo sapiens cDNA |
| 10807 | 23141 | | 2.02 | 4.8E-01 | X83502.1 | NT | 602184267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5' |
| 11786 | 24170 | | 1.28 | 4.8E-01 | AL163227.2 | NT | S.cerevisiae ORFs from chromosome X |
| 12016 | 24842 | | 3.04 | 4.8E-01 | AF227565.1 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 12846 | 24895 | | 3.36 | 4.8E-01 | AJ132884.1 | NT | Trypanosoma cruzi transposon V1P II SIRE repeat region |
| 8638 | 19234 | 32038 | 8.72 | 4.7E-01 | BF217173.1 | EST_HUMAN | Chlamydomonas reinhardtii cap gene, exons 1-8 |
| 7107 | 19447 | 32263 | 0.78 | 4.7E-01 | AJ204374.1 | EST_HUMAN | 601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086387 5' |
| 7806 | 20349 | 33257 | 0.52 | 4.7E-01 | T11414.1 | EST_HUMAN | q772a09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1756544 3' |
| 7808 | 20349 | 33258 | 0.52 | 4.7E-01 | T11414.1 | EST_HUMAN | hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end |
| 9005 | 21542 | 34473 | 0.6 | 4.7E-01 | 8881501 | NT | hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end |
| 10467 | 22861 | 35972 | 0.79 | 4.7E-01 | AW087791.1 | EST_HUMAN | Rattus norvegicus Spermine binding protein (Sbp), mRNA |
| 10727 | 23253 | | 4.94 | 4.7E-01 | AF102873.1 | NT | xb88e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581580 3' |
| 10963 | 23478 | 36503 | 2.19 | 4.7E-01 | U41069.1 | NT | Influenza A virus isolate HK51697 hemagglutinin (HA) gene, partial cds |
| 11163 | 23870 | 36715 | 11.61 | 4.7E-01 | BF528658.1 | EST_HUMAN | Human collagen alpha2(XI)(COL11A2) gene, exons 6 through 16, and partial cds |
| 11254 | 23784 | 36840 | 2.89 | 4.7E-01 | AW889448.1 | EST_HUMAN | 602043889F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181303 5' |
| 11804 | 24243 | | 1.92 | 4.7E-01 | BE887763.1 | EST_HUMAN | RC8-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA |
| 12036 | 24325 | | 1.33 | 4.7E-01 | AW341561.1 | EST_HUMAN | 601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3812488 5' |
| 12666 | 24736 | | 1.38 | 4.7E-01 | AF000007.1 | NT | hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909188 3' |
| 3797 | 16397 | 28862 | 2.23 | 4.6E-01 | AW818638.1 | EST_HUMAN | Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt. position (7/7) |
| 3806 | 16406 | 28870 | 1.68 | 4.6E-01 | BF683300.1 | EST_HUMAN | RC1-ST0278-040400-018-b08 ST0278 Homo sapiens cDNA |
| 3808 | 16406 | 28871 | 1.68 | 4.6E-01 | BF683300.1 | EST_HUMAN | 602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5' |
| 5323 | 17885 | | 1.03 | 4.6E-01 | M11267.1 | NT | 602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5' |
| 5428 | 17886 | 30390 | 22.08 | 4.6E-01 | AL163248.2 | NT | Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C048 |
| | | | | | | | AMILORIDE-SENSITIVE SODIUM CHANNEL GAMMA-SUBUNIT (EPITHELIAL NA+ CHANNEL GAMMA SUBUNIT) (GAMMA ENAC) (NONVOL TAGE-GATED SODIUM CHANNEL 1 GAMMA SUBUNIT) (SCNEG) (GAMMA NACH) |
| 5440 | 17885 | 30400 | 1.37 | 4.6E-01 | PS1170 | SWISSPROT | |
| 5612 | 18241 | 30680 | 1.12 | 4.6E-01 | BF313583.1 | EST_HUMAN | 601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128472 5' |
| 5612 | 18241 | 30691 | 1.12 | 4.6E-01 | BF313583.1 | EST_HUMAN | 601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128472 5' |
| 5663 | 18280 | 30768 | 3.27 | 4.6E-01 | Q80643 | SWISSPROT | INTERFERON REGULATORY FACTOR 3 (IRF-3) |
| 5663 | 18280 | 30769 | 3.27 | 4.6E-01 | Q80643 | SWISSPROT | INTERFERON REGULATORY FACTOR 3 (IRF-3) |
| 5735 | 18361 | 31067 | 2.39 | 4.6E-01 | BE734781.1 | EST_HUMAN | 601568756F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5748 | 18374 | 31082 | 4.22 | 4.6E-01 | A1247678.1 | EST_HUMAN | q55h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.; |
| 5748 | 18374 | 31083 | 4.22 | 4.6E-01 | A1247678.1 | EST_HUMAN | q55h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.; |
| 5758 | 18382 | 31094 | 1.4 | 4.6E-01 | P20050 | SWISSPROT | MEIOSIS SPECIFIC PROTEIN HOP1 |
| 5828 | 18452 | | 1.05 | 4.6E-01 | AF212124.1 | NT | Andis schwartzii cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product |
| 5907 | 18529 | | 0.88 | 4.6E-01 | BE817247.1 | EST_HUMAN | Pfmo-BNC280-120600-001-F07 BNC280 Homo sapiens cDNA |
| 6058 | 18675 | 31417 | 0.75 | 4.6E-01 | D28215.1 | NT | Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA |
| 6404 | 19007 | 31788 | 1.05 | 4.6E-01 | AE000894.1 | NT | Methanobacterium thermoautotrophicum from bases 1165761 to 1176238 (section 100 of 148) of the complete genome |
| 6865 | 19569 | 32429 | 1.36 | 4.6E-01 | U82332.1 | NT | Emmericella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds |
| 6865 | 19569 | 32430 | 1.38 | 4.6E-01 | U82332.1 | NT | Emmericella nidulans NEMPA (nemPA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds |
| 7712 | 20221 | 33108 | 0.88 | 4.6E-01 | AA493577.1 | EST_HUMAN | nt04h05.s1 NC1_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element; |
| 8282 | 20803 | 33721 | 13.23 | 4.6E-01 | BF697399.1 | EST_HUMAN | 602130953F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4287828 5' |
| 9225 | 21741 | 34684 | 1.04 | 4.6E-01 | P55202 | SWISSPROT | ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE) |
| 9225 | 21741 | 34685 | 1.04 | 4.6E-01 | P55202 | SWISSPROT | ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE) |
| 9583 | 22083 | 35046 | 0.55 | 4.6E-01 | AF162283.1 | NT | Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product |
| 9583 | 22083 | 35047 | 0.55 | 4.6E-01 | AF162283.1 | NT | Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product |
| 9886 | 22383 | 35358 | 2.63 | 4.6E-01 | AI015634.1 | EST_HUMAN | wg73a12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3' |
| 9886 | 22383 | 35359 | 2.63 | 4.6E-01 | AI015634.1 | EST_HUMAN | wg73a12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3' |
| 10870 | 23391 | | 3.09 | 4.6E-01 | P88163 | SWISSPROT | PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL) |
| 10879 | 23400 | 36416 | 4.13 | 4.6E-01 | BE185449.1 | EST_HUMAN | IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA |
| 10879 | 23400 | 36417 | 4.13 | 4.6E-01 | BE185449.1 | EST_HUMAN | IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA |
| 11346 | 23044 | 36054 | 5.52 | 4.6E-01 | AF019369.1 | NT | Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds |
| 11346 | 23044 | 36055 | 5.52 | 4.6E-01 | AF019369.1 | NT | Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds |
| 12854 | 24726 | | 1.26 | 4.6E-01 | M22360.1 | NT | Rat plasma proteinase inhibitor alpha-1-inhibitor III group 3 variants 6J, 12J, 13J, and 17J mRNA, partial cds |

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Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1954 | 14538 | 27094 | 1.89 | 4.5E-01 | AE001831.1 | NT | Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1 |
| 1954 | 14538 | 27085 | 1.89 | 4.5E-01 | AE001831.1 | NT | Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1 |
| 2895 | 15512 | 27982 | 4.77 | 4.5E-01 | AA877088.1 | EST_HUMAN | 255d02.01 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3' |
| 3348 | 15956 | 28431 | 0.84 | 4.5E-01 | AW083781.1 | EST_HUMAN | xc25c06.x1 NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585280 3' similar to gb:L07807 |
| 3348 | 15958 | 28432 | 0.84 | 4.5E-01 | AW083781.1 | EST_HUMAN | DYNAMIN-1 (HUMAN); |
| 3359 | 15967 | 28444 | 5.18 | 4.5E-01 | Q05783 | SWISSPROT | BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN |
| 3424 | 18032 | 28512 | 1.15 | 4.5E-01 | AF128378.1 | NT | PRECURSOR (HSPG) (PERLECAN) (PLC) |
| 4100 | 18884 | | 1.35 | 4.5E-01 | Q28247 | SWISSPROT | Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12 |
| 4149 | 18741 | 29185 | 0.73 | 4.5E-01 | A708808.1 | EST_HUMAN | COLLAGEN ALPHA 5(V) CHAIN |
| 4255 | 18015 | | 4.04 | 4.5E-01 | AW873485.1 | EST_HUMAN | ss86009.x1 Berstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3' |
| 5078 | 17651 | 30092 | 1.18 | 4.5E-01 | BE883445.2 | EST_HUMAN | h60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3' |
| 5427 | 17984 | | 26.74 | 4.5E-01 | AF060185.1 | NT | 60165722R1 NH_MGC_67 Homo sapiens cDNA clone IMAGE:3868023 3' |
| 5737 | 18063 | 31070 | 1.37 | 4.5E-01 | AW808814.1 | EST_HUMAN | Mus musculus proteasome regulator PA28 beta subunit gene, complete cds |
| 6719 | 18313 | | 1.38 | 4.5E-01 | Q00956 | SWISSPROT | QV2-PT0012-140100-031-c09 FT0012 Homo sapiens cDNA |
| 7449 | 19867 | 32834 | 1.89 | 4.5E-01 | M37036.1 | NT | COAT PROTEIN |
| 7804 | 20117 | 32893 | 2.53 | 4.5E-01 | A1858849.1 | EST_HUMAN | Rat nuclear proteins B23.1 and B23.2 |
| 8249 | 20780 | | 0.97 | 4.5E-01 | M32881.1 | NT | w832a02.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2428818 3' similar to TR:Q82923 Q82923 |
| 8342 | 20883 | 33904 | 4.02 | 4.5E-01 | A1848596.1 | EST_HUMAN | SWISNF COMPLEX 170 KDA SUBUNIT ; |
| | | | | | | | D.melanogaster Shaw2 protein mRNA, complete cds |
| | | | | | | | ts56g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282844 3' |
| 8494 | 21033 | 33954 | 0.89 | 4.5E-01 | Q82728 | SWISSPROT | POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE) |
| 8716 | 21255 | | 1.74 | 4.5E-01 | 11444789 | NT | Homo sapiens hypothetical protein DKFZp47G183 (DKFZp47G183), mRNA |
| 8928 | 21457 | 34395 | 0.89 | 4.5E-01 | AE000218.1 | NT | Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome |
| 9833 | 22351 | | 1.02 | 4.5E-01 | 9830816 | NT | Bombyx mori nuclear polyhedrosis virus, complete genome |
| 10389 | 22883 | 35877 | 23.95 | 4.5E-01 | M86008.1 | EST_HUMAN | EST025331 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBCY17 |
| 10389 | 22883 | 35878 | 23.85 | 4.5E-01 | M86008.1 | EST_HUMAN | EST025331 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBCY17 |
| 10744 | 23288 | 36285 | 3.01 | 4.5E-01 | AW591271.1 | EST_HUMAN | xc1401.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703885 3' similar to SW:NT8_MOUSE Q84252 VIRAL INTEGRATION SITE PROTEIN INT-6 [1]; |
| 11131 | 23639 | | 1.9 | 4.5E-01 | AV719382.1 | EST_HUMAN | AV719382 GLC Homo sapiens cDNA clone GLOCED12 5' |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11378 | 23828 | 36880 | 1.68 | 4.5E-01 | BE068472.1 | EST_HUMAN | RC3-BT0333-160300-018-e03 BT0333 Homo sapiens cDNA |
| 11871 | 26070 | | 3.3 | 4.5E-01 | BE871481.1 | EST_HUMAN | 60144820F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3652861 5' |
| 12370 | 24540 | | 2.13 | 4.5E-01 | BF337531.1 | EST_HUMAN | 602035275F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183280 5' |
| 12442 | 24578 | | 6.25 | 4.5E-01 | 11422000 | NT | Homo sapiens testis-specific kinase 2 (TESK2), mRNA |
| 2081 | 14662 | | 1.39 | 4.4E-01 | 0680503 | NT | Mus musculus integral membrane-associated protein 1 (limap1), mRNA |
| 2432 | 14899 | 27572 | 3.26 | 4.4E-01 | P40785 | SWISSPROT | VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (MEGF RELATED FACTOR) |
| 3357 | 15985 | 28442 | 1.27 | 4.4E-01 | AF058790.1 | NT | Rattus norvegicus SynGAP-b mRNA, complete cds |
| 3357 | 15985 | 28443 | 1.27 | 4.4E-01 | AF058790.1 | NT | Rattus norvegicus SynGAP-b mRNA, complete cds |
| 3361 | 15989 | 28446 | 2.31 | 4.4E-01 | BF086728.1 | EST_HUMAN | 7891402.Y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3383785 5' |
| 4318 | 16804 | | 1.28 | 4.4E-01 | BE378707.1 | EST_HUMAN | 601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608393 5' |
| 5134 | 17706 | | 2.07 | 4.4E-01 | BE141398.1 | EST_HUMAN | MRO-HT0078-131288-007-g05 HT0078 Homo sapiens cDNA |
| 5277 | 17839 | 30285 | 0.94 | 4.4E-01 | U81154.1 | NT | Buzura suppressaria nucleopolydnavirus ecdysteroid UDP-glucosyltransferase (egt) gene, complete cds |
| 5417 | 17874 | | 0.8 | 4.4E-01 | AW814885.1 | EST_HUMAN | MR1-ST0206-120400-022-g07 ST0206 Homo sapiens cDNA |
| 5613 | 18242 | 30892 | 4.06 | 4.4E-01 | PO4829 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 5613 | 18242 | 30893 | 4.06 | 4.4E-01 | PO4829 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 5887 | 18489 | 31215 | 1.72 | 4.4E-01 | S65019.1 | NT | much [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt] |
| 5883 | 18505 | 31231 | 1.9 | 4.4E-01 | AV720408.1 | EST_HUMAN | AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5' |
| 6108 | 18724 | 31476 | 1.53 | 4.4E-01 | A1189413.1 | EST_HUMAN | q62h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR-Q29168 Q29168 UNKNOWN PROTEIN |
| 6108 | 18724 | 31477 | 1.53 | 4.4E-01 | A1189413.1 | EST_HUMAN | q62h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR-Q29168 Q29168 UNKNOWN PROTEIN |
| 6387 | 18990 | 31771 | 1.69 | 4.4E-01 | AW080785.1 | EST_HUMAN | xc-27e08.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR-O85154 O85154 AFLATOXIN B1-ALDEHYDE REDUCTASE |
| 6470 | 19071 | | 1.02 | 4.4E-01 | AA776132.1 | EST_HUMAN | ae85d11.s1 Stratiotes schizobrain S11 Homo sapiens cDNA clone IMAGE:970865 3' similar to gb.M16038 TYROSINE-PROTEIN KINASE LYN (HUMAN); |
| 7429 | 19853 | 32818 | 0.89 | 4.4E-01 | AE000571.1 | NT | Helicobacter pylori 26695 section 49 of 134 of the complete genome |
| 7782 | 20325 | | 10.05 | 4.4E-01 | Z11679.1 | NT | S. luteusum mRNA for induced stolon tip protein (partial) |
| 8688 | 21237 | 34160 | 1.01 | 4.4E-01 | AA058427.1 | EST_HUMAN | z68a03.s1 Stratiotes schizobrain (#637204) Homo sapiens cDNA clone IMAGE:508836 3' |
| 9078 | 21814 | 34549 | 0.76 | 4.4E-01 | AF112540.1 | NT | HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds |
| 9111 | 21847 | 34587 | 0.56 | 4.4E-01 | AW612578.1 | EST_HUMAN | h05c08.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 |
| 8214 | 21731 | 34874 | 1.13 | 4.4E-01 | O62836 | SWISSPROT | ZINC FINGER X-CHROMOSOMAL PROTEIN |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9872 | 22369 | 35347 | 1.69 | 4.4E-01 | A1268650.1 | EST_HUMAN | q03909.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910821 3' |
| 9873 | 22370 | | 2.12 | 4.4E-01 | P28822 | SWISSPROT | GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14) |
| 10009 | 22504 | 35495 | 4.51 | 4.4E-01 | P35590 | SWISSPROT | TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR |
| 10276 | 22771 | 35759 | 1.43 | 4.4E-01 | S76404.1 | NT | beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2] |
| 10276 | 22771 | 35760 | 1.43 | 4.4E-01 | S76404.1 | NT | beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2] |
| 11939 | 24271 | 31016 | 4.68 | 4.4E-01 | 6877874 | NT | Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA |
| 11952 | 25000 | | 14.98 | 4.4E-01 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 12517 | 24635 | | 1.5 | 4.4E-01 | P54725 | SWISSPROT | UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A) |
| 436 | 13069 | 25584 | 1.77 | 4.3E-01 | AF155218.1 | NT | Calitritix jacobus MW/LW opsin gene, upstream flanking region |
| 436 | 13069 | 25585 | 1.77 | 4.3E-01 | AF155218.1 | NT | Calitritix jacobus MW/LW opsin gene, upstream flanking region |
| 3096 | 15711 | 28182 | 0.91 | 4.3E-01 | AW698477.1 | EST_HUMAN | MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA |
| 4231 | 16819 | 29268 | 1.21 | 4.3E-01 | J00306.1 | NT | Human somatostatin 1 gene and flanks |
| 4495 | 13069 | 25584 | 3.96 | 4.3E-01 | AF155218.1 | NT | Calitritix jacobus MW/LW opsin gene, upstream flanking region |
| 4495 | 13069 | 25585 | 3.96 | 4.3E-01 | AF155218.1 | NT | Calitritix jacobus MW/LW opsin gene, upstream flanking region |
| 5567 | 18188 | 30645 | 0.76 | 4.3E-01 | P48634 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 5567 | 18188 | 30646 | 0.76 | 4.3E-01 | P48634 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 6049 | 18688 | 31407 | 1.34 | 4.3E-01 | BE181655.1 | EST_HUMAN | QV1-HT0638-070500-181-408 HT0638 Homo sapiens cDNA |
| 6065 | 18682 | 31424 | 2.06 | 4.3E-01 | AF179825.1 | NT | Salimiri sciureus olfactory receptor (SSC186) gene, partial cds |
| 6809 | 19400 | 32215 | 4.28 | 4.3E-01 | AJ001678.1 | NT | Columix columix japonica ifnG gene |
| 6949 | 19528 | | 0.78 | 4.3E-01 | Q33367 | SWISSPROT | DNA GYRASE SUBUNIT B |
| 7456 | 19860 | | 1.76 | 4.3E-01 | BF348001.1 | EST_HUMAN | 602023134F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158298 5' |
| 8366 | 20906 | | 2.66 | 4.3E-01 | U97040.1 | NT | Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds |
| 9179 | 21756 | 34702 | 0.7 | 4.3E-01 | Y14604.1 | NT | Erwinia amylovora rcsV gene |
| 9642 | 22142 | 35109 | 2.63 | 4.3E-01 | AW630048.1 | EST_HUMAN | hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5' |
| 9642 | 22142 | 35110 | 2.63 | 4.3E-01 | AW630048.1 | EST_HUMAN | hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5' |
| | | | | | | | xt63a05.x1 Soares_NHCoC_cervical_tumor Homo sapiens cDNA clone IMAGE:2968400 3' similar to |
| 10126 | 22623 | 35614 | 0.57 | 4.3E-01 | AW170559.1 | EST_HUMAN | TR:000189 000189 MU-ADAPTIN-RELATED PROTEIN 2 ; |
| 10811 | 19316 | 32451 | 2.52 | 4.3E-01 | AF075629.1 | NT | Equus caballus microsatellite LEX027 |
| 11588 | 24031 | 37101 | 1.54 | 4.3E-01 | A1874332.1 | EST_HUMAN | t284404.x1 NCL_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2283351 3' |
| 11632 | 18198 | 30645 | 1.55 | 4.3E-01 | P48634 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 11632 | 18198 | 30646 | 1.55 | 4.3E-01 | P48634 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 12616 | 24696 | | 2.81 | 4.3E-01 | AJ003022.1 | NT | Streptomyces coelicolor whiH gene |
| 1402 | 15440 | 26524 | 1.39 | 4.2E-01 | Q39102 | SWISSPROT | CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR |
| 1991 | 14573 | | 1.04 | 4.2E-01 | AA761653.1 | EST_HUMAN | n224a09.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288686 3' |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2068 | 14648 | | 1.37 | 4.2E-01 | AF258325.1 | NT | Plasmodium falciparum multidrug resistance protein Pgh1 gene, complete cds |
| 3689 | 16270 | 28738 | 4.91 | 4.2E-01 | AE003947.1 | NT | Xylella fastidiosa, section 93 of Z29 of the complete genome |
| 3689 | 16300 | 28768 | 1 | 4.2E-01 | AI280338.1 | EST_HUMAN | q194b01.x1 Soares_NHt-MP_u_S1 Homo sapiens cDNA clone IMAGE:1878945 3' |
| 3773 | 18014 | | 0.6 | 4.2E-01 | N81203.1 | EST_HUMAN | 788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07879, Z40488 |
| 3948 | 18548 | 28014 | 0.73 | 4.2E-01 | AW83527.1 | EST_HUMAN | QV0-L T0015-180200-127-h01 LT0015 Homo sapiens cDNA |
| 4054 | 18851 | 29118 | 0.88 | 4.2E-01 | Q04888 | SWISSPROT | SOX-8 PROTEIN |
| 4807 | 17395 | 28835 | 4.3 | 4.2E-01 | AA534088.1 | EST_HUMAN | np68h01.s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:987777 similar to gb.M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN); |
| 4895 | 17470 | 28928 | 4.04 | 4.2E-01 | R13467.1 | EST_HUMAN | Y77601.r1 Soares Infant brain IN1B Homo sapiens cDNA clone IMAGE:28278 5' |
| 5232 | 17708 | | 3.77 | 4.2E-01 | U08071.1 | NT | Human familial Alzheimer's disease (STM2) gene, complete cds |
| 5881 | 18514 | 31241 | 1.52 | 4.2E-01 | BF242055.1 | EST_HUMAN | 601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108483 5' |
| 5953 | 18575 | 31308 | 2.16 | 4.2E-01 | AW854182.1 | EST_HUMAN | RC3-CT0254-080400-029-g04 CT0254 Homo sapiens cDNA |
| 6352 | 18957 | 31738 | 1.06 | 4.2E-01 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 7031 | 19565 | 32382 | 10.28 | 4.2E-01 | AU158472.1 | EST_HUMAN | AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3' |
| 7031 | 19565 | 32383 | 10.28 | 4.2E-01 | AU158472.1 | EST_HUMAN | AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3' |
| 7082 | 24776 | 32492 | 1.97 | 4.2E-01 | S82504.1 | NT | Brcal1=breast cancer gene [rats, W.F. spleen, Genomic, 419 nt, segment 2 of 2] |
| 7150 | 19883 | 32524 | 5.91 | 4.2E-01 | AL161547.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47 |
| 7834 | 20476 | 33385 | 2.61 | 4.2E-01 | AW957448.1 | EST_HUMAN | EST369413 IMAGE ressequences, MAGE Homo sapiens cDNA |
| 7834 | 20476 | 33388 | 2.61 | 4.2E-01 | AW957448.1 | EST_HUMAN | EST369413 IMAGE ressequences, MAGE Homo sapiens cDNA |
| 8148 | 20689 | 33602 | 0.55 | 4.2E-01 | 4756039 | NT | Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA |
| 8235 | 21761 | 34708 | 0.52 | 4.2E-01 | U57431.1 | NT | Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds |
| 8235 | 21761 | 34707 | 0.52 | 4.2E-01 | U57431.1 | NT | Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds |
| 8980 | 22377 | | 0.81 | 4.2E-01 | AA705007.1 | EST_HUMAN | z89f01.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462849 3' |
| 10083 | 22578 | 35571 | 0.5 | 4.2E-01 | AF181854.1 | NT | Lassa virus strain 803273 glycoprotein precursor and nucleoprotein genes, complete cds |
| 10390 | 22884 | 35879 | 1.35 | 4.2E-01 | AW865688.1 | EST_HUMAN | MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA |
| 10921 | 23440 | 38461 | 3.68 | 4.2E-01 | AB023488.1 | NT | Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds |
| 11273 | 23728 | 36780 | 2.65 | 4.2E-01 | BE968485.2 | EST_HUMAN | 801680352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3806085 3' |
| 12561 | 24661 | | 1.49 | 4.2E-01 | AV731815.1 | EST_HUMAN | AV731815 HTF Homo sapiens cDNA clone HTFBHH05 5' |
| 1133 | 13736 | 26245 | 1.59 | 4.1E-01 | A1805481.1 | EST_HUMAN | RC-BT091-210189-142 BT091 Homo sapiens cDNA |
| 1142 | 13745 | 26254 | 1.54 | 4.1E-01 | AV705243.1 | EST_HUMAN | AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5' |
| 1142 | 13745 | 26255 | 1.54 | 4.1E-01 | AV705243.1 | EST_HUMAN | AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5' |
| 2735 | 15280 | 27858 | 1.58 | 4.1E-01 | 7705283 | NT | Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA |
| 2807 | 15582 | 28061 | 2.11 | 4.1E-01 | AL161536.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38 |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2967 | 15682 | 28062 | 2.11 | 4.1E-01 | AL161538.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38 |
| 3342 | 15652 | 28428 | 0.68 | 4.1E-01 | AA906344.1 | EST_HUMAN | q94b08.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3' |
| 3839 | 16438 | 28899 | 0.58 | 4.1E-01 | AW961202.1 | EST_HUMAN | EST1373364 IMAGE resequences, MAGG Homo sapiens cDNA |
| 3839 | 16438 | 28900 | 0.58 | 4.1E-01 | AW961292.1 | EST_HUMAN | EST1373364 IMAGE resequences, MAGG Homo sapiens cDNA |
| 4381 | 16848 | 29390 | 2.82 | 4.1E-01 | AJ248207.1 | NT | Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE and isoAF genes |
| 4383 | 16878 | | 0.76 | 4.1E-01 | AA908257.1 | EST_HUMAN | cm33d02.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3' |
| 4774 | 17355 | 29807 | 1.31 | 4.1E-01 | AV747880.1 | EST_HUMAN | AV747880 NPC Homo sapiens cDNA clone NPC8DF10 5' |
| 6141 | 18755 | 31513 | 3.97 | 4.1E-01 | BF681383.1 | EST_HUMAN | 602156580F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4287319 5' |
| 7480 | 19883 | 32848 | 2.74 | 4.1E-01 | U87535.1 | NT | Methanococcus jannaschii section 77 of 150 of the complete genome |
| 7979 | 20521 | 33427 | 1.31 | 4.1E-01 | BF574604.1 | EST_HUMAN | 602133261F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4288238 5' |
| 9019 | 21558 | 34484 | 1.26 | 4.1E-01 | 6755321 | NT | Mus musculus signalling intermediate in Toll pathway-evolutionarily conserved (Sitpec-pending), mRNA |
| 9484 | 21941 | | 0.61 | 4.1E-01 | AF160597.1 | NT | Volvox gymnocaudus Vgym580 cytochrome b (cytb) gene, complete cds, mitochondrial gene for |
| 10184 | 22859 | | 1.26 | 4.1E-01 | AL138076.2 | NT | mitochondrial product |
| 10310 | 22804 | 35786 | 0.79 | 4.1E-01 | AV649578.1 | EST_HUMAN | Campylobacter jejuni NCTC11168 complete genome, segment 3/6 |
| 10401 | 22895 | 35800 | 0.51 | 4.1E-01 | P18584 | SWISSPROT | AV649578 GLC Homo sapiens cDNA clone GLC8VD12 3' |
| 10401 | 22895 | 35891 | 0.51 | 4.1E-01 | P18584 | SWISSPROT | PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59) |
| 10471 | 22885 | | 2.28 | 4.1E-01 | BF348382.1 | EST_HUMAN | PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59) |
| 10719 | 23247 | 36282 | 45.22 | 4.1E-01 | X68700.1 | NT | CM2-HT0137-200989-010-408 HT0137 Homo sapiens cDNA |
| 11270 | 23008 | 36015 | 3.57 | 4.1E-01 | Q08470 | SWISSPROT | Zea mays ZmPMS2 gene for 19 kDa zain protein |
| 12280 | 25049 | | 2.6 | 4.1E-01 | D67875.1 | NT | VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1) |
| 147 | 15408 | | 4.55 | 4.0E-01 | AW847123.1 | EST_HUMAN | Homo sapiens DNA for amyloid precursor protein, complete cds |
| 1077 | 13681 | 28191 | 0.82 | 4.0E-01 | 8404858 | NT | RC2-CT0201-200989-012-410 CT0201 Homo sapiens cDNA |
| 1394 | 13978 | 28505 | 1.51 | 4.0E-01 | AF203478.1 | NT | Laqueus rubellus mitochondrion, complete genome |
| 1532 | 14124 | | 4.1 | 4.0E-01 | 6879258 | NT | Drosophila melanogaster Dalmation (dnt) mRNA, complete cds |
| 2049 | 15458 | 27200 | 1.22 | 4.0E-01 | Z98833.1 | NT | Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA |
| 2049 | 15458 | 27201 | 1.22 | 4.0E-01 | Z98833.1 | NT | Aesobolus limmatus mesc2 gene |
| 2204 | 14780 | 27352 | 17.82 | 4.0E-01 | AE001931.1 | NT | Aesobolus limmatus mesc2 gene |
| 2204 | 14780 | 27353 | 17.82 | 4.0E-01 | AE001931.1 | NT | Deinococcus radiodurans R1 section 68 of 228 of the complete chromosome 1 |
| 2831 | 12811 | 25289 | 1.45 | 4.0E-01 | 6878490 | NT | Deinococcus radiodurans R1 section 68 of 228 of the complete chromosome 1 |
| 2895 | 15511 | 28090 | 1.23 | 4.0E-01 | AL163280.2 | NT | Mus musculus ubiquitin-protein ligase e3 component n-recognition (Ubr1), mRNA |
| 2895 | 15511 | 28091 | 1.23 | 4.0E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 2895 | 15511 | 28091 | 1.23 | 4.0E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3758 | 16359 | 28828 | 2.17 | 4.0E-01 | AF088903.1 | NT | Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds |
| 3889 | 16408 | 28900 | 3.04 | 4.0E-01 | AJ277511.1 | NT | Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1 |
| 3889 | 16408 | 28901 | 3.04 | 4.0E-01 | AJ277511.1 | NT | Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1 |
| 4942 | 17517 | | 8.41 | 4.0E-01 | Q31849 | SWISSPROT | NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST |
| 6069 | 18696 | 31428 | 1.16 | 4.0E-01 | AW970610.1 | EST_HUMAN | EST382691 IMAGE resequences, MAGK Homo sapiens cDNA |
| 6567 | 19165 | 31961 | 0.87 | 4.0E-01 | P27285 | SWISSPROT | STRUCTURAL POLYPEPTIDE (P139) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE] |
| 7777 | 20286 | 33183 | 0.72 | 4.0E-01 | P27546 | SWISSPROT | MICROTUBULE-ASSOCIATED PROTEIN 4 |
| 7869 | 20411 | 33317 | 0.46 | 4.0E-01 | BF082634.1 | EST_HUMAN | MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA |
| 7954 | 20490 | 33408 | 0.99 | 4.0E-01 | AB016025.1 | NT | Homo sapiens OCTN2 gene, complete cds |
| 8836 | 21474 | 34394 | 0.98 | 4.0E-01 | AA323289.1 | EST_HUMAN | EST28068 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat |
| 11443 | 23893 | | 1.95 | 4.0E-01 | BF030262.1 | EST_HUMAN | 601558283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3628092 5' |
| 11568 | 24015 | | 3.52 | 4.0E-01 | L76800.1 | NT | Synechocystis sp. PCC 9413 transposase gene, complete cds |
| 11658 | 24801 | | 2.5 | 4.0E-01 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 12518 | 24936 | | 1.42 | 4.0E-01 | P38049 | SWISSPROT | HYPOTHEICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION |
| 1420 | 14013 | 26543 | 1.98 | 3.9E-01 | AF206618.1 | NT | Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds |
| 2668 | 15226 | 27798 | 3.8 | 3.9E-01 | AB033019.1 | NT | Homo sapiens mRNA for KIAA1183 protein, partial cds |
| 2730 | 15265 | 27851 | 3.79 | 3.9E-01 | X82032.1 | NT | H. sapiens B-myb gene |
| 2730 | 15286 | 27852 | 3.79 | 3.9E-01 | X82032.1 | NT | H. sapiens B-myb gene |
| 3131 | 15745 | 28214 | 3.95 | 3.9E-01 | AJ225896.1 | NT | Stenotrophomonas maltophilia egl, syb2, cys3 genes and orf3 |
| 4153 | 16745 | 29199 | 1.49 | 3.9E-01 | BF582611.1 | EST_HUMAN | 7161401.x1 NC1_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3' |
| 5130 | 17702 | 30136 | 1.86 | 3.9E-01 | BE728687.1 | EST_HUMAN | 601563949F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833689 5' |
| 6090 | 18706 | 31454 | 6.44 | 3.9E-01 | BF208036.1 | EST_HUMAN | 601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5' |
| 8428 | 18028 | 31812 | 0.68 | 3.9E-01 | U82895.2 | NT | Homo sapiens zinc finger protein 82 (ZFP82), expressed-Xg28STS protein (XG28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 7896 | 20438 | 33343 | 0.78 | 3.9E-01 | U79415.1 | NT | Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds |
| 8795 | 21334 | 34269 | 0.73 | 3.9E-01 | AW177011.1 | EST_HUMAN | CM3-CT0105-170898-004-b08 CT0105 Homo sapiens cDNA |
| 8804 | 21343 | | 0.7 | 3.9E-01 | BF348634.1 | EST_HUMAN | 602018944F1 NC1_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158322 5' |
| 9161 | 21696 | 34840 | 1.24 | 3.9E-01 | AW195888.1 | EST_HUMAN | m86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821 |
| | | | | | | | OB4821 KIAA0713 PROTEIN ; |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9484 | 21889 | 34845 | 1.42 | 3.8E-01 | A687337.1 | EST_HUMAN | wp76a02.x1 NCL_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2467688 3' similar to SW_RFX5_HUMAN P48382 BINDING REGULATORY FACTOR.; |
| 9782 | 22280 | 35274 | 3.68 | 3.8E-01 | M19878.1 | NT | Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats |
| 9858 | 22354 | | 0.5 | 3.8E-01 | 11485630 | NT | Porphyra purpurea mitochondrion, complete genome |
| 10071 | 22588 | 35581 | 0.69 | 3.8E-01 | D88722.1 | NT | Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds |
| 10482 | 22886 | 35883 | 0.46 | 3.8E-01 | M18440.1 | NT | Human beta-B2-crystallin (B2-1) gene, exon 4, partial cds |
| 10700 | 23229 | | 1.82 | 3.8E-01 | AV685974.1 | EST_HUMAN | AV685974 GKC Homo sapiens cDNA clone GKCBQC11 5' |
| 11729 | 24977 | | 3.42 | 3.8E-01 | AF304354.1 | NT | Homo sapiens proteoglycan 3 (PRG3) gene, complete cds |
| 11854 | 24214 | | 1.42 | 3.8E-01 | Q61670 | SWISSPROT | HOMEOBOX PROTEIN HLX1 |
| 11880 | 24285 | 31015 | 1.58 | 3.8E-01 | AE001811.1 | NT | Thermotoga maritima section 123 of 136 of the complete genome |
| 12389 | 24551 | | 1.37 | 3.8E-01 | 11433335 | NT | Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA |
| 171 | 12834 | | 19.28 | 3.8E-01 | 7018488 | NT | Homo sapiens protein kinase PKNbeta (pknbeta), mRNA |
| 531 | 13182 | | 3.11 | 3.8E-01 | AB029281.1 | NT | Mus musculus pcn-1 mRNA for pericentriolar material-1, complete cds |
| 1811 | 14488 | | 0.89 | 3.8E-01 | AE003870.1 | NT | Xylella fastidiosa, section 18 of 229 of the complete genome |
| 2805 | 15167 | 27734 | 1.89 | 3.8E-01 | AF214117.1 | NT | Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds |
| 2881 | 15473 | 27781 | 3.94 | 3.8E-01 | 8578002 | NT | Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA |
| 3034 | 15650 | | 0.89 | 3.8E-01 | AJ251057.1 | NT | Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP-1213) |
| 3084 | 15889 | 28173 | 2.2 | 3.8E-01 | AF043383.1 | NT | Pleurococcus americanus aminopeptidase N (ampN) gene, partial cds |
| 3530 | 16135 | 28815 | 9.83 | 3.8E-01 | AL161518.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30 |
| 3582 | 16188 | | 0.59 | 3.8E-01 | AB072719.1 | EST_HUMAN | wf38b12.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2357855 3' |
| 3609 | 16188 | | 0.75 | 3.8E-01 | AB072719.1 | EST_HUMAN | wf38b12.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2357855 3' |
| 3820 | 16420 | 28882 | 0.94 | 3.8E-01 | BE154080.1 | EST_HUMAN | PMO-H10339-200400-010-G01 HTD339 Homo sapiens cDNA |
| 3989 | 16587 | 29058 | 0.8 | 3.8E-01 | 6754096 | NT | Mus musculus general transcription factor III (Gt2), mRNA |
| 4138 | 16730 | 29183 | 0.69 | 3.8E-01 | AJ271361.2 | NT | Takifugu rubripes wt12 (partial), frank1, cfr and frank2 (partial) genes |
| 5271 | 17833 | 30259 | 0.89 | 3.8E-01 | BE544853.1 | EST_HUMAN | 601074110F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154 5' |
| | | | | | | | yf8a11.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:210428 5' similar to gb U87833 HUMALU384 Human carcinoma cell-derived Alu RNA transcript. (fRNA); gb U88658 EPIDERMAL GROWTH FACTOR-LIKE CRYPTO PROTEIN (HUMAN); contains Alu repetitive element; contains MER4 repetitive element; |
| 5412 | 17889 | 30378 | 1.07 | 3.8E-01 | H84627.1 | EST_HUMAN | TRANSCRIPTION FACTOR SOX-10 |
| 5794 | 18419 | 31135 | 1.11 | 3.8E-01 | Q04888 | SWISSPROT | p10n protein [mink, Genomic, 2446 nt] |
| 6481 | 18082 | | 0.68 | 3.8E-01 | S48825.1 | NT | QV3-BT0537-271289-049-402 BT0537 Homo sapiens cDNA |
| 6737 | 19331 | 32137 | 5.29 | 3.8E-01 | BE072389.1 | EST_HUMAN | la54f11.x1 Soares total fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:2047817 3' similar to contains Alu repetitive element; |
| 6857 | 19391 | 32423 | 3.97 | 3.8E-01 | A1374601.1 | EST_HUMAN | |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7019 | 19517 | 32339 | 1.33 | 3.8E-01 | AL161513.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25 |
| 7626 | 20045 | | 4.75 | 3.8E-01 | X61597.1 | NT | M. musculus gene for kallikrein-binding protein |
| 8238 | 20779 | 33700 | 0.49 | 3.8E-01 | M81385.1 | NT | Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds |
| 8492 | 21031 | 33951 | 2.34 | 3.8E-01 | AB046851.1 | NT | Homo sapiens mRNA for KIAA1631 protein, partial cds |
| 8560 | 21089 | 34019 | 1.14 | 3.8E-01 | 11441284 | NT | Homo sapiens FOS-like antigen-1 (FOSL1), mRNA |
| 8751 | 21280 | 34210 | 1.12 | 3.8E-01 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 9480 | 21879 | | 4.03 | 3.8E-01 | T95413.1 | EST_HUMAN | ye43h06.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element |
| 11408 | 23859 | | 3.5 | 3.8E-01 | BE718219.1 | EST_HUMAN | RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA |
| 11541 | 23989 | 37080 | 2.95 | 3.8E-01 | R42550.1 | EST_HUMAN | Y62h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3' |
| 11541 | 23989 | 37081 | 2.95 | 3.8E-01 | R42550.1 | EST_HUMAN | Y62h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3' |
| 11940 | 24272 | | 2.81 | 3.8E-01 | AE001124.1 | NT | Borrelia burgdorferi (section 10 of 70) of the complete genome |
| 12068 | 24688 | | 1.75 | 3.8E-01 | U94788.1 | NT | Human p53 (TP53) gene, complete cds |
| 12189 | 24421 | | 1.45 | 3.8E-01 | BE829258.1 | EST_HUMAN | QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA |
| 12565 | 24884 | | 2.22 | 3.8E-01 | U78031.1 | NT | Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds |
| 12838 | 24713 | 30886 | 1.25 | 3.8E-01 | AF194972.1 | NT | Mus musculus developmental control protein mRNA, partial cds |
| 2521 | 15085 | 27657 | 15.01 | 3.7E-01 | AB037831.1 | NT | Homo sapiens mRNA for KIAA1410 protein, partial cds |
| 3507 | 16112 | 28589 | 10.94 | 3.7E-01 | AF056336.1 | NT | Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds |
| 3838 | 16538 | 29003 | 0.88 | 3.7E-01 | AA319482.1 | EST_HUMAN | EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end |
| 4313 | 16889 | 29344 | 9.19 | 3.7E-01 | AL218707.1 | EST_HUMAN | ck9c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510186 3' |
| 4412 | 16997 | 29440 | 1.18 | 3.7E-01 | AW878037.1 | EST_HUMAN | MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA |
| 4479 | 17064 | 29514 | 3.13 | 3.7E-01 | AE002408.1 | NT | Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome |
| 5838 | 18557 | 31285 | 1.27 | 3.7E-01 | AF135187.1 | NT | Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds |
| 6105 | 18721 | 31474 | 0.94 | 3.7E-01 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 6633 | 19229 | 32033 | 1 | 3.7E-01 | M10808.1 | NT | Chicken (White Leghorn) delta-1 and delta-2 crystallin genes, complete cds |
| 6651 | 19247 | | 0.81 | 3.7E-01 | L10353.1 | NT | Mus saxicola heptoglobin mRNA, complete cds |
| 7197 | 19728 | 32579 | 4.44 | 3.7E-01 | 11525843 | NT | Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA |
| 8271 | 20812 | 33733 | 1.88 | 3.7E-01 | 11436739 | NT | Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA |
| 8271 | 20812 | 33734 | 1.88 | 3.7E-01 | 11436739 | NT | Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA |
| 8306 | 20847 | 33770 | 0.76 | 3.7E-01 | AA902812.1 | EST_HUMAN | ck43b11.s1 NC1_CGAP_La2 Homo sapiens cDNA clone IMAGE:1516701 3' |
| 9129 | 21664 | | 1.54 | 3.7E-01 | AJ271386.1 | NT | Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene) |
| 10074 | 22569 | | 0.46 | 3.7E-01 | K00691.1 | NT | mouse Ig germline alpha membrane exon region |
| 10111 | 22808 | 35568 | 4.17 | 3.7E-01 | AF388411.1 | EST_HUMAN | qt46b07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950987 3' |
| 10809 | 23428 | 36446 | 3.47 | 3.7E-01 | AJ297357.1 | NT | Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10909 | 23428 | 38447 | 3.47 | 3.7E-01 | AJ287357.1 | NT | Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene |
| 11341 | 23039 | 36048 | 4.81 | 3.7E-01 | X04122.1 | NT | Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31) |
| 11549 | 23907 | | 1.8 | 3.7E-01 | AA973540.1 | EST_HUMAN | ccf6d03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:M77698 |
| 11603 | 24046 | | 2.76 | 3.7E-01 | 6877878 | NT | TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN); |
| 11640 | 24601 | | 1.82 | 3.7E-01 | J04982.1 | NT | Mus musculus retinoblastoma 1 (Rb1), mRNA |
| 11821 | 24191 | | 4.15 | 3.7E-01 | AJ243525.1 | NT | Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds |
| 11913 | 24251 | | 4.72 | 3.7E-01 | D88878.1 | NT | Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1 |
| 12302 | 24489 | | 2.94 | 3.7E-01 | AL121154.1 | EST_HUMAN | Human mRNA for KIAA0223 gene, partial cds |
| 12377 | 24545 | 30804 | 7.01 | 3.7E-01 | Y18000.1 | NT | DKFZp762K075_r1 782 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5' |
| 282 | 12638 | 25424 | 1.07 | 3.6E-01 | AJ009609.1 | NT | Homo sapiens NF2 gene |
| 1033 | 13643 | | 8.45 | 3.6E-01 | U89241.1 | NT | Brassica napus mRNA for MAP4K alpha2 protein |
| 1357 | 13951 | 28477 | 4.32 | 3.6E-01 | T80255.1 | EST_HUMAN | Human mibp gene, partial cds |
| 1357 | 13951 | 28478 | 4.32 | 3.6E-01 | T80255.1 | EST_HUMAN | y03g05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5' |
| 1959 | 14543 | 27089 | 6.39 | 3.6E-01 | AW580184.1 | EST_HUMAN | y03g05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443 5' |
| 1959 | 14543 | 27100 | 6.39 | 3.6E-01 | AW580184.1 | EST_HUMAN | hg33102.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2847419 3' |
| 1994 | 14576 | 27138 | 7.23 | 3.6E-01 | AF216207.1 | NT | hg33102.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2847419 3' |
| 2088 | 14877 | | 0.88 | 3.6E-01 | AF056927.1 | NT | Mus musculus ribosomal protein S19 (Rps19) gene, complete cds |
| 2309 | 14881 | | 1.13 | 3.6E-01 | AB002321.1 | NT | Rattus norvegicus repeat element associated with the Rasgrf1 gene |
| 2433 | 15000 | | 2.49 | 3.6E-01 | X76725.1 | NT | Human mRNA for KIAA0323 gene, partial cds |
| 2528 | 15062 | 27665 | 3.34 | 3.6E-01 | AW812033.1 | EST_HUMAN | P. irregularis (P3804) gene for actin |
| | | | | | | | RC5-STD171-181089-011-g07 ST0171 Homo sapiens cDNA |
| 2859 | 15218 | 27789 | 1.38 | 3.6E-01 | P24206 | SWISSPROT | PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) |
| 2824 | 18012 | | 10.38 | 3.6E-01 | AF169485.1 | NT | Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds |
| 3516 | 16121 | 28600 | 2.16 | 3.6E-01 | X76758.1 | NT | H. sapiens serotonine transporter gene, exons 9 and 10 |
| 3516 | 16121 | 28601 | 2.16 | 3.6E-01 | X76758.1 | NT | H. sapiens serotonine transporter gene, exons 9 and 10 |
| 4497 | 17081 | 28530 | 1.97 | 3.6E-01 | BE707883.1 | EST_HUMAN | RC1-HT0545-150800-014-B12 HT0545 Homo sapiens cDNA |
| 4850 | 17428 | 28680 | 0.94 | 3.6E-01 | AJ009609.1 | NT | Brassica napus mRNA for MAP4K alpha2 protein |
| 4867 | 17443 | 28684 | 0.65 | 3.6E-01 | Y11526.1 | NT | Z. mays mRNA for casein kinase II alpha subunit |
| 5153 | 17723 | 30154 | 2.28 | 3.6E-01 | AW336389.1 | EST_HUMAN | hs02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872568 3' |
| 5261 | 17824 | 30249 | 0.58 | 3.6E-01 | BE067689.1 | EST_HUMAN | MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA |
| 6236 | 18845 | 31616 | 1.16 | 3.6E-01 | P10431 | SWISSPROT | FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E) |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6604 | 18201 | 32008 | 1.88 | 3.0E-01 | Y10198.1 | NT | Homo sapiens PH1EX gene |
| 7202 | 19733 | | 4.57 | 3.0E-01 | R94090.1 | EST_HUMAN | Y74406.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5' |
| 7327 | 19854 | 32717 | 1.73 | 3.0E-01 | AW027174.1 | EST_HUMAN | w472c10.x1 Soares thymus NHFTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117 |
| 8168 | 20707 | 33623 | 0.68 | 3.0E-01 | P98167 | SWISSPROT | O15117 FYN BINDING PROTEIN. [1]; |
| 8221 | 20762 | 33676 | 13.59 | 3.0E-01 | AL161583.2 | NT | SCO-SPONDIN |
| | | | | | | | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79 |
| 8832 | 21470 | 34388 | 3.06 | 3.0E-01 | 4504956 | NT | Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA |
| 8832 | 21470 | 34388 | 3.06 | 3.0E-01 | 4504956 | NT | Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA |
| 9120 | 21658 | 34597 | 1.32 | 3.0E-01 | AL183204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 9320 | 21834 | 34784 | 0.92 | 3.0E-01 | X17550.1 | NT | D. melanogaster singed gene, exons 3, 4, 5 & 6 |
| 9320 | 21834 | 34785 | 0.92 | 3.0E-01 | X17550.1 | NT | D. melanogaster singed gene, exons 3, 4, 5 & 6 |
| 9390 | 21813 | | 0.54 | 3.0E-01 | X62825.1 | NT | C. perfringens plc gene for phospholipase C upstream region containing bent DNA fragment |
| 9777 | 22275 | 35260 | 18.15 | 3.0E-01 | Q53194 | SWISSPROT | PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS |
| 9804 | 22401 | 35374 | 0.53 | 3.0E-01 | AW752801.1 | EST_HUMAN | MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA |
| 9904 | 22401 | 35376 | 0.53 | 3.0E-01 | AW752801.1 | EST_HUMAN | MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA |
| 10823 | 23344 | 36359 | 2.51 | 3.0E-01 | BE902390.1 | EST_HUMAN | 601678418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958897 5' |
| 10987 | 23501 | 36531 | 4.15 | 3.0E-01 | AB004293.1 | NT | Arabidopsis thaliana mRNA for SigB, complete cds |
| 11065 | 23577 | 36815 | 2.02 | 3.0E-01 | L41687.1 | NT | Mus musculus T-cell receptor V region delta 1 chain gene, 5' region |
| | | | | | | | Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome |
| 11318 | 23016 | 36025 | 4.07 | 3.0E-01 | AE000856.1 | NT | Homo sapiens h1b5 gene for hair keratin, exons 1 to 9 |
| 11680 | 25109 | | 2.45 | 3.0E-01 | Y19210.1 | NT | Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome |
| 11788 | 24159 | | 5.79 | 3.0E-01 | AE000335.1 | NT | Mus musculus Enr1 mRNA, complete cds |
| 11823 | 24258 | | 4.7 | 3.0E-01 | U66888.1 | NT | Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (vithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA |
| 12308 | 24502 | | 2.16 | 3.0E-01 | 11432598 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38 |
| 120 | 12781 | 25273 | 1.35 | 3.0E-01 | AL161536.2 | NT | Mus musculus mannose receptor, C type 2 (Mrc2), mRNA |
| 223 | 12884 | 25369 | 2.67 | 3.0E-01 | 6678933 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77 |
| 706 | 13327 | 25814 | 4.48 | 3.0E-01 | AL161581.2 | NT | Homo sapiens GAP-like protein (LOC51306), mRNA |
| 754 | 13373 | 25868 | 1.39 | 3.0E-01 | 7706136 | NT | Homo sapiens GAP-like protein (LOC51306), mRNA |
| 754 | 13373 | 25868 | 1.39 | 3.0E-01 | 7706136 | NT | Homo sapiens GAP-like protein (LOC51306), mRNA |
| 812 | 13430 | 25935 | 3.83 | 3.0E-01 | BF128796.1 | EST_HUMAN | 601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1682 | 14274 | 26807 | 1.91 | 3.5E-01 | U35778.1 | NT | Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds |
| 2322 | 14893 | 27469 | 1.12 | 3.5E-01 | P06708 | SWISSPROT | HOMEOBOX PROTEIN HOXA-4 (HOX-1.4) (MH-3) |
| 2637 | 15472 | 27770 | 1.92 | 3.5E-01 | AA223262.1 | EST_HUMAN | z08a09.s1 Striatagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3' |
| 2729 | 15284 | | 11.8 | 3.5E-01 | U05897.1 | NT | Fibroblast succinoglycogen S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds |
| 3030 | 15946 | 28124 | 0.57 | 3.5E-01 | AA057891.1 | EST_HUMAN | z04f03.r1 Striatagene corneal stroma (#837222) Homo sapiens cDNA clone IMAGE:512285 5' |
| 3878 | 16476 | | 1.27 | 3.5E-01 | AA842138.1 | EST_HUMAN | m00403.s1 NCL CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3' |
| 4349 | 16936 | 29377 | 2.3 | 3.5E-01 | AF071253.1 | NT | Danio rerio homeobox protein (hox5b) gene, complete cds |
| 5014 | 17588 | 30031 | 0.57 | 3.5E-01 | N81203.1 | EST_HUMAN | 788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07878, Z40498 |
| 5066 | 17639 | 30082 | 4.33 | 3.5E-01 | M18349.1 | NT | Rat leukocyte common antigen (L-Ca) gene, exons 1 through 5 |
| 5537 | 18169 | 30583 | 0.74 | 3.5E-01 | Q86887 | SWISSPROT | EARLY E2A DNA-BINDING PROTEIN |
| 5537 | 18169 | 30584 | 0.74 | 3.5E-01 | Q86887 | SWISSPROT | EARLY E2A DNA-BINDING PROTEIN |
| 5738 | 18364 | 31071 | 1.42 | 3.5E-01 | D42045.1 | NT | Human mRNA for KIAA0098 gene, complete cds |
| 6384 | 18988 | | 0.9 | 3.5E-01 | AW863816.1 | EST_HUMAN | PM4-SN0012-030400-001-at11 SN0012 Homo sapiens cDNA |
| 6540 | 19139 | 31932 | 0.75 | 3.5E-01 | AA431833.1 | EST_HUMAN | z07903.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782428 5' similar to TR: 1068935 |
| 6578 | 19176 | 31976 | 0.72 | 3.5E-01 | U37150.1 | NT | G1068935 F10F2.1; |
| 6770 | 19363 | 32172 | 0.93 | 3.5E-01 | O24357 | SWISSPROT | Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds |
| 7116 | 19458 | | 3.51 | 3.5E-01 | X86605.1 | NT | GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD) |
| 8016 | 20558 | | 2.02 | 3.5E-01 | 1148042 | NT | S. scrofa mRNA for CD31 protein (PECAM-1) |
| 8019 | 20561 | 33482 | 0.65 | 3.5E-01 | BF358871.1 | EST_HUMAN | Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA |
| 8403 | 20943 | | 0.61 | 3.5E-01 | AF061691.1 | NT | RC4-ET0024-280900-014-007 ET0024 Homo sapiens cDNA |
| 8857 | 21396 | 34319 | 1.12 | 3.5E-01 | 4507810 | NT | Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds |
| 9851 | 22150 | 35120 | 1.93 | 3.5E-01 | Q02294 | SWISSPROT | Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA |
| 9801 | 22288 | 35284 | 4.91 | 3.5E-01 | Z28825.1 | NT | VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII) |
| 9877 | 22374 | 35351 | 1.14 | 3.5E-01 | BE174794.1 | EST_HUMAN | X. laevis gene for albumin including HP1 enhancer |
| 10613 | 23146 | 36157 | 4 | 3.5E-01 | X61084.1 | NT | QV2-HT0577-080400-128-c07 HT0577 Homo sapiens cDNA |
| 10902 | 23422 | 36440 | 2.09 | 3.5E-01 | AJ243178.1 | NT | C. griseus rhodopsin gene for opsin protein |
| 10902 | 23422 | 36441 | 2.09 | 3.5E-01 | AJ243178.1 | NT | Gallus gallus SPARC gene for osteonectin, promoter and exon 1 |
| 11482 | 23912 | 36978 | 1.93 | 3.5E-01 | N77597.1 | EST_HUMAN | Gallus gallus SPARC gene for osteonectin, promoter and exon 1 |
| 11532 | 23980 | 37050 | 1.71 | 3.5E-01 | L05145.1 | NT | y080h12.r1 Soares_multiple_sclerosis_2NbrMSP Homo sapiens cDNA clone IMAGE:290375 5' |
| | | | | | | | Human glucokinase (GCK) gene, repeat polymorphism |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11778 | 25112 | | 1.51 | 3.5E-01 | AF297468.1 | NT | Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds |
| 11851 | 24211 | | 7.56 | 3.5E-01 | X64565.1 | NT | B.taurus atpA1 gene for F(0F(1)ATP synthase alpha-subunit |
| 12014 | 24313 | | 2.03 | 3.5E-01 | AE001774.1 | NT | Thermotoga maritima section 88 of 138 of the complete genome |
| 12209 | 24433 | | 2.21 | 3.5E-01 | AE001691.1 | NT | Thermotoga maritima section 3 of 138 of the complete genome |
| 12643 | 24950 | 30625 | 2.84 | 3.5E-01 | H80814.1 | EST_HUMAN | ys64f11.J1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5' |
| 12843 | 24950 | 30628 | 2.84 | 3.5E-01 | H80814.1 | EST_HUMAN | ys64f11.J1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5' |
| 736 | 13356 | | 1.5 | 3.4E-01 | AJ242858.1 | NT | Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line |
| 1011 | 13621 | 26136 | 7.62 | 3.4E-01 | Y09798.2 | NT | Pseudomonas fluorescens cdlR, cdlS genes, crf222 and partial inaA gene |
| 1013 | 13623 | 26138 | 8.97 | 3.4E-01 | AW380120.1 | EST_HUMAN | QV3-HT0281-241189-019-g10 HT0281 Homo sapiens cDNA |
| 1371 | 13665 | 28491 | 1.86 | 3.4E-01 | Y00554.1 | NT | Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element) |
| 2445 | 15012 | 27594 | 2.6 | 3.4E-01 | D80809.1 | NT | Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418 |
| 3032 | 15648 | 28126 | 0.73 | 3.4E-01 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3032 | 15648 | 28127 | 0.73 | 3.4E-01 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3163 | 15798 | 28268 | 0.66 | 3.4E-01 | D80809.1 | NT | Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418 |
| 3197 | 15809 | 28282 | 6.78 | 3.4E-01 | U83905.1 | NT | Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds |
| 3387 | 15896 | 28473 | 0.84 | 3.4E-01 | AF034862.1 | NT | Homo sapiens pulmonary surfactant protein D, promoter region and exon 1 |
| 3594 | 16188 | 28671 | 4.84 | 3.4E-01 | AF106835.1 | NT | Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds |
| 3858 | 16456 | | 1.32 | 3.4E-01 | BF449010.1 | EST_HUMAN | 7H94a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8LU15 |
| 4108 | 16702 | | 1.23 | 3.4E-01 | AF184614.1 | NT | Q8LU15 DJ18C9.1 ; |
| 4126 | 16718 | | 1.56 | 3.4E-01 | AA584196.1 | EST_HUMAN | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 4594 | 17177 | 28624 | 0.7 | 3.4E-01 | AF166341.1 | NT | no11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3' |
| 4749 | 17330 | 28773 | 2 | 3.4E-01 | BE068912.1 | EST_HUMAN | Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23 |
| 4765 | 17348 | 28795 | 1.01 | 3.4E-01 | BF314688.1 | EST_HUMAN | MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA |
| 5087 | 17660 | | 4.2 | 3.4E-01 | A1240873.1 | EST_HUMAN | 601901632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130335 5' |
| 5864 | 18486 | 31210 | 2.9 | 3.4E-01 | AL101594.2 | NT | q85c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1667208 3' similar to contains Alu repetitive element |
| 5979 | 18569 | | 5.68 | 3.4E-01 | AA065313.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80 |
| 6158 | 18771 | | 2.44 | 3.4E-01 | U02871.1 | NT | zn12d11.s1 Streptococcus hnt neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3' |
| | | | | | | | Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6181 | 18791 | 31560 | 0.69 | 3.4E-01 | BE748912.1 | EST_HUMAN | 60157181T1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3839826 3' |
| 6258 | 18895 | 31635 | 2.45 | 3.4E-01 | AW204505.1 | EST_HUMAN | UI-H-B11-est-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718582 3' |
| 6382 | 18996 | 31766 | 1.02 | 3.4E-01 | AL120544.1 | EST_HUMAN | DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5' |
| 6841 | 19431 | | 1.32 | 3.4E-01 | N86225.1 | EST_HUMAN | zb53e12.s1 Soares_fetal_lung_NihHL19W Homo sapiens cDNA clone IMAGE:307342 3' |
| | | | | | | EST_HUMAN | hm63g05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 |
| 7027 | 19561 | 32388 | 1.09 | 3.4E-01 | AI468082.1 | EST_HUMAN | LAMININ RECEPTOR (HUMAN); |
| 7847 | 20369 | | 0.51 | 3.4E-01 | AE000493.1 | NT | Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome |
| 8179 | 20720 | 33635 | 0.51 | 3.4E-01 | Y14930.1 | NT | Homo sapiens TCRV28 gene, allele A4, partial |
| 8424 | 20804 | | 1.92 | 3.4E-01 | AA337063.1 | EST_HUMAN | EST41765 Endometrial tumor Homo sapiens cDNA 5' end |
| 8498 | 21037 | 33958 | 0.88 | 3.4E-01 | L04690.1 | NT | Cricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds |
| 8788 | 21325 | 34249 | 1.63 | 3.4E-01 | | NT | Bovine enterovirus strain K2577, complete genome |
| 9139 | 21674 | 34616 | 3.89 | 3.4E-01 | P28013 | SWISSPROT | INTEGRIN BETA-8 PRECURSOR |
| 9139 | 21674 | 34617 | 3.89 | 3.4E-01 | P28013 | SWISSPROT | INTEGRIN BETA-8 PRECURSOR |
| 9342 | 21856 | | 0.59 | 3.4E-01 | AB017610.1 | NT | Epithelial fibroblast mRNA for PLC-gammaS, complete cds |
| 9367 | 20306 | 33208 | 4.77 | 3.4E-01 | U19492.1 | NT | Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds |
| 9367 | 20306 | 33209 | 4.77 | 3.4E-01 | U19492.1 | NT | Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds |
| 9612 | 22112 | 35075 | 0.86 | 3.4E-01 | U88763.1 | NT | Glycine max putative transcription factor SCOF-1 (scsf-1) mRNA, complete cds |
| 9804 | 22302 | 35288 | 1.99 | 3.4E-01 | AJ225084.1 | NT | Homo sapiens FAA gene, exon 16, 17 and 18 |
| 10373 | 22867 | | 0.54 | 3.4E-01 | AE004098.1 | NT | Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome |
| | | | | | | NT | Methanobacterium thermoautotrophicum from bases 1018444 to 1028212 (section 87 of 148) of the complete genome |
| 10895 | 23416 | | 4.42 | 3.4E-01 | AE000881.1 | NT | PROBABLE E4 PROTEIN. |
| 10932 | 23450 | 36471 | 2.61 | 3.4E-01 | P08923 | SWISSPROT | |
| 10989 | 23484 | 36512 | 2.72 | 3.4E-01 | AF045981.1 | NT | Rudius erussii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds |
| 11164 | 23671 | 36716 | 1.89 | 3.4E-01 | M25956.1 | NT | Human von Willebrand factor gene, exons 36 and 37 |
| 11164 | 23671 | 36717 | 1.89 | 3.4E-01 | M25956.1 | NT | Human von Willebrand factor gene, exons 36 and 37 |
| 11372 | 23824 | 36887 | 2.27 | 3.4E-01 | AB035507.1 | NT | Rattus norvegicus mRNA for s-glycerol/ALC18, complete cds |
| 11401 | 23852 | 36917 | 4.36 | 3.4E-01 | AL161515.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 11614 | 24056 | 37121 | 1.75 | 3.4E-01 | BF081948.1 | EST_HUMAN | 7688d12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3480846 3' |
| 11655 | 24082 | | 2.12 | 3.4E-01 | U93604.1 | NT | Citrus variegation virus putative replicase gene, partial cds |
| 11771 | 24180 | | 1.44 | 3.4E-01 | Z21621.1 | NT | S. cerevisiae RIB5 gene encoding Riboflavin synthase |
| 11873 | 24836 | | 1.8 | 3.4E-01 | AF254351.1 | NT | Schistosoma haematobium Cwifp (cwifp) gene, complete cds |
| 11998 | 24303 | | 14.59 | 3.4E-01 | L26339.1 | NT | Human autoantigen mRNA, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12023 | 24865 | | 3.18 | 3.4E-01 | BE218652.1 | EST_HUMAN | h42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13 |
| 12078 | 24974 | | 2.44 | 3.4E-01 | 9838361 | NT | PTR5 repetitive element; |
| 12198 | 24424 | 30650 | 2.68 | 3.4E-01 | AJ297131.1 | NT | Beta vulgaris mitochondrion, complete genome |
| 12427 | 25068 | | 1.25 | 3.4E-01 | AJ288948.1 | NT | Mus musculus SIL_MAP_17, CYP_a, SCL & CYP_b genes |
| | | | | | | | Clostridium cellulosum partial spoVB gene and spoOA gene, strain ATCC 35319 |
| 12623 | 24639 | | 2.55 | 3.4E-01 | AF010413.1 | NT | Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes;> |
| 12651 | 24723 | | 2.71 | 3.4E-01 | 11406174 | NT | Neisseria glabrata mitochondrion, complete genome |
| 16 | 12685 | 25151 | 13.68 | 3.3E-01 | X07980.1 | NT | Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene |
| 110 | 12686 | 25151 | 3.75 | 3.3E-01 | X07980.1 | NT | Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene |
| 473 | 13108 | 25589 | 1.08 | 3.3E-01 | AL161545.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45 |
| 661 | 13265 | 25766 | 1.87 | 3.3E-01 | 7682485 | NT | Homo sapiens KIAA1100 protein (KIAA1100), mRNA |
| 1242 | 13940 | 26358 | 2.96 | 3.3E-01 | Q12448 | SWISSPROT | PROLINE-RICH PROTEIN LAS17 |
| 1350 | 13945 | 26468 | 3.58 | 3.3E-01 | BF568880.1 | EST_HUMAN | 602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4900251 3' |
| 1648 | 14241 | 26775 | 1.43 | 3.3E-01 | 6753685 | NT | Mus musculus disintegrin 5 (Dign5), mRNA |
| 1773 | 14363 | | 1.44 | 3.3E-01 | AA332734.1 | EST_HUMAN | EST38722 Embryo, 8 week I Homo sapiens cDNA 5' end |
| 2075 | 14655 | | 1.22 | 3.3E-01 | AF031148.1 | NT | Methylobacterium capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds |
| 2450 | 15017 | | 5.41 | 3.3E-01 | 4507834 | NT | Homo sapiens uridine monophosphate synthetase (urate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMP5) mRNA |
| 2976 | 15592 | 28074 | 2.14 | 3.3E-01 | AJ251805.1 | NT | Bacteriophage phi-Ye03-12 complete genome |
| 3049 | 15665 | | 0.68 | 3.3E-01 | O02743 | SWISSPROT | INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35) |
| 3061 | 15706 | 28178 | 0.82 | 3.3E-01 | AJ007832.2 | NT | Streptomyces argillaceus nitramycin biosynthetic genes |
| 3542 | 16147 | 28628 | 0.99 | 3.3E-01 | AB012822.1 | NT | Homo sapiens MTA1-L1 gene, complete cds |
| 3882 | 16480 | 28942 | 2.14 | 3.3E-01 | O94645 | SWISSPROT | EXOEXOXYRIBONUCLEASE V BETA CHAIN |
| 3890 | 16489 | 28949 | 0.85 | 3.3E-01 | P22602 | SWISSPROT | GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3] |
| 4037 | 16635 | 29104 | 1.49 | 3.3E-01 | AL161498.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10 |
| 4073 | 16669 | 29130 | 1.95 | 3.3E-01 | AF200446.1 | NT | Hypoxylon fragiforme chitin synthase gene, partial cds |
| 4457 | 17043 | | 1.44 | 3.3E-01 | D31682.1 | NT | Rattus norvegicus DNA for regucalcin, partial cds |
| 4789 | 17377 | | 1.57 | 3.3E-01 | A1539114.1 | EST_HUMAN | tp78b12.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN); |
| 4964 | 17538 | 28980 | 1.44 | 3.3E-01 | D94003.1 | NT | Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766 |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5527 | 18159 | 30573 | 2.75 | 3.3E-01 | X89819.1 | NT | R.norvegicus mRNA for 3'UTR of ubiquitin-like protein |
| 5527 | 18159 | 30574 | 2.75 | 3.3E-01 | X89819.1 | NT | R.norvegicus mRNA for 3'UTR of ubiquitin-like protein |
| 6101 | 18171 | 31468 | 1.72 | 3.3E-01 | BE819650.1 | EST_HUMAN | 601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3' |
| 6101 | 18171 | 31469 | 1.72 | 3.3E-01 | BE819650.1 | EST_HUMAN | 601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3' |
| 6188 | 18798 | 31567 | 12.71 | 3.3E-01 | P05691 | SWISSPROT | CIRCULIMSPOROZOITE PROTEIN (CS) |
| 6869 | 19546 | 32369 | 4.8 | 3.3E-01 | A1628131.1 | EST_HUMAN | tye4h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ; |
| 6869 | 19546 | 32370 | 4.8 | 3.3E-01 | A1628131.1 | EST_HUMAN | tye4h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ; |
| 7758 | 20268 | 33182 | 1.61 | 3.3E-01 | N85148.1 | EST_HUMAN | J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT |
| 8497 | 21038 | 33957 | 17.55 | 3.3E-01 | BF883954.1 | EST_HUMAN | 602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5' |
| 8663 | 21202 | 34120 | 0.48 | 3.3E-01 | BF210322.1 | EST_HUMAN | 601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5' |
| 8696 | 21235 | 34157 | 0.49 | 3.3E-01 | AU128115.1 | EST_HUMAN | AU128115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5' |
| 8696 | 21235 | 34158 | 0.49 | 3.3E-01 | AU128115.1 | EST_HUMAN | AU128115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5' |
| 9042 | 21578 | 34508 | 0.83 | 3.3E-01 | Q62925 | SWISSPROT | MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1) |
| 9300 | 21900 | 34848 | 0.99 | 3.3E-01 | BE828481.1 | EST_HUMAN | CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA |
| 9300 | 21900 | 34849 | 0.99 | 3.3E-01 | BE828481.1 | EST_HUMAN | CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA |
| 9430 | 21939 | 34887 | 3.24 | 3.3E-01 | N69866.1 | EST_HUMAN | z687h01.s1 Soares_fetal_kung_NihHL19W Homo sapiens cDNA clone IMAGE:297849 3' |
| 9471 | 21970 | 34819 | 2.93 | 3.3E-01 | BF376745.1 | EST_HUMAN | RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA |
| 9902 | 22399 | | 2.16 | 3.3E-01 | L41044.1 | NT | Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds |
| 10600 | 23134 | 36147 | 2.83 | 3.3E-01 | X63953.1 | NT | D.mauritiana Adh gene |
| 10600 | 23134 | 36148 | 2.83 | 3.3E-01 | X63953.1 | NT | D.mauritiana Adh gene |
| 10905 | 23424 | | 1.8 | 3.3E-01 | BF628488.1 | EST_HUMAN | 602070802F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4213585 5' |
| 11110 | 23620 | 36861 | 17.52 | 3.3E-01 | BE219351.1 | EST_HUMAN | hw51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3' |
| | | | | | | | GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (ICE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30) |
| 11223 | 23754 | 36812 | 4.97 | 3.3E-01 | P47953 | SWISSPROT | cb71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3' |
| 11565 | 24012 | | 4.68 | 3.3E-01 | AA806821.1 | EST_HUMAN | Rhizobium leguminosarum sym plasmid pRL5LJ nodX gene |
| 11584 | 12895 | 25151 | 2.48 | 3.3E-01 | X07890.1 | NT | Homo sapiens aldehyde oxidase 1 (AOX1), mRNA |
| 11759 | 24153 | 36771 | 1.96 | 3.3E-01 | 6598319 | NT | Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (277) |
| 12510 | 24631 | | 36.28 | 3.3E-01 | AP000002.1 | NT | Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds |
| 482 | 13115 | | 1.79 | 3.2E-01 | AF018261.1 | NT | |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 747 | 13387 | | 0.76 | 3.2E-01 | AL161581.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61 |
| 1204 | 13804 | 26317 | 27.96 | 3.2E-01 | AF047013.1 | NT | Fusarium rose virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds |
| 1325 | 13918 | 26441 | 1.39 | 3.2E-01 | Z50202.1 | NT | P. vulgaris arc5-1 gene |
| 1434 | 14027 | 26555 | 7.37 | 3.2E-01 | Q48624 | SWISSPROT | LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN) |
| 1811 | 14401 | 26946 | 0.92 | 3.2E-01 | Z36041.1 | NT | S. cerevisiae chromosome II reading frame ORF YBR172c |
| 1819 | 14408 | 26954 | 6.36 | 3.2E-01 | AW957194.1 | EST_HUMAN | EST369264 IMAGE resequences, MAGD Homo sapiens cDNA |
| 1819 | 14409 | 26955 | 6.36 | 3.2E-01 | AW957194.1 | EST_HUMAN | EST369264 IMAGE resequences, MAGD Homo sapiens cDNA |
| 1883 | 14468 | 27028 | 1.22 | 3.2E-01 | AL111655.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 2205 | 14781 | 27354 | 2.89 | 3.2E-01 | BF203817.1 | EST_HUMAN | 601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5' |
| 2578 | 15140 | | 2.24 | 3.2E-01 | 7710079 | NT | Mus musculus Pbx/knotted 1 homeobox (Pbxact1), mRNA |
| 2734 | 15288 | 27857 | 1.09 | 3.2E-01 | AF060588.1 | NT | Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds |
| 3668 | 16268 | | 0.78 | 3.2E-01 | D10872.1 | NT | Human h NAT allele 3-2 gene for arylamine N-acetyltransferase |
| 4023 | 16821 | | 0.61 | 3.2E-01 | AL161548.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46 |
| 4483 | 17088 | 28518 | 1.64 | 3.2E-01 | M18818.1 | NT | Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds |
| 4587 | 17181 | 28628 | 1.56 | 3.2E-01 | Q10288 | SWISSPROT | HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR |
| 4844 | 17422 | | 6.52 | 3.2E-01 | BF683817.1 | EST_HUMAN | 602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5' |
| | | | | | | | CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P99) |
| 5009 | 17582 | 30025 | 0.63 | 3.2E-01 | Q57061 | SWISSPROT | 601465581F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868799 5' |
| 5174 | 17741 | 30170 | 0.58 | 3.2E-01 | BE782748.1 | EST_HUMAN | Homo sapiens Interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds |
| 5392 | 17850 | 30363 | 0.93 | 3.2E-01 | AY008947.1 | NT | CMO-HT05689-080300-289-f10 HT05689 Homo sapiens cDNA |
| 5478 | 18110 | 30519 | 2.5 | 3.2E-01 | BE173884.1 | EST_HUMAN | Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes |
| 6112 | 18728 | 31481 | 1.18 | 3.2E-01 | L27221.1 | NT | Human mRNA for KIAA0361 gene, KIAA0361 protein |
| 6831 | 19421 | | 1.03 | 3.2E-01 | AB002359.1 | NT | Rat ISO-atrial natriuretic factor gene, complete cds |
| 8113 | 20654 | 33563 | 1.33 | 3.2E-01 | M60266.1 | NT | Rattus norvegicus repeat, map NOS-D12Wax1 |
| 8210 | 20751 | 33665 | 0.51 | 3.2E-01 | AJ231001.1 | NT | |
| 8308 | 20849 | 33772 | 11.34 | 3.2E-01 | X02508.1 | NT | H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region |
| 8311 | 20852 | 33777 | 16.78 | 3.2E-01 | BF311635.1 | EST_HUMAN | 601867107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5' |
| 8388 | 20838 | | 1.43 | 3.2E-01 | AL161574.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70 |
| 8437 | 20977 | 33891 | 1.22 | 3.2E-01 | BF246771.1 | EST_HUMAN | 601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5' |
| 8437 | 20977 | 33892 | 1.22 | 3.2E-01 | BF246771.1 | EST_HUMAN | 601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5' |
| 8508 | 21047 | 33968 | 2.72 | 3.2E-01 | AE02015.1 | NT | Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1 |
| 8605 | 21144 | 34058 | 0.69 | 3.2E-01 | U51026.1 | NT | Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 8805 | 21144 | 34059 | 0.89 | 3.2E-01 | U51028.1 | NT | Oryzobolus curticulus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds |
| 8897 | 21535 | 34485 | 0.58 | 3.2E-01 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 9007 | 21544 | | 2.08 | 3.2E-01 | M86511.1 | NT | Human monocyte antigen CD14 (CD14) mRNA, complete cds |
| 9077 | 21613 | 34547 | 0.48 | 3.2E-01 | AF041828.1 | NT | Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13 |
| 9077 | 21613 | 34548 | 0.48 | 3.2E-01 | AF041828.1 | NT | Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13 |
| 9805 | 22402 | 35378 | 3.22 | 3.2E-01 | U44914.1 | NT | Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes |
| 10100 | 22585 | 35588 | 0.51 | 3.2E-01 | BE326230.1 | EST_HUMAN | h89805.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181568 3' |
| 10213 | 22708 | | 3.03 | 3.2E-01 | AB011399.1 | NT | Homo sapiens gene for AF-6, complete cds |
| 10548 | 23084 | 36088 | 3.28 | 3.2E-01 | T08813.1 | EST_HUMAN | EST04702 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFB0221 |
| 11786 | 24989 | | 4.31 | 3.2E-01 | L07288.1 | NT | Drosophila melanogaster leminin A (Lam-A) mRNA, complete cds |
| 12344 | 24525 | | 4.85 | 3.2E-01 | O83217 | SWISSPROT | ELONGATION FACTOR TU (EF-TU) |
| 12441 | 24819 | | 3.37 | 3.2E-01 | AF157625.1 | NT | Bos taurus insulin 1,4,5-trisphosphate receptor type I mRNA, complete cds |
| 12488 | 24818 | | 1.94 | 3.2E-01 | L39874.1 | NT | Homo sapiens deoxycytidylate deaminase gene, complete cds |
| 12550 | 25041 | 30504 | 1.98 | 3.2E-01 | BE385778.1 | EST_HUMAN | 801275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3818748 5' |
| 2685 | 15252 | 27823 | 2.39 | 3.1E-01 | R18051.1 | EST_HUMAN | ye801h08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:MB4241 QM PROTEIN (HUMAN); |
| 2722 | 15403 | 27843 | 3.67 | 3.1E-01 | 7681971 | NT | Homo sapiens KIAA0174 gene product (KIAA0174), mRNA |
| 2722 | 15403 | 27844 | 3.67 | 3.1E-01 | 7681971 | NT | Homo sapiens KIAA0174 gene product (KIAA0174), mRNA |
| 2883 | 15501 | | 1.35 | 3.1E-01 | AW628038.1 | EST_HUMAN | h46h08.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2975391 3' |
| 3208 | 15820 | | 3.53 | 3.1E-01 | AB028068.1 | NT | Mus musculus gene for Ser/Thr kinase KIAA0174, exon 8 |
| 3978 | 16578 | 29046 | 0.91 | 3.1E-01 | AJ251598.1 | NT | Daucus carota mRNA for transcription factor E2F (E2F gene) |
| 5055 | 17628 | 30072 | 0.78 | 3.1E-01 | S88245.1 | NT | carbonic anhydrase IV [rats, Sprague-Dawley, lung, mRNA, 1205 nt] |
| 5097 | 17670 | 30109 | 0.82 | 3.1E-01 | AE003984.1 | NT | Xylella fastidiosa, section 130 of 229 of the complete genome |
| 5208 | 17771 | 30194 | 0.98 | 3.1E-01 | AL161503.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15 |
| 5688 | 18298 | 30776 | 10.8 | 3.1E-01 | AF176111.1 | NT | Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1 |
| 5786 | 18411 | 31127 | 0.75 | 3.1E-01 | Z74883.1 | NT | S.cerevisiae chromosome XV reading frame ORF YOL141w |
| 5798 | 18421 | | 0.99 | 3.1E-01 | Y13278.1 | NT | Mus musculus mRNA for polyoystin |
| 5945 | 18565 | 31285 | 2.18 | 3.1E-01 | AF184122.1 | NT | Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22 |
| 6582 | 19189 | 31882 | 2.63 | 3.1E-01 | AJ983549.1 | EST_HUMAN | RC3-HN0001-310300-011-404 HN0001 Homo sapiens cDNA |
| 6854 | 18250 | 32052 | 0.87 | 3.1E-01 | AJ284458.1 | EST_HUMAN | q139d01.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1874689 3' |
| 6784 | 19375 | 32181 | 0.81 | 3.1E-01 | X71887.1 | NT | H.sapiens gene for immunoglobulin kappa light chain variable region AB and A9 |
| 6883 | 19567 | | 0.9 | 3.1E-01 | AW377354.1 | EST_HUMAN | MR2-CT0222-261089-005-h05 CT0222 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7048 | 24741 | 30458 | 2.4 | 3.1E-01 | BE737392.1 | EST_HUMAN | 601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3840420 5' |
| 7671 | 20183 | 33071 | 1.18 | 3.1E-01 | 4885390 | NT | Homo sapiens hyaluronan synthase 2 (HAS2), mRNA |
| 8582 | 21121 | 34041 | 1.22 | 3.1E-01 | R45318.1 | EST_HUMAN | YG46101.s1 Soares infant brain T11B Homo sapiens cDNA clone IMAGE:35639 3' |
| 9818 | 22314 | 35295 | 0.45 | 3.1E-01 | 6878322 | NT | Mus musculus phosphatidylinositol 4-phosphate 5-kinase, type 1 gamma (Pip5K1c), mRNA |
| 9879 | 22474 | 35456 | 0.81 | 3.1E-01 | BF686839.1 | EST_HUMAN | 602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281811 5' |
| 9879 | 22474 | 35457 | 0.81 | 3.1E-01 | BF686839.1 | EST_HUMAN | 602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281811 5' |
| 10035 | 22530 | 35525 | 1.7 | 3.1E-01 | A1244001.1 | EST_HUMAN | q81e11.x1 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S65700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN); |
| 10204 | 22699 | | 0.54 | 3.1E-01 | T55325.1 | EST_HUMAN | y64708.s1 Stratagene fetal spleen (8637205) Homo sapiens cDNA clone IMAGE:74987 3' similar to similar to gb:1461036_m22 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN) |
| 10717 | 23245 | 36261 | 1.86 | 3.1E-01 | BF216117.1 | EST_HUMAN | 601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5' |
| 11411 | 23862 | 36823 | 2.03 | 3.1E-01 | 7662281 | NT | Homo sapiens KIAA0764 gene product (KIAA0764), mRNA |
| 11821 | 24257 | | 2.13 | 3.1E-01 | AF294308.1 | NT | Andis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds, mitochondrial gene for mitochondrial product |
| 11880 | 24282 | | 1.95 | 3.1E-01 | AF304182.1 | NT | Sitosterolemia vitreum 40S ribosomal protein S11 mRNA, partial cds |
| 12108 | 24370 | | 3.31 | 3.1E-01 | AF185953.1 | NT | Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds |
| 12496 | 24624 | | 3.89 | 3.1E-01 | AF108779.1 | NT | Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, complete cds; and L-type calcium channel α |
| 12535 | 25035 | | 1.62 | 3.1E-01 | 10946623 | NT | Mus musculus peptidoglycan recognition protein-like (Pglyrp-pending), mRNA |
| 76 | 15382 | 25234 | 1.37 | 3.0E-01 | 6755083 | NT | Mus musculus protein kinase C, epsilon (Ptkce), mRNA |
| 275 | 12932 | 25419 | 11.51 | 3.0E-01 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 1268 | 13883 | 26380 | 2.05 | 3.0E-01 | AW300400.1 | EST_HUMAN | xs63f08.x1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2774343 3' |
| 1555 | 14147 | 26680 | 6.84 | 3.0E-01 | AJ006755.1 | NT | Balanoptera physalus gene encoding atrial natriuretic peptide |
| 3248 | 15880 | | 1.4 | 3.0E-01 | AB030481.1 | NT | Corynebacterium sp. ALY-1 alyP gene for polydextranase lyase, complete cds |
| 3832 | 16530 | 26897 | 2.1 | 3.0E-01 | AW817785.1 | EST_HUMAN | PM1-ST0262-261189-001-g01 ST0262 Homo sapiens cDNA |
| 4046 | 16643 | 29109 | 1.01 | 3.0E-01 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 4611 | 17184 | 29640 | 1.78 | 3.0E-01 | AJ006755.1 | NT | Balanoptera physalus gene encoding atrial natriuretic peptide |
| 5554 | 18186 | 30601 | 5.34 | 3.0E-01 | BE741629.1 | EST_HUMAN | 601894900F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5' |
| 5627 | 18258 | 30726 | 0.88 | 3.0E-01 | AF228247.1 | NT | Canigado orthopoxvirus hemagglutinin gene, complete cds |
| 5685 | 18321 | 30820 | 4.03 | 3.0E-01 | BE688575.1 | EST_HUMAN | RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA |
| 5685 | 18321 | 30821 | 4.03 | 3.0E-01 | BE688575.1 | EST_HUMAN | RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA |
| 5731 | 18357 | 31062 | 4.57 | 3.0E-01 | U01247.1 | NT | Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds |
| 6819 | 19578 | 32407 | 3.14 | 3.0E-01 | D16131.1 | NT | Mouse cytokeratin 15 gene, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6844 | 18052 | 30476 | 0.7 | 3.0E-01 | U02369.1 | NT | Strongylocentrotus purpuratus 34/87 kDa laminin-binding protein mRNA, partial cds |
| 7005 | 18503 | 32322 | 0.86 | 3.0E-01 | AF229247.1 | NT | Carthago orthopoxvirus hemagglutinin gene, complete cds |
| 7175 | 19707 | 32555 | 0.78 | 3.0E-01 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 7367 | 19893 | 32758 | 6 | 3.0E-01 | 10947007 | NT | Mus musculus midbrain (Midn-pending), mRNA |
| 7512 | 20033 | 32899 | 1.88 | 3.0E-01 | AF071810.1 | NT | Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds |
| 7867 | 20409 | 33318 | 1.07 | 3.0E-01 | AE001755.1 | NT | Thermotoga maritima section 67 of 138 of the complete genome |
| 8314 | 20855 | | 3.82 | 3.0E-01 | 8910101 | NT | Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec9f), mRNA |
| 8411 | 20951 | 33870 | 1.27 | 3.0E-01 | BE589083.1 | EST_HUMAN | 601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5' |
| 8763 | 21302 | 34223 | 0.82 | 3.0E-01 | AF141676.1 | NT | Streptomyces sulfonolactans isopenicillin N synthase (pcbc) gene, partial cds |
| 8805 | 21344 | | 0.95 | 3.0E-01 | 7661685 | NT | Homo sapiens DKFZP680M0122 protein (DKFZP586M0122), mRNA |
| 9145 | 21680 | 34624 | 0.88 | 3.0E-01 | AF220507.1 | NT | Arabidopsis POC7120 cytosine-specific DNA methyltransferase (dmlb) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene |
| 9493 | 21963 | 34949 | 0.55 | 3.0E-01 | P76389 | SWISSPROT | HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASNA INTERGENIC REGION |
| 9878 | 22375 | 35352 | 0.84 | 3.0E-01 | BF574612.1 | EST_HUMAN | 602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288338 5' |
| 10294 | 22788 | 35778 | 0.58 | 3.0E-01 | AW118111.1 | EST_HUMAN | 6030410.X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808035 3' |
| 10296 | 22790 | 35780 | 1.85 | 3.0E-01 | AB030231.1 | NT | Aspergillus oryzae bpa gene for ER chaperone BiP, complete cds |
| 10315 | 22809 | 35801 | 0.73 | 3.0E-01 | BF883841.1 | EST_HUMAN | 602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301087 5' |
| 10315 | 22809 | 35802 | 0.73 | 3.0E-01 | BF883841.1 | EST_HUMAN | 602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301087 5' |
| 11604 | 24047 | 37112 | 2.87 | 3.0E-01 | H51029.1 | EST_HUMAN | yp84b10.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5' |
| 11604 | 24047 | 37113 | 2.87 | 3.0E-01 | H51029.1 | EST_HUMAN | yp84b10.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5' |
| 11975 | 24287 | | 1.37 | 3.0E-01 | PS4680 | SWISSPROT | PONTICULIN PRECURSOR |
| 12227 | 24984 | | 2.93 | 3.0E-01 | AJ297631.1 | NT | Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene) |
| 12529 | 25033 | | 2.51 | 3.0E-01 | 6677788 | NT | Mus musculus ribose 5-phosphate isomerase A (RpiA), mRNA |
| 1824 | 14509 | 27064 | 2.27 | 2.9E-01 | 5174502 | NT | Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA |
| 2070 | 14650 | 27221 | 1.38 | 2.9E-01 | AE000736.1 | NT | Aquifex seductus section 68 of 109 of the complete genome |
| 2524 | 15088 | | 1.22 | 2.9E-01 | M32360.1 | NT | Mouse apolipoprotein A-II (ApoA2) gene, complete cds |
| 3289 | 15900 | 28379 | 2.07 | 2.9E-01 | AW754239.1 | EST_HUMAN | PM1-CT0328-171289-001-412 CT0328 Homo sapiens cDNA |
| 3289 | 15900 | 28380 | 2.07 | 2.9E-01 | AW754239.1 | EST_HUMAN | PM1-CT0328-171289-001-412 CT0328 Homo sapiens cDNA |
| 3965 | 16563 | 29032 | 0.71 | 2.9E-01 | A610836.1 | EST_HUMAN | tp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A |
| 4159 | 18751 | | 0.67 | 2.9E-01 | AW002802.1 | EST_HUMAN | ZINC FINGER PROTEIN (HUMAN) contains element L1 repetitive element; |
| 4583 | 17168 | 28609 | 1.21 | 2.9E-01 | AA284468.1 | EST_HUMAN | z57d12.1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element; |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|---|
| 4793 | 17372 | | 0.63 | 2.9E-01 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 5148 | 17718 | | 1.02 | 2.9E-01 | U80756.1 | NT | Lymnaea dispar vitellogenin gene, complete cds |
| 5154 | 17724 | 30155 | 1.43 | 2.9E-01 | 7682169 | NT | Homo sapiens KIAA0537 gene product (KIAA0537), mRNA |
| 5285 | 17847 | | 1.7 | 2.9E-01 | AI870888.1 | EST_HUMAN | we08003.x1 NCI_CGAP_Kid111 Homo sapiens cDNA clone IMAGE:2297308 3' similar to contains L1.12 L1 repetitive element; |
| 5463 | 18098 | | 1.25 | 2.9E-01 | R37485.1 | EST_HUMAN | y77612.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28281 3' |
| 5562 | 19522 | 32344 | 0.79 | 2.9E-01 | AF321001.1 | NT | Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds |
| 5837 | 18558 | 31286 | 5.1 | 2.9E-01 | X56098.1 | NT | B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase |
| 5837 | 18558 | 31286 | 5.1 | 2.9E-01 | X56098.1 | NT | B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase |
| 5949 | 18570 | 31302 | 6.06 | 2.9E-01 | 6678662 | NT | Mus musculus Eph receptor A8 (EphA8), mRNA |
| 6208 | 18816 | 31587 | 1.28 | 2.9E-01 | AA418145.1 | EST_HUMAN | z697612.r1 Soares NIHIMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5' |
| 6427 | 19030 | 31813 | 0.93 | 2.9E-01 | AI797128.1 | EST_HUMAN | we27c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.11 L1 repetitive element; |
| 6467 | 19068 | 31854 | 2.3 | 2.9E-01 | U03420.1 | NT | Bos taurus myosin I mRNA, complete cds |
| 6585 | 19183 | 31983 | 0.72 | 2.9E-01 | R69194.1 | EST_HUMAN | y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5' |
| 6585 | 19183 | 31984 | 0.72 | 2.9E-01 | R69194.1 | EST_HUMAN | y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5' |
| 7082 | 18081 | 30437 | 1.35 | 2.9E-01 | AF142329.1 | NT | Mus musculus Flii protein (Flii) gene, complete cds; and Flii protein (Flii) gene, partial cds |
| 7153 | 19885 | 32527 | 2.87 | 2.9E-01 | Q04399 | SWISSPROT | PUTATIVE MULTICOPIER OXIDASE YDR508C |
| | | | | | | | Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RafGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr> |
| 7213 | 19744 | 32598 | 1.61 | 2.9E-01 | AF100958.1 | NT | |
| 7860 | 20402 | 33308 | 1.82 | 2.9E-01 | BE540422.1 | EST_HUMAN | 601085830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5' |
| 7860 | 20402 | 33309 | 1.82 | 2.9E-01 | BE540422.1 | EST_HUMAN | 601085830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5' |
| 8103 | 20844 | | 0.88 | 2.9E-01 | BF217743.1 | EST_HUMAN | 601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5' |
| 8531 | 21070 | 33990 | 0.68 | 2.9E-01 | AI150910.1 | EST_HUMAN | AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3' |
| 8856 | 21395 | 34318 | 1.07 | 2.9E-01 | AF225608.1 | NT | Arabidopsis thaliana sulfonylurea receptor-like protein mRNA, complete cds |
| 8963 | 21501 | 34423 | 0.71 | 2.9E-01 | M22452.1 | NT | Baboon lymphocyte homing/adhesion receptor mRNA, complete cds |
| 9170 | 21747 | 34688 | 0.77 | 2.9E-01 | AJ248287.1 | NT | Pyrococcus abyssi complete genome; segment 5/6 |
| 9170 | 21747 | 34690 | 0.77 | 2.9E-01 | AJ248287.1 | NT | Pyrococcus abyssi complete genome; segment 5/6 |
| 10773 | 23287 | 36302 | 2.24 | 2.9E-01 | AJ128843.1 | NT | Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds |
| 11041 | 23555 | 36589 | 2.88 | 2.9E-01 | V01394.1 | NT | Torpedo californica mRNA encoding acetylcholine receptor gamma subunit |
| 11041 | 23555 | 36590 | 2.88 | 2.9E-01 | V01394.1 | NT | Torpedo californica mRNA encoding acetylcholine receptor gamma subunit |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11453 | 23903 | 36970 | 2.07 | 2.9E-01 | AA855373.1 | EST_HUMAN | ny55402.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element; |
| 11458 | 23906 | 36973 | 5.52 | 2.9E-01 | AL139078.2 | NT | Campylobacter jejuni NCTC11168 complete genome; segment 5/6 |
| 12172 | 24411 | 30944 | 1.64 | 2.9E-01 | AW005671.1 | EST_HUMAN | wz8805.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565621 3' similar to contains element |
| 12262 | 24472 | 30832 | 1.47 | 2.9E-01 | AF082453.1 | NT | MER29 repetitive element; |
| 12313 | 24505 | | 1.4 | 2.9E-01 | BE788186.1 | EST_HUMAN | Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds |
| 12588 | 24679 | 30877 | 1.57 | 2.9E-01 | Y08837.1 | NT | 601482059F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5' |
| 12588 | 24679 | 30878 | 1.57 | 2.9E-01 | Y08837.1 | NT | Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus |
| 594 | 13224 | | 2.06 | 2.8E-01 | U67136.1 | NT | Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus |
| 599 | 13228 | | 0.75 | 2.8E-01 | L28145.1 | NT | Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds |
| 1122 | 13725 | 26238 | 3.14 | 2.8E-01 | AF168050.1 | NT | Pruva dwarf virus movement protein, complete cds; coat protein, complete cds |
| 1320 | 13914 | 26435 | 3.51 | 2.8E-01 | BE313442.1 | EST_HUMAN | Guinea guinea oocyte maturation factor Mos (c-mos) gene, partial cds |
| 1320 | 13914 | 26436 | 3.51 | 2.8E-01 | BE313442.1 | EST_HUMAN | 601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5' |
| 1334 | 13928 | 26448 | 1.03 | 2.8E-01 | D86550.1 | NT | 601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5' |
| 1765 | 14355 | 26902 | 2.01 | 2.8E-01 | AW860020.1 | EST_HUMAN | Human mRNA for serine/threonine protein kinase, complete cds |
| 2057 | 14638 | 27210 | 2.12 | 2.8E-01 | AL047620.1 | EST_HUMAN | QV1-CT0364-120200-065-005 CT0364 Homo sapiens cDNA |
| 2175 | 14752 | 27322 | 3.53 | 2.8E-01 | AW511195.1 | EST_HUMAN | DKFZp598I2321_r1 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp598I2321 |
| 2511 | 15075 | 27648 | 2.41 | 2.8E-01 | AE000494.1 | NT | hd44503.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3' |
| 2511 | 15075 | 27649 | 2.41 | 2.8E-01 | AE000494.1 | NT | Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome |
| 2584 | 15147 | | 2.75 | 2.8E-01 | AL161565.2 | NT | Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome |
| 2688 | 15246 | 27813 | 1.21 | 2.8E-01 | AB020975.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65 |
| 2688 | 15614 | | 1.7 | 2.8E-01 | AF179480.1 | NT | Arabidopsis thaliana mRNA for lipoyltransferase, complete cds |
| 2689 | 15615 | 28094 | 2.36 | 2.8E-01 | Z14037.1 | NT | Toxoplasma gondii 80kDa heat-shock protein (HSP90) mRNA, partial cds |
| 2689 | 15615 | 28095 | 2.36 | 2.8E-01 | Z14037.1 | NT | B. taurus microsatellite (ETH121) |
| 3425 | 16033 | 28513 | 1.28 | 2.8E-01 | AP000004.1 | NT | B. taurus microsatellite (ETH121) |
| 4068 | 16894 | 28125 | 2.06 | 2.8E-01 | AE001180.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 777001-884000 nt. position (477) |
| 4202 | 16791 | | 0.62 | 2.8E-01 | AE004450.1 | NT | Borrelia burgdorferi (section 66 of 70) of the complete genome |
| 4276 | 16862 | | 2.75 | 2.8E-01 | AE008888.1 | EST_HUMAN | Pseudomonas aeruginosa PAO1, section 11 of 529 of the complete genome |
| 4553 | -17136 | 29584 | 1.32 | 2.8E-01 | AL021127.2 | NT | ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element/contains element MER22 repetitive element; |
| 4559 | 17142 | 29590 | 2.47 | 2.8E-01 | P13615 | SWISSPROT | Mus musculus chromosome X contigA; putative Mages9 gene, Caltractin, NAD(P) ⁺ steroid dehydrogenase and Zinc finger protein 185 |
| 4887 | 17472 | 29628 | 1.07 | 2.8E-01 | D15050.1 | NT | RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN) |
| | | | | | | | Human mRNA for transcription factor AREB6, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4897 | 17472 | 29629 | 1.07 | 2.8E-01 | D15050.1 | NT | Human mRNA for transcription factor AREB8, complete cds |
| 4937 | 17512 | 29658 | 1.02 | 2.8E-01 | AW594539.1 | EST_HUMAN | hg68405.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2950569 3' |
| 4949 | 17524 | 29665 | 1.17 | 2.8E-01 | AF075238.1 | NT | Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds |
| 4955 | 17530 | 29672 | 3.5 | 2.8E-01 | AF030154.1 | NT | Bovine adenovirus 3 complete genome |
| 4986 | 17560 | 30003 | 1.67 | 2.8E-01 | BF528186.1 | EST_HUMAN | 602042601F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4180129 5' |
| 5013 | 17587 | 30030 | 2.82 | 2.8E-01 | AI272699.1 | EST_HUMAN | gb86c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876828 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element; |
| 5514 | 24744 | 30558 | 21.59 | 2.8E-01 | AA349997.1 | EST_HUMAN | EST57072 Infant brain Homo sapiens cDNA 5' end |
| 5781 | 18416 | 31132 | 2.78 | 2.8E-01 | AB018025.1 | NT | Homo sapiens OCTN2 gene, complete cds |
| 5983 | 18603 | | 0.97 | 2.8E-01 | AW992583.1 | EST_HUMAN | CH1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA |
| 6078 | 18695 | 31442 | 0.69 | 2.8E-01 | AA785286.1 | EST_HUMAN | ca01d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK508-BINDING PROTEIN (HUMAN); |
| 6323 | 25114 | | 0.75 | 2.8E-01 | M36668.1 | NT | Bovine 680 bp repeated unit of 1.723 satellite DNA |
| 6368 | 18970 | 31748 | 1.55 | 2.8E-01 | AF003124.1 | NT | Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds |
| 6368 | 18970 | 31749 | 1.55 | 2.8E-01 | AF003124.1 | NT | Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds |
| 6829 | 19419 | 32235 | 8.4 | 2.8E-01 | BF511215.1 | EST_HUMAN | U1H-B14-4d-4-04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3' |
| 7467 | 19689 | | 1.19 | 2.8E-01 | U05633.1 | NT | Maretea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds |
| 7708 | 20276 | 33174 | 0.69 | 2.8E-01 | BE537151.1 | EST_HUMAN | 601063105F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449568 5' |
| 8036 | 20578 | 33482 | 1.12 | 2.8E-01 | A1346126.1 | EST_HUMAN | gp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1828289 3' similar to gb:X068323_cds1 |
| 8036 | 20578 | 33483 | 1.12 | 2.8E-01 | A1346126.1 | EST_HUMAN | MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN); |
| 8150 | 20681 | 33605 | 2.18 | 2.8E-01 | U51698.1 | NT | gp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1828289 3' similar to gb:X068323_cds1 |
| 8451 | 20991 | 33909 | 0.47 | 2.8E-01 | AA911629.1 | EST_HUMAN | MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN); |
| 8525 | 21064 | | 6.69 | 2.8E-01 | BF347847.1 | EST_HUMAN | Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5 |
| 8987 | 21910 | 34761 | 1.22 | 2.8E-01 | U17251.1 | NT | c02h05.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1419993 3' similar to gb:M67769 IG |
| 9627 | 22127 | | 1.03 | 2.8E-01 | L13654.1 | NT | GAMMA-1 CHAIN C REGION (HUMAN); |
| 9803 | 22301 | 35286 | 1.04 | 2.8E-01 | AF132728.1 | NT | 602022987F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4158525 5' |
| 9803 | 22301 | 35287 | 1.04 | 2.8E-01 | AF132728.1 | NT | Neurospora crassa negative regulator sulfur controller-2 (scot-2) gene, complete cds |
| 9861 | 22558 | 35338 | 0.84 | 2.8E-01 | AF294393.1 | NT | Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds |
| 9972 | 22467 | 35451 | 1.91 | 2.8E-01 | 7706163 | NT | Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds |
| | | | | | | | Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds |
| | | | | | | | Rattus norvegicus glyceral-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product |
| | | | | | | | Homo sapiens hypothetical protein (LOC51319), mRNA |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10215 | 22710 | | 0.81 | 2.8E-01 | 8626154 | NT | Fujinami sarcoma virus, complete genome |
| 10255 | 22750 | 35738 | 0.47 | 2.8E-01 | BE959727.2 | EST_HUMAN | 601654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3639765 3' |
| 10622 | 23154 | 36166 | 2.26 | 2.8E-01 | BF241062.1 | EST_HUMAN | 601880784F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108350 5' |
| 10622 | 23154 | 36167 | 2.26 | 2.8E-01 | BF241062.1 | EST_HUMAN | 601880784F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108350 5' |
| 10651 | 23183 | 36197 | 2.83 | 2.8E-01 | BF695970.1 | EST_HUMAN | 601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5' |
| 10760 | 23284 | 36297 | 3.31 | 2.8E-01 | AF051682.1 | NT | Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds |
| 11158 | 23665 | | 4.56 | 2.8E-01 | BF974023.1 | EST_HUMAN | 602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5' |
| 12213 | 24436 | | 15.74 | 2.8E-01 | D83329.1 | NT | Mus musculus DNA for prostaglandin D2 synthase, complete cds |
| 12328 | 24514 | 30920 | 8.89 | 2.8E-01 | BE178699.1 | EST_HUMAN | PM4-HT0608-030400-001-007 HT0608 Homo sapiens cDNA |
| 12356 | 24533 | 30927 | 1.25 | 2.8E-01 | BE800116.1 | EST_HUMAN | 601679020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955698 5' |
| 12519 | 24988 | | 2.21 | 2.8E-01 | 11433629 | NT | Homo sapiens CDC42-binding protein kinase beta (DMIPK-like) (CDC42BPB), mRNA |
| 502 | 13134 | 25622 | 3.21 | 2.7E-01 | Y17324.1 | NT | Rattus norvegicus CDK104 mRNA |
| 641 | 13284 | 25740 | 2.53 | 2.7E-01 | AA450061.1 | EST_HUMAN | z39b10.s1 Soares_tet_Nb2H18_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element |
| 1304 | 13888 | 26418 | 1.89 | 2.7E-01 | AB004906.1 | NT | Ipomoea purpurea transposable element 1p100 gene for transposase, complete cds |
| 1662 | 14255 | | 2.17 | 2.7E-01 | X78815.1 | NT | Glomalia SR2 gene |
| 1767 | 14357 | 26903 | 3.34 | 2.7E-01 | W56067.1 | EST_HUMAN | z39b10.s1 Soares_tet_Nb2H18_9w Homo sapiens cDNA clone IMAGE:341443 5' |
| 1813 | 14403 | 26948 | 4.14 | 2.7E-01 | P03341 | SWISSPROT | GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] |
| 2181 | 15459 | | 2.77 | 2.7E-01 | AF047575.1 | NT | Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1 |
| 2405 | 14973 | 27545 | 7.35 | 2.7E-01 | Y13688.1 | NT | Feline immunodeficiency virus env gene, isolate ITT0088P1U (M88), partial |
| 2496 | 15060 | 27634 | 3.82 | 2.7E-01 | A1310858.1 | EST_HUMAN | ta43c11.x2 NC1_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element |
| 3013 | 15629 | | 0.73 | 2.7E-01 | BF088284.1 | EST_HUMAN | CM1-HT0875-060800-385-e05 HT0875 Homo sapiens cDNA |
| 4062 | 16678 | 28136 | 1.98 | 2.7E-01 | AI928015.1 | EST_HUMAN | w02a11.x1 NC1_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2462828 3' |
| 4066 | 16691 | 28147 | 0.79 | 2.7E-01 | AF216214.1 | NT | Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds |
| 4066 | 16691 | 28148 | 0.79 | 2.7E-01 | AF216214.1 | NT | Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds |
| 4101 | 16695 | 28151 | 2.31 | 2.7E-01 | L177516.1 | NT | Homo sapiens DiGeorge syndrome critical region, telomeric end |
| 5020 | 17594 | 30037 | 0.98 | 2.7E-01 | L27516.1 | NT | Triticum aestivum (Wcs68) gene, complete cds |
| 5183 | 17758 | | 3.82 | 2.7E-01 | AW856131.1 | EST_HUMAN | RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA |
| 5471 | 18105 | 30424 | 2.07 | 2.7E-01 | P17277 | SWISSPROT | HOMEBOX PROTEIN HOXA4 (CHOX-1.4) |
| 5681 | 18308 | | 0.86 | 2.7E-01 | AB033171.1 | NT | Astrocopa myriophthalma mitochondrial cytb gene for cytochrome b, partial cds |
| 6724 | 19318 | 32122 | 1.07 | 2.7E-01 | AE001094.1 | NT | Archaeoglobus fulgidus section 13 of 172 of the complete genome |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6724 | 18318 | 32123 | 1.07 | 2.7E-01 | AE001094.1 | NT | Archaeoglobus fulgidus section 13 of 172 of the complete genome |
| 6875 | 18609 | 32443 | 2.03 | 2.7E-01 | Q81554 | SWISSPROT | FIBRILLIN 1 PRECURSOR |
| 7085 | 18656 | 32495 | 0.76 | 2.7E-01 | U15987.1 | NT | Drosophila melanogaster rib-40 protein, Rop protein (Rop), and small GTP binding protein (DRac2) genes, complete cds |
| 7383 | 18918 | 32782 | 0.87 | 2.7E-01 | Q11079 | SWISSPROT | HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X |
| 7562 | 20079 | 32854 | 0.95 | 2.7E-01 | Q01168 | SWISSPROT | NITROGEN REGULATORY PROTEIN NUT1 |
| 7562 | 20079 | 32955 | 0.95 | 2.7E-01 | Q01168 | SWISSPROT | NITROGEN REGULATORY PROTEIN NUT1 |
| 7677 | 20188 | 33078 | 2.21 | 2.7E-01 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 7677 | 20188 | 33077 | 2.21 | 2.7E-01 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 7720 | 20228 | 33116 | 0.82 | 2.7E-01 | AA351121.1 | EST_HUMAN | EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H |
| 7720 | 20228 | 33117 | 0.82 | 2.7E-01 | AA351121.1 | EST_HUMAN | EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H |
| 7805 | 20348 | 33256 | 0.95 | 2.7E-01 | AA013147.1 | EST_HUMAN | z035b11.s1 Soares retina N2b-4-IR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element |
| 7989 | 20511 | | 0.51 | 2.7E-01 | AF048820.1 | NT | Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds |
| 8079 | 20621 | 33534 | 0.59 | 2.7E-01 | AW868503.1 | EST_HUMAN | MR1-SN0062-100500-002-d09 SN0062 Homo sapiens cDNA |
| 8127 | 20668 | 33577 | 0.48 | 2.7E-01 | R39257.1 | EST_HUMAN | yc91h06.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3' |
| 8232 | 20773 | 33694 | 0.94 | 2.7E-01 | AL161552.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52 |
| 8684 | 21233 | 34154 | 0.83 | 2.7E-01 | Q14784 | SWISSPROT | MAJOR VALLT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) |
| 8957 | 21495 | 34418 | 0.53 | 2.7E-01 | X03216.1 | NT | Staphylococcus aureus transposon Tn554 |
| 9256 | 21782 | 34734 | 9.83 | 2.7E-01 | O83809 | SWISSPROT | THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS) |
| 9256 | 21782 | 34735 | 9.83 | 2.7E-01 | O83809 | SWISSPROT | THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS) |
| 9259 | 21785 | | 2.02 | 2.7E-01 | P37828 | SWISSPROT | FIMBRIAE W PROTEIN |
| 9718 | 22214 | 35188 | 0.67 | 2.7E-01 | D86680.1 | NT | Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds |
| 9883 | 22488 | 35476 | 0.91 | 2.7E-01 | AF091848.1 | NT | Oryctolagus cuniculus calgranulin C mRNA, partial cds |
| 10026 | 22521 | 35517 | 2.5 | 2.7E-01 | AF087434.1 | NT | Mus musculus transcription factor NF-A7c isoform a (NF-A7c) mRNA, complete cds |
| 10148 | 22643 | 35634 | 0.69 | 2.7E-01 | AF156539.1 | NT | Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9 |
| 10148 | 22643 | 35635 | 0.69 | 2.7E-01 | AF156539.1 | NT | Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9 |
| 10691 | 23221 | 36233 | 2.31 | 2.7E-01 | AV705043.1 | EST_HUMAN | AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5' |
| 10691 | 23221 | 36234 | 2.31 | 2.7E-01 | AV705043.1 | EST_HUMAN | AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10702 | 23231 | 36244 | 3.65 | 2.7E-01 | AJ133268.1 | NT | Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2) |
| 12298 | 24863 | | 1.72 | 2.7E-01 | AB008782.1 | NT | Arabidopsis thaliana mRNA for sulfate transporter, complete cds |
| 12501 | 24627 | | 3.98 | 2.7E-01 | AF217491.1 | NT | Homo sapiens fragile 18D oxidoreductase (FOR) gene, exon 6 |
| 495 | 15416 | 25615 | 2.06 | 2.6E-01 | P78411 | SWISSPROT | IROQUOIS-CLASS HOMEODOMAIN PROTEIN RX-2 |
| 508 | 13139 | | 1.24 | 2.6E-01 | D16459.1 | NT | Bos taurus mRNA for mb-1, complete cds |
| 1437 | 14030 | 26558 | 2.19 | 2.6E-01 | BE885087.1 | EST_HUMAN | 607510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5' |
| 1485 | 14078 | 26616 | 1.36 | 2.6E-01 | AB013290.1 | NT | Glycine max pseudogene for Bd 30K |
| 1941 | 14525 | 27080 | 6.59 | 2.6E-01 | AL161472.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2 |
| 1941 | 14525 | 27081 | 6.59 | 2.6E-01 | AL161472.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2 |
| | | | | | | | bb04d10 x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2858451 3' similar to gb:M36072 605 |
| | | | | | | | RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfactant protein 3 protein gene (MOUSE); |
| 2140 | 14718 | | 13.12 | 2.6E-01 | AW733152.1 | EST_HUMAN | Human prealbumin gene, complete cds |
| 2197 | 14773 | 27347 | 1.41 | 2.6E-01 | M11844.1 | NT | B. maritimus rbcL gene |
| 2512 | 15076 | | 2.09 | 2.6E-01 | Y12996.1 | NT | |
| 2593 | 15146 | | 10.77 | 2.6E-01 | BE272440.1 | EST_HUMAN | 601128016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2860043 5' |
| 3640 | 16243 | 28719 | 0.86 | 2.6E-01 | M22342.1 | NT | Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds |
| | | | | | | | |
| 3705 | 16306 | 28775 | 2.13 | 2.6E-01 | AF228118.1 | NT | Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5 |
| 4175 | 16786 | 28214 | 0.7 | 2.6E-01 | AW959510.1 | EST_HUMAN | EST371580 MAGE resequenced, MAGF Homo sapiens cDNA |
| 4234 | 16822 | 28273 | 19.88 | 2.6E-01 | BE080596.1 | EST_HUMAN | QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA |
| | | | | | | | Enterococcus faecium strain N87-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene |
| 4448 | 17034 | 29477 | 1.57 | 2.6E-01 | AF175293.1 | NT | Gallus gallus mRNA for skeletal myosin heavy chain, complete cds |
| 4593 | 17176 | 29622 | 0.76 | 2.6E-01 | AB021180.1 | NT | Gallus gallus mRNA for skeletal myosin heavy chain, complete cds |
| 4593 | 17176 | 29623 | 0.76 | 2.6E-01 | AB021180.1 | NT | sa89d07.r1 Strabagene fetal retina B37202 Homo sapiens cDNA clone IMAGE:839477 5' |
| 4846 | 17228 | 29684 | 1.35 | 2.6E-01 | AA457817.1 | EST_HUMAN | Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3-1) mRNA, complete cds |
| 4752 | 17333 | 29776 | 1.63 | 2.6E-01 | U01103.1 | NT | |
| | | | | | | | |
| 4825 | 17403 | 29856 | 1.47 | 2.6E-01 | AF142703.1 | NT | Ophrestia radiciosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product |
| 5107 | 17679 | 30118 | 3.56 | 2.6E-01 | H04658.1 | EST_HUMAN | y51e06.r1 Soares placenta Nb24P Homo sapiens cDNA clone IMAGE:162288 5' |
| 5195 | 17760 | | 0.58 | 2.6E-01 | AA884625.1 | EST_HUMAN | sm33b11.s1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1468805 3' |
| 5544 | 18176 | | 1.29 | 2.6E-01 | AB035972.1 | NT | Peromyscus caudatus gene for PAP, complete cds |
| | | | | | | | |
| 5840 | 18289 | 30742 | 0.68 | 2.6E-01 | M86060.1 | NT | Acetabacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CopAx genes, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6760 | 18398 | | 0.81 | 2.6E-01 | AI862398.1 | EST_HUMAN | ts02a03.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER36 repetitive element; |
| 6847 | 18568 | 31289 | 0.89 | 2.6E-01 | AF207550.1 | NT | Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g> |
| 8221 | 25113 | | 2.36 | 2.6E-01 | AE001811.1 | NT | Thermoboga maritima section 123 of 136 of the complete genome |
| 8348 | 18953 | 31732 | 1.89 | 2.6E-01 | AI582557.1 | EST_HUMAN | ts02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84288 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ; |
| 8348 | 18953 | 31733 | 1.89 | 2.6E-01 | AI582557.1 | EST_HUMAN | ts02a12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84288 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ; |
| 8554 | 19182 | 31948 | 1.05 | 2.6E-01 | AL162757.2 | NT | Neisseria meningitidis serogroup A strain Z2491 complete genomes, segment 67 |
| 7103 | 19873 | 32512 | 0.97 | 2.6E-01 | AI814380.1 | EST_HUMAN | w048c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331368 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN); |
| 7457 | 24783 | | 0.98 | 2.6E-01 | AL139077.2 | NT | Campylobacter jejuni NCTC11168 complete genome; segment 48 |
| 7721 | 20229 | 33118 | 1.6 | 2.6E-01 | R10365.1 | EST_HUMAN | y037a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN); |
| 7791 | 20334 | 33240 | 1.14 | 2.6E-01 | R02411.1 | EST_HUMAN | y082a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5' |
| 7845 | 20387 | 33280 | 1.18 | 2.6E-01 | BE144331.1 | EST_HUMAN | MR0-HT0166-181198-003-412 HT0166 Homo sapiens cDNA |
| 8083 | 20625 | 33538 | 0.67 | 2.6E-01 | X82841.1 | NT | D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin) |
| 8083 | 20625 | 33539 | 0.67 | 2.6E-01 | X82841.1 | NT | D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin) |
| 8276 | 20817 | 33738 | 2.99 | 2.6E-01 | BF343588.1 | EST_HUMAN | 602014422F1 NCI_CGAP_Brr64 Homo sapiens cDNA clone IMAGE:4150398 5' |
| 8349 | 20890 | 33810 | 1.89 | 2.6E-01 | Q10109 | SWISSPROT | HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II |
| 8627 | 21166 | 34080 | 4.49 | 2.6E-01 | BE830339.1 | EST_HUMAN | RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA |
| 8627 | 21166 | 34081 | 4.49 | 2.6E-01 | BE830339.1 | EST_HUMAN | RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA |
| 9388 | 21811 | 34762 | 0.96 | 2.6E-01 | X17604.1 | NT | S. occidentalis INV gene for Invertase (EC 3.2.1.26) |
| 9654 | 22153 | | 0.5 | 2.6E-01 | AF057121.1 | NT | Lentia canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds |
| 9782 | 22280 | 35265 | 0.93 | 2.6E-01 | P87368 | SWISSPROT | GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G) |
| 9782 | 22280 | 35266 | 0.93 | 2.6E-01 | P87368 | SWISSPROT | GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G) |
| 10083 | 22588 | | 0.5 | 2.6E-01 | Q28285 | SWISSPROT | VON WILLEBRAND FACTOR PRECURSOR (VWF) |
| 10403 | 22897 | | 0.81 | 2.6E-01 | Y10196.1 | NT | Homo sapiens PHEX gene |
| 10500 | 22994 | | 0.51 | 2.6E-01 | AI978681.1 | EST_HUMAN | wf58509.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2491865 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11300 | 23752 | 36809 | 2.18 | 2.6E-01 | P48280 | SWISSPROT | CELL DIVISION PROTEIN FTSW HOMOLOG |
| 11400 | 23851 | | 30.88 | 2.6E-01 | X51755.1 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 11777 | 24165 | | 1.72 | 2.6E-01 | 10190855 | NT | Mus musculus jerky (Jrk), mRNA |
| 11973 | 24601 | | 4.06 | 2.6E-01 | BE883491.1 | EST_HUMAN | 601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5' |
| 12042 | 24329 | 30986 | 4.8 | 2.6E-01 | AF316896.1 | NT | Homo sapiens NaK-ATPase gamma subunit (FXD2) gene, complete cds, alternatively spliced |
| 12398 | 24556 | | 1.34 | 2.6E-01 | D88425.1 | NT | Caenorhabditis elegans mRNA for serine/threonine kinase, complete cds |
| 12478 | 24612 | | 1.96 | 2.6E-01 | AE001713.1 | NT | Thermoboga maritima section 25 of 138 of the complete genome |
| 12526 | 24641 | | 1.37 | 2.6E-01 | AF141325.2 | NT | Homo sapiens insulin-like growth factor 1-phosphatase (INPP1) gene, complete cds |
| 12567 | 24666 | | 3.74 | 2.6E-01 | P47285 | SWISSPROT | HYPOPHOSPHATASE PROTEIN MG039 |
| 262 | 12921 | 25407 | 1.48 | 2.5E-01 | 4502298 | NT | Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA |
| 263 | 12921 | 25407 | 1.77 | 2.5E-01 | 4502298 | NT | Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA |
| 276 | 12933 | | 4.29 | 2.5E-01 | M26501.1 | NT | Starfish (P. ochreus) cytoplasmic actin gene, complete cds |
| 865 | 13480 | 25994 | 1.02 | 2.5E-01 | U09094.1 | NT | Mus musculus (ICR) Swiss glycerinaldehyde 3-phosphate dehydrogenase (G6pd-S) gene, complete cds |
| 1098 | 13703 | | 1.03 | 2.5E-01 | AE002156.1 | NT | Ureaplasma urealyticum section 57 of 59 of the complete genome |
| 1160 | 13763 | 26274 | 11.59 | 2.5E-01 | T89837.1 | EST_HUMAN | ye11g07.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5' |
| 1506 | 14156 | 26689 | 0.87 | 2.5E-01 | AL115624.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 1766 | 14356 | | 6.09 | 2.5E-01 | 4885408 | NT | Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA |
| 1827 | 15454 | 27067 | 1.29 | 2.5E-01 | BE696804.1 | EST_HUMAN | PM4-CT0400-310700-005-008 CT0400 Homo sapiens cDNA |
| 1927 | 15454 | 27068 | 1.29 | 2.5E-01 | BE696804.1 | EST_HUMAN | PM4-CT0400-310700-005-008 CT0400 Homo sapiens cDNA |
| 2452 | 15019 | | 12.93 | 2.5E-01 | AE000675.1 | NT | Aquifex aeolicus section 7 of 109 of the complete genome |
| 2536 | 15100 | 27673 | 0.93 | 2.5E-01 | 6079216 | NT | Mus musculus protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 (Pcm1t), mRNA |
| 2540 | 15104 | | 1.49 | 2.5E-01 | AA251987.1 | EST_HUMAN | zs11a12.r1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:684862 5' |
| 3459 | 16066 | | 3.41 | 2.5E-01 | AW973471.1 | EST_HUMAN | EST385484 IMAGE resources, MAGM Homo sapiens cDNA |
| 3587 | 16191 | 28675 | 0.84 | 2.5E-01 | AF233875.1 | NT | Danio rerio peptide YY precursor gene, complete cds |
| 3603 | 16207 | 28685 | 7.97 | 2.5E-01 | AL161517.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28 |
| 4143 | 16735 | | 1.36 | 2.5E-01 | P32323 | SWISSPROT | A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR |
| 4409 | 16894 | | 0.9 | 2.5E-01 | Q03314 | SWISSPROT | RHIB PROTEIN |
| 4722 | 17303 | 28747 | 0.59 | 2.5E-01 | AF242431.1 | NT | Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds, and Naip3 gene, exons 2-9 and 11-16 |
| 4860 | 17438 | | 1.47 | 2.5E-01 | Q27225 | SWISSPROT | MOLT-INHIBITING HORMONE PRECURSOR (MIH) |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4889 | 17445 | 28898 | 4.69 | 2.5E-01 | AF007768.1 | NT | Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds |
| 4890 | 17471 | 28927 | 2.82 | 2.5E-01 | AE004416.1 | NT | Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome |
| 4924 | 17489 | | 3.21 | 2.5E-01 | AJ230113.1 | NT | Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MAERV-L (murine endogenous retrovirus) element |
| 4959 | 17534 | 28976 | 0.61 | 2.5E-01 | BE880785.1 | EST_HUMAN | 601437488F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922800 5' |
| 5262 | 12933 | | 0.65 | 2.5E-01 | M26501.1 | NT | Starfish (P. ochraceus) cytoplasmic actin gene, complete cds |
| 5529 | 18161 | 30576 | 12.86 | 2.5E-01 | S83390.1 | NT | T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2890 nt] |
| 6114 | 18730 | | 0.84 | 2.5E-01 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 6738 | 18332 | 32138 | 0.83 | 2.5E-01 | AJ251973.1 | NT | Homo sapiens partial steatrin-1 gene |
| 7389 | 18914 | 32778 | 0.82 | 2.5E-01 | U13992.1 | NT | Feline calicivirus CFU68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polypeptide precursor and capsid protein precursor, genes, complete cds; and unknown gene |
| 7413 | 18938 | | 1.35 | 2.5E-01 | AF134119.1 | NT | Mus musculus SKD1 (Skd1) gene, complete cds |
| 7632 | 20144 | 33025 | 4.48 | 2.5E-01 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 7786 | 20329 | 33236 | 2.31 | 2.5E-01 | BF109040.1 | EST_HUMAN | 7157a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3' |
| 7797 | 20340 | 33248 | 0.7 | 2.5E-01 | BE860712.1 | EST_HUMAN | 601683391R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3' |
| 8168 | 20709 | 33625 | 2.2 | 2.5E-01 | BF038595.1 | EST_HUMAN | 601459238F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862809 5' |
| 8338 | 20877 | 33798 | 0.72 | 2.5E-01 | P04482 | SWISSPROT | ETB PROTEIN, SMALL T-ANTIGEN (ETB 18K) |
| 8571 | 21110 | 34029 | 3.03 | 2.5E-01 | H53236.1 | EST_HUMAN | y84f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5' |
| 8808 | 21347 | 34271 | 0.88 | 2.5E-01 | M88828.1 | NT | Mouse testis-specific protein (TPX-1) gene, exon 10 |
| 9435 | 21961 | 34909 | 15.98 | 2.5E-01 | U88851.2 | NT | Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region |
| 9435 | 21961 | 34910 | 15.98 | 2.5E-01 | U88851.2 | NT | Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region |
| 9492 | 21948 | 34887 | 2.09 | 2.5E-01 | AF085184.1 | NT | Hordeum vulgare receptor-like kinase LRK10 gene, partial cds |
| 9492 | 21948 | 34888 | 2.09 | 2.5E-01 | AF085184.1 | NT | Hordeum vulgare receptor-like kinase LRK10 gene, partial cds |
| 10010 | 22505 | 35498 | 1.68 | 2.5E-01 | AW581987.1 | EST_HUMAN | RC3-ST0188-130100-015-e07 ST0188 Homo sapiens cDNA |
| 10438 | 22930 | 35937 | 1.53 | 2.5E-01 | AW152246.1 | EST_HUMAN | xg40c10.x1 NCI_CGAP_Uh1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ; |
| 10439 | 22933 | 35941 | 1.31 | 2.5E-01 | X59491.1 | NT | Mouse L1Md LINE DNA |
| 10459 | 22953 | 35962 | 2.03 | 2.5E-01 | AL161505.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17 |
| 10459 | 22953 | 35963 | 2.03 | 2.5E-01 | AL161505.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17 |
| 10955 | 23470 | 36495 | 4.3 | 2.5E-01 | D50814.1 | NT | Human mRNA for KIAA0124 gene, partial cds |
| 11712 | 24122 | 37153 | 5.28 | 2.5E-01 | AF200528.1 | NT | Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds |
| 11740 | 25075 | | 10.13 | 2.5E-01 | AL161541.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41 |
| 579 | 13209 | 25887 | 1.67 | 2.4E-01 | AA836316.1 | EST_HUMAN | on70d04.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582023 3' |
| 881 | 13495 | 26014 | 2.4 | 2.4E-01 | BF76124.1 | EST_HUMAN | 602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1347 | 13942 | 28464 | 21.36 | 2.4E-01 | AJ269880.1 | NT | Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene |
| 1347 | 13942 | 28465 | 21.36 | 2.4E-01 | AJ269880.1 | NT | Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene |
| 1427 | 14020 | 28548 | 0.83 | 2.4E-01 | Y17263.1 | NT | Homo sapiens FLI-1 gene, partial |
| 1801 | 14476 | 27277 | 27.27 | 2.4E-01 | AF267753.1 | NT | Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds |
| 1944 | 14528 | 27084 | 1.17 | 2.4E-01 | AF251708.1 | NT | Zaocys diummedes fructose-1,6-bisphosphatase mRNA, complete cds |
| 2079 | 14659 | 27230 | 1.49 | 2.4E-01 | A1742958.1 | EST_HUMAN | wg76405.x1 Soares NSF F8 GW OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:060267 KIAA0512 PROTEIN. ; |
| 2183 | 14759 | 27328 | 1.04 | 2.4E-01 | AF111108.2 | NT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| 2213 | 14788 | 27451 | 1.04 | 2.4E-01 | P45384 | SWISSPROT | IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE) |
| 2302 | 14875 | 27451 | 1.78 | 2.4E-01 | AE000880.1 | NT | Aquifex aeolicus section 12 of 109 of the complete genome |
| 2425 | 14893 | 27568 | 1.26 | 2.4E-01 | BF002171.1 | EST_HUMAN | 7h23d04.x1 NCI CGAP Cor16 Homo sapiens cDNA clone IMAGE:3318807 3' similar to SW:FRSB_XENLA |
| 2575 | 15138 | 27708 | 3.05 | 2.4E-01 | Z38534.1 | NT | O42588 26S PROTEASE REGULATORY SUBUNIT 6A ; |
| 2760 | 15343 | 27813 | 1.79 | 2.4E-01 | X71783.1 | NT | D. discoideum (A3-K) pona gene |
| 2812 | 15384 | 27833 | 3.88 | 2.4E-01 | AF030154.1 | NT | S. pombe swi6 gene |
| 3168 | 15780 | | 3.27 | 2.4E-01 | U72728.1 | NT | Bovine adenovirus 3 complete genome |
| 3182 | 15795 | 28267 | 1.39 | 2.4E-01 | X74209.1 | NT | Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds |
| 3724 | 16325 | 28792 | 1.26 | 2.4E-01 | AF169793.1 | NT | H. sapiens AGT gene, Pcd fragment of intron 4 |
| 3824 | 16424 | 28886 | 0.83 | 2.4E-01 | AE000312.1 | NT | Podospira arisaria HET-C protein (Het-c) gene, complete cds |
| 4103 | 16897 | | 0.6 | 2.4E-01 | D28680.1 | NT | Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome |
| 5008 | 17581 | 30024 | 1.09 | 2.4E-01 | AE000305.1 | NT | Rattus norvegicus mRNA for alpha8 crystallin-related protein, complete cds |
| 5220 | 17785 | 30203 | 0.93 | 2.4E-01 | BE737592.1 | EST_HUMAN | Escherichia coli K-12 MG1655 section 195 of 400 of the complete genome |
| 5302 | 17884 | | 1.65 | 2.4E-01 | K02402.1 | NT | 601572862F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:3839775 5' |
| 5653 | 18280 | 30758 | 0.83 | 2.4E-01 | A825707.1 | EST_HUMAN | Human coagulation factor IX gene, complete cds |
| 5653 | 18280 | 30759 | 0.83 | 2.4E-01 | A825707.1 | EST_HUMAN | wc33405.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457128 3' |
| 5676 | 18303 | 30785 | 0.85 | 2.4E-01 | D50871.1 | NT | wc33405.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457128 3' |
| 5836 | 18480 | 31182 | 7.92 | 2.4E-01 | AF081216.1 | NT | Glycine max mRNA for mitotic cyclin b1-type, complete cds |
| 5836 | 18480 | 31183 | 7.92 | 2.4E-01 | AF081216.1 | NT | Mus musculus Wm protein (Wm) gene, complete cds |
| 6050 | 24764 | | 1.02 | 2.4E-01 | AJ133838.2 | NT | Mus musculus Wm protein (Wm) gene, complete cds |
| | | | | | | NT | Branchiostoma floridae mRNA for calmodulin 2 (cam2 gene) |
| 6054 | 18872 | 31411 | 2.36 | 2.4E-01 | BF582338.1 | EST_HUMAN | 7154404.x1 NCI CGAP BR16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN |
| 6138 | 18752 | 31510 | 2.5 | 2.4E-01 | AF035546.1 | NT | Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element ; |
| | | | | | | NT | Drosophila melanogaster p38a MAP kinase gene, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6240 | 18949 | 31619 | 2.28 | 2.4E-01 | 7861801 | NT | Homo sapiens HSPC142 protein (HSPC142), mRNA |
| 6280 | 18898 | 31689 | 0.8 | 2.4E-01 | AV733787.1 | EST_HUMAN | AV733787 cDNA Homo sapiens cDNA clone cDAAD11.5' |
| 6656 | 18252 | 32055 | 2.43 | 2.4E-01 | AI698889.1 | EST_HUMAN | wc82c11.x1 NC1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03484 |
| 7381 | 19907 | 32772 | 8.84 | 2.4E-01 | L93001.1 | NT | PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN); |
| 7709 | 20218 | 33106 | 1.06 | 2.4E-01 | AF228644.1 | NT | Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds |
| 8139 | 20680 | 33591 | 0.71 | 2.4E-01 | AJ006397.1 | NT | Mus musculus DDX48a protein (DDX48a) mRNA, complete cds |
| 8139 | 20680 | 33592 | 0.71 | 2.4E-01 | AJ006397.1 | NT | Streptococcus pneumoniae r08 and h108 genes; two component system 08 |
| 8290 | 20631 | 33752 | 1.66 | 2.4E-01 | AJ012585.1 | NT | Streptococcus pneumoniae r08 and h108 genes; two component system 08 |
| 8535 | 21074 | 33994 | 0.97 | 2.4E-01 | BF242794.1 | EST_HUMAN | Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2 |
| 8588 | 21127 | | 0.58 | 2.4E-01 | BF678275.1 | EST_HUMAN | 80187767F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106208 5' |
| 9059 | 21598 | 34526 | 0.58 | 2.4E-01 | AL138077.2 | NT | 802086188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5' |
| 9059 | 21598 | 34527 | 0.58 | 2.4E-01 | AL138077.2 | NT | Campylobacter jejuni NCTC11168 complete genome, segment 4/8 |
| 9482 | 21881 | 34826 | 6.84 | 2.4E-01 | AI693515.1 | EST_HUMAN | Campylobacter jejuni NCTC11168 complete genome, segment 4/8 |
| 9620 | 22120 | 35083 | 0.8 | 2.4E-01 | AF220067.1 | NT | wk43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains MER22.b1 TAR1 repetitive element; |
| 9620 | 22120 | 35084 | 0.8 | 2.4E-01 | AF220067.1 | NT | Drosophila melanogaster SKPB gene, complete cds |
| 10335 | 22829 | 35823 | 1.95 | 2.4E-01 | Q03682 | SWISSPROT | Drosophila melanogaster SKPB gene, complete cds |
| 10647 | 23179 | 36182 | 3.25 | 2.4E-01 | AL161494.2 | NT | COLLAGEN ALPHA 1(X) CHAIN PRECURSOR |
| 10715 | 23243 | 36280 | 2.9 | 2.4E-01 | AF030189.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6 |
| 11081 | 23583 | | 2.28 | 2.4E-01 | Z21847.1 | NT | Mus musculus type 1 sigma receptor gene, complete cds |
| 11665 | 24089 | 37145 | 1.91 | 2.4E-01 | AF217491.1 | NT | P. asiatica mosaic virus genomic RNA |
| 11807 | 24953 | | 2.65 | 2.4E-01 | AF004213.1 | NT | Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6 |
| 11868 | 24220 | | 2.02 | 2.4E-01 | AJ278191.1 | NT | Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds |
| 12086 | 24638 | | 2.18 | 2.4E-01 | V01507.1 | NT | Mus musculus mRNA for putative mc7 protein (mc7 gene) |
| 12320 | 25061 | | 1.5 | 2.4E-01 | BF229975.1 | EST_HUMAN | Gallus gallus gene coding for a-actin |
| 12562 | 24962 | | 2.31 | 2.4E-01 | AL163281.2 | NT | RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA |
| 412 | 13047 | 25538 | 0.91 | 2.3E-01 | U75898.1 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 685 | 13289 | | 4.4 | 2.3E-01 | S97913.1 | NT | aromatase [P. ophiophila guttata-zabara finches, ovary, mRNA, 3188 nt] |
| 695 | 13318 | 25803 | 17.02 | 2.3E-01 | U67598.1 | NT | Mycoplasma genitalium section 35 of 51 of the complete genome |
| 968 | 13590 | 26092 | 3.44 | 2.3E-01 | BE311893.1 | EST_HUMAN | Methanococcus jannaschii section 138 of 150 of the complete genome |
| 1847 | 14239 | 28774 | 1.19 | 2.3E-01 | AJ245480.1 | NT | 801142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3503818 5' |
| 1674 | 14288 | 28800 | 2.75 | 2.3E-01 | Y10887.2 | NT | Brassica napus seg gene for S-b locus glycoprotein, cultivar T2 |
| 2089 | 14689 | | 1.29 | 2.3E-01 | AJ235353.1 | NT | Mus musculus cdh5 gene, exon 1, partial |
| | | | | | | NT | Homo sapiens partial intron 3 of the wild type AF-4/FEL gene |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2489 | 15054 | 27626 | 2.03 | 2.3E-01 | BE297718.1 | EST_HUMAN | 60175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5' |
| 2678 | 15236 | 27803 | 1.16 | 2.3E-01 | M11319.1 | NT | Human erythropoietin gene, complete cds |
| 2651 | 14024 | 26552 | 1.42 | 2.3E-01 | AB015033.1 | NT | Marinibacteria agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957 |
| 2690 | 15606 | 28086 | 0.93 | 2.3E-01 | AA601379.1 | EST_HUMAN | no16d06.s1 NC1_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element TH-R repetitive element; |
| 3120 | 15734 | | 6.96 | 2.3E-01 | R21732.1 | EST_HUMAN | Y121b07.s1 Soares, placenta Nb2-IP Homo sapiens cDNA clone IMAGE:130357 3' |
| 3417 | 16025 | 28507 | 0.78 | 2.3E-01 | H68836.1 | EST_HUMAN | Y187h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5' |
| 3908 | 16507 | 28968 | 1.02 | 2.3E-01 | S82821.1 | NT | GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3] |
| 4009 | 16607 | | 5.14 | 2.3E-01 | 7682133 | NT | Homo sapiens KIAA0450 gene product (KIAA0450), mRNA |
| 4442 | 17026 | 29468 | 0.83 | 2.3E-01 | R82252.1 | EST_HUMAN | Y17701.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:148017 5' |
| 4489 | 17074 | | 2.4 | 2.3E-01 | L78789.1 | NT | Mus musculus renin (Ren-1c) gene, promoter region |
| 4548 | 17131 | 28578 | 0.87 | 2.3E-01 | D80989.1 | NT | Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859 |
| 4586 | 17189 | 28613 | 2.16 | 2.3E-01 | AF092535.1 | NT | Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds |
| 4652 | 17234 | 29690 | 6.13 | 2.3E-01 | 5031984 | NT | Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA |
| 5180 | 17585 | 30028 | 0.82 | 2.3E-01 | J03280.1 | NT | Human phenylethanolamine N-methyltransferase gene, complete cds |
| 5202 | 17767 | 30191 | 0.62 | 2.3E-01 | AB032400.1 | NT | Mus musculus tulip 1 mRNA, complete cds |
| 5403 | 17981 | 30372 | 0.9 | 2.3E-01 | AE000240.1 | NT | Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome |
| 5507 | 18140 | 30552 | 2.39 | 2.3E-01 | AB040945.1 | NT | Homo sapiens mRNA for KIAA1512 protein, partial cds |
| 5821 | 18250 | 30718 | 2.05 | 2.3E-01 | BF058381.1 | EST_HUMAN | 7130b06.x1 NC1_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW-GAG_SMSAV P03330 GAG POLYPEPTIDE [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] ; |
| 5721 | 18347 | 31050 | 4.58 | 2.3E-01 | X86587.1 | NT | C.fantasma rom1 gene |
| 5831 | 18455 | | 1.19 | 2.3E-01 | L39112.1 | NT | Vitis vinifera corneum small subunit ribosomal RNA gene |
| 5928 | 18648 | 31274 | 0.78 | 2.3E-01 | S80371.1 | NT | 23S rRNA [Leuconostoc carnosum, Genomic, 2868 nt] |
| 6086 | 18712 | 31461 | 2.34 | 2.3E-01 | A1708840.1 | EST_HUMAN | as27e12.x1 Barslead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN); |
| 6098 | 18712 | 31462 | 2.34 | 2.3E-01 | A1708840.1 | EST_HUMAN | as27e12.x1 Barslead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN); |
| 6762 | 19355 | 32184 | 0.76 | 2.3E-01 | AF198089.1 | NT | Oryctolagus cuniculus cytochrome oxidase subunit Via (coxVia2) mRNA, complete cds; nuclear gene for mitochondrial product |
| 6859 | 19336 | 32360 | 4.1 | 2.3E-01 | A1718148.1 | EST_HUMAN | as42f12.x1 Barslead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318887 3' similar to contains Alu repetitive element; |
| 7165 | 19697 | 32544 | 0.7 | 2.3E-01 | 8823323 | NT | Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7331 | 19858 | 32721 | 0.68 | 2.3E-01 | AF000227.1 | NT | Secale cereale omega secalin gene, complete cds |
| 7445 | 19889 | 32837 | 2.42 | 2.3E-01 | AF175389.1 | NT | Glycine max resistance protein LM17 precursor RNA, partial cds |
| 7603 | 20116 | | 3.63 | 2.3E-01 | 8754779 | NT | Mus musculus myosin XV (Myo15), mRNA |
| 7608 | 20121 | 32898 | 1.63 | 2.3E-01 | BE888071.1 | EST_HUMAN | 601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5' |
| 7732 | 20240 | | 2.68 | 2.3E-01 | N80883.1 | EST_HUMAN | zai2a08.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:292358 5' |
| 7783 | 20338 | 33243 | 0.58 | 2.3E-01 | AL161558.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58 |
| 7835 | 20477 | 33387 | 1.83 | 2.3E-01 | M88831.1 | NT | Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds |
| 8430 | 20870 | 33882 | 0.6 | 2.3E-01 | U57899.1 | NT | Mus musculus prosaposin (psap/SGP-1) gene, complete cds |
| 9087 | 21804 | 34534 | 0.87 | 2.3E-01 | AA372184.1 | EST_HUMAN | EST84061 Rhodomyosarcoma Homo sapiens cDNA 5' and similar to DnaJ homolog (GB:X633388) |
| 9087 | 21804 | 34535 | 0.87 | 2.3E-01 | AA372184.1 | EST_HUMAN | EST84061 Rhodomyosarcoma Homo sapiens cDNA 5' and similar to DnaJ homolog (GB:X633388) |
| 9501 | 22001 | 34858 | 0.65 | 2.3E-01 | 6678318 | NT | Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (PIK3cd), mRNA |
| 9644 | 22144 | 35112 | 0.51 | 2.3E-01 | BE277860.1 | EST_HUMAN | 601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2968739 5' |
| 9697 | 22188 | 35189 | 0.78 | 2.3E-01 | AW964480.1 | EST_HUMAN | EST7376533 MAGE resequences, MAGE1 Homo sapiens cDNA |
| 9748 | 22244 | 35225 | 1.22 | 2.3E-01 | X52124.1 | NT | Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4)) |
| 9781 | 22279 | 35284 | 0.55 | 2.3E-01 | AW364633.1 | EST_HUMAN | PM2-DT0036-281290-001-04 DT0036 Homo sapiens cDNA |
| 9847 | 22345 | 35326 | 2.6 | 2.3E-01 | BE173080.1 | EST_HUMAN | MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA |
| 9803 | 22400 | 35373 | 1.83 | 2.3E-01 | AJ293261.1 | NT | Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes |
| 10339 | 22833 | 35828 | 0.94 | 2.3E-01 | AF201929.1 | NT | Murine hepatitis virus strain 2, complete genome |
| 10351 | 22845 | | 5.88 | 2.3E-01 | BF133577.1 | EST_HUMAN | 60184615R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3' |
| 10883 | 23414 | 36432 | 1.85 | 2.3E-01 | AF004833.1 | NT | Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds |
| 10893 | 23414 | 36433 | 1.85 | 2.3E-01 | AF004833.1 | NT | Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds |
| 11068 | 23580 | 36619 | 1.85 | 2.3E-01 | AJ250189.1 | NT | Mus musculus partial mRNA for muscle protein S34 (mg534 gene) |
| 11068 | 23580 | 36620 | 1.85 | 2.3E-01 | AJ250189.1 | NT | Mus musculus partial mRNA for muscle protein S34 (mg534 gene) |
| 11230 | 23781 | 36817 | 2.49 | 2.3E-01 | AE002187.2 | NT | Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome |
| 11624 | 24066 | | 1.6 | 2.3E-01 | AV709736.1 | EST_HUMAN | AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5' |
| 11788 | 24172 | | 2.82 | 2.3E-01 | U45426.1 | NT | Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds |
| 11878 | 24228 | | 57.94 | 2.3E-01 | T27231.1 | EST_HUMAN | HCOEST44 HT29M8 Homo sapiens cDNA clone HCOE44 5' |
| 11899 | 24804 | | 1.31 | 2.3E-01 | AA088819.1 | EST_HUMAN | chm1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5' |
| 11908 | 24240 | | 1.61 | 2.3E-01 | AW803940.1 | EST_HUMAN | PIMA-SIN0012-030400-001-006 SIN0012 Homo sapiens cDNA |
| 11969 | 25002 | 30810 | 3.1 | 2.3E-01 | AW303623.1 | EST_HUMAN | xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR-Q82175 Q82175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.b2 TAR1 repetitive element; |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | RF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12007 | 25053 | 30511 | 10.98 | 2.3E-01 | BE882484.1 | EST_HUMAN | 601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3308689 5' |
| 12057 | 24340 | | 1.94 | 2.3E-01 | BF063319.1 | EST_HUMAN | 602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4287719 5' |
| 12107 | 24369 | | 3.11 | 2.3E-01 | AJ006519.1 | NT | Rattus norvegicus mRNA for acid gated ion channel |
| 12205 | 24429 | | 1.36 | 2.3E-01 | U48945.1 | NT | Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds |
| 12211 | 24369 | | 1.67 | 2.3E-01 | AJ006519.1 | NT | Rattus norvegicus mRNA for acid gated ion channel |
| 12490 | 24614 | | 2.67 | 2.3E-01 | BF476811.1 | EST_HUMAN | nec30h12.x1 Lupschi_sclafic_nerve Homo sapiens cDNA clone IMAGE:3305950 3' similar to contains element |
| 12608 | 24898 | 30710 | 1.26 | 2.3E-01 | AA094108.1 | EST_HUMAN | MER38 repetitive element ; |
| 83 | 12769 | 25252 | 0.91 | 2.2E-01 | AI052190.1 | EST_HUMAN | cl1894.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5' |
| 1611 | 14204 | 28738 | 2.85 | 2.2E-01 | AF167850.1 | NT | oz14a10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to |
| 2063 | 14643 | | 3.89 | 2.2E-01 | AF171801.1 | NT | TR:Q13040 Q13040 A TP-BINDING CASSETTE PROTEIN ; |
| 2136 | 14714 | 27287 | 3.16 | 2.2E-01 | M34840.1 | NT | Homo sapiens PPAR delta gene, promoter region |
| 2447 | 15014 | 27588 | 5.61 | 2.2E-01 | BF677638.1 | EST_HUMAN | Trimeresurus malabaricus cytb gene, partial cds; mitochondrial gene for mitochondrial product |
| 2623 | 15185 | 27751 | 1.27 | 2.2E-01 | BE618258.1 | EST_HUMAN | Fresh-water sponge Emf1 alpha collagen (COLF1) gene |
| 2623 | 15185 | 27752 | 1.27 | 2.2E-01 | BE618258.1 | EST_HUMAN | 602085603F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249989 5' |
| 2703 | 15260 | | 1.17 | 2.2E-01 | AL163218.2 | NT | 601462829F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866180 5' |
| 2908 | 15523 | 27993 | 4.28 | 2.2E-01 | BE155625.1 | EST_HUMAN | 601462829F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866180 5' |
| 2908 | 15523 | 27994 | 4.28 | 2.2E-01 | BE155625.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C018 |
| 2947 | 15563 | | 1.04 | 2.2E-01 | AF020503.1 | NT | PM2-HT0353-281289-003-a12-HT0353 Homo sapiens cDNA |
| 3439 | 16047 | | 2.67 | 2.2E-01 | AL161562.2 | NT | PM2-HT0353-281289-003-a12-HT0353 Homo sapiens cDNA |
| 3896 | 16484 | | 1.18 | 2.2E-01 | AF156728.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5 |
| 4291 | 16877 | | 1.26 | 2.2E-01 | AF119102.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62 |
| 4300 | 16886 | 28330 | 7.03 | 2.2E-01 | AF155142.1 | NT | Xiphophorus maculatus truncated Rax1 retrotransposon reverse transcriptase (RT) pseudogene |
| 4350 | 16937 | 28378 | 2.59 | 2.2E-01 | AF117340.1 | NT | Drosophila melanogaster UNC-119 (unc-119) gene, complete cds |
| 4350 | 16937 | 28379 | 2.59 | 2.2E-01 | AF117340.1 | NT | Mus musculus ribonuclease kinase 3 (Mlck3) and two pore domain K+ channel subunit (Kcnid6) genes, complete cds |
| 4447 | 17033 | 29475 | 1.36 | 2.2E-01 | U01307.1 | NT | Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds |
| 4447 | 17033 | 29476 | 1.36 | 2.2E-01 | U01307.1 | NT | Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds |
| 4952 | 17527 | | 1.35 | 2.2E-01 | D50804.1 | NT | Human scRNA (BC200 beta) pseudogene |
| 4957 | 17532 | 28974 | 2.86 | 2.2E-01 | AA211216.1 | EST_HUMAN | Human beta-cytoplasmic actin (ACTBP9) pseudogene |
| 5198 | 17781 | | 1.33 | 2.2E-01 | L13289.1 | NT | zq87c05.r1 Streptococcus NNT neuron (8837233) Homo sapiens cDNA clone IMAGE:648988 5' |
| 5203 | 17788 | | 1.79 | 2.2E-01 | AE001137.1 | NT | Mus musculus vinculin gene, exon 3 |
| | | | | | | | Borrelia burgdorferi (section 23 of 70) of the complete genome |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5281 | 17853 | 30277 | 1.2 | 2.2E-01 | BE141035.1 | EST_HUMAN | MRO-HT0067-201089-002-c10 HT0067 Homo sapiens cDNA |
| 5316 | 17878 | | 0.9 | 2.2E-01 | S57565.1 | NT | histamine H2-receptor [rats, Genomic, 1928 nt] |
| 5919 | 18541 | 31267 | 2.46 | 2.2E-01 | 5803002 | NT | Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 158, mRNA |
| 5930 | 18552 | | 3.53 | 2.2E-01 | D04000.1 | NT | Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2539899 |
| 6150 | 18763 | 31525 | 0.73 | 2.2E-01 | U67087.1 | NT | Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds |
| 6150 | 18763 | 31526 | 0.73 | 2.2E-01 | U67087.1 | NT | Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds |
| 6807 | 19368 | 32212 | 0.85 | 2.2E-01 | A8038480.1 | NT | Homo sapiens gene for fukutin, complete cds |
| 7063 | 19684 | 32503 | 9.14 | 2.2E-01 | AV756238.1 | EST_HUMAN | AV756238 BM Homo sapiens cDNA clone BMFAHC08 5' |
| 7183 | 19715 | 32562 | 1.46 | 2.2E-01 | AF082738.1 | NT | Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spa) genes, complete cds; and unknown genes |
| 7183 | 19715 | 32563 | 1.46 | 2.2E-01 | AF082738.1 | NT | Streptococcus pyogenes phosphotidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (spa) genes, complete cds; and unknown genes |
| 7333 | 19660 | 32723 | 2.01 | 2.2E-01 | M24136.1 | NT | Human glycoprotein B gene, exon 4 |
| 7333 | 19660 | 32724 | 2.01 | 2.2E-01 | M24136.1 | NT | Human glycoprotein B gene, exon 4 |
| 7688 | 20197 | 33085 | 0.68 | 2.2E-01 | AF287987.1 | NT | Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds |
| 7863 | 20505 | | 3.06 | 2.2E-01 | AF155143.1 | NT | Mus musculus nm23-M1 gene, promoter region |
| 8032 | 20574 | 33479 | 0.84 | 2.2E-01 | Z48933.1 | NT | E. coli sepA and sepB genes |
| 8815 | 21354 | 34277 | 0.57 | 2.2E-01 | L23312.1 | NT | Mouse HD protein mRNA, complete cds |
| 8815 | 21354 | 34278 | 0.57 | 2.2E-01 | L23312.1 | NT | Mouse HD protein mRNA, complete cds |
| 8827 | 21366 | 34290 | 3.48 | 2.2E-01 | AE001713.1 | NT | Thermotoga maritima section 25 of 136 of the complete genome |
| 8847 | 21368 | 34310 | 1.02 | 2.2E-01 | U09884.1 | NT | Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds |
| 8852 | 21480 | | 3.12 | 2.2E-01 | AW850339.1 | EST_HUMAN | PM9-CT0263-241289-008-b07 CT0263 Homo sapiens cDNA |
| 9043 | 21580 | 34509 | 1.82 | 2.2E-01 | 8393247 | NT | Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA |
| 9126 | 21661 | 34804 | 1.95 | 2.2E-01 | BF376354.1 | EST_HUMAN | MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA |
| 9213 | 21730 | 34673 | 1.24 | 2.2E-01 | W02988.1 | EST_HUMAN | zod4f08.1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:291581 5' |
| 9231 | 21853 | 34803 | 14.03 | 2.2E-01 | P48834 | SWISSPROT | LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2) |
| 9274 | 21800 | 34750 | 0.74 | 2.2E-01 | AJ009839.1 | NT | Xenopus laevis mRNA for kinesin-like protein 3 (xldp3) |
| 9285 | 21855 | 34830 | 0.71 | 2.2E-01 | 7657428 | NT | Mus musculus osteoblast specific factor 2 (OSF-2), mRNA |
| 9288 | 21868 | 34845 | 3.69 | 2.2E-01 | M80643.1 | NT | Brachydanio rerio opandynin beta and gamma chains (Epd) gene, complete cds |
| 9639 | 22039 | 35000 | 0.59 | 2.2E-01 | Q90880 | SWISSPROT | CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3) |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9729 | 22227 | 35204 | 3.1 | 2.2E-01 | AF197841.1 | NT | Funaria hygrometrica chloroplast-localized small heat shock protein (CPaHSP21) mRNA, complete cds; nuclear gene for chloroplast product |
| 9854 | 22361 | 35341 | 2.23 | 2.2E-01 | BF206507.1 | EST_HUMAN | 601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5' |
| 10079 | 22574 | 35568 | 0.87 | 2.2E-01 | 6825671 | NT | Human herpesvirus 5, complete genome |
| 10340 | 22834 | | 0.61 | 2.2E-01 | AF071001.1 | NT | Mus musculus PIR1 (Pir1) gene, partial cds |
| 10384 | 22878 | 35870 | 0.72 | 2.2E-01 | AE001562.1 | NT | Helicobacter pylori, strain J99 section 123 of 132 of the complete genome |
| 10384 | 22878 | 35871 | 0.72 | 2.2E-01 | AE001562.1 | NT | Helicobacter pylori, strain J99 section 123 of 132 of the complete genome |
| 11005 | 23519 | 36554 | 1.8 | 2.2E-01 | AF257772.1 | NT | Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced |
| 11299 | 23751 | 36808 | 5.58 | 2.2E-01 | X01818.1 | NT | Drosophila 68C glue gene cluster |
| 11335 | 23033 | 36042 | 3.18 | 2.2E-01 | 7706215 | NT | Homo sapiens H-2K binding factor-2 (LOC51580), mRNA |
| 11715 | 24125 | | 1.8 | 2.2E-01 | BE870859.1 | EST_HUMAN | 601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5' |
| 11827 | 25065 | | 6.34 | 2.2E-01 | UB2671.2 | NT | Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1> |
| 11910 | 24248 | | 5.37 | 2.2E-01 | AF188843.1 | NT | Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds |
| 12024 | 18029 | 30491 | 1.7 | 2.2E-01 | AW361088.1 | EST_HUMAN | RC1-CT0249-141189-021-g04 CT0249 Homo sapiens cDNA |
| 12025 | 24317 | | 1.85 | 2.2E-01 | AW681822.1 | EST_HUMAN | h17602.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3' |
| 12575 | 25058 | | 4.05 | 2.2E-01 | AV694801.1 | EST_HUMAN | AV694801 GK6 Homo sapiens cDNA clone GKCAHB02 5' |
| 12659 | 24730 | 30855 | 2.44 | 2.2E-01 | BF243095.1 | EST_HUMAN | 601876452F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104998 5' |
| 1009 | 13617 | 26132 | 1.36 | 2.1E-01 | AA569289.1 | EST_HUMAN | mm31e11.s1 NCI_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:1061804 |
| 1009 | 13619 | 26134 | 1.27 | 2.1E-01 | AL161504.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16 |
| 1163 | 13765 | | 2.41 | 2.1E-01 | AE002314.2 | NT | Chlamydia muridarum, section 45 of 85 of the complete genome |
| 1240 | 13838 | 26354 | 0.85 | 2.1E-01 | 6754289 | NT | Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA |
| 1240 | 13838 | 26355 | 0.85 | 2.1E-01 | 6754289 | NT | Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes |
| 1557 | 14149 | 26681 | 3.45 | 2.1E-01 | AJ246895.1 | NT | Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes |
| 1957 | 14541 | 27097 | 1.84 | 2.1E-01 | AA906824.1 | EST_HUMAN | dk73602.s1 NCI_CGAP_GCA1 Homo sapiens cDNA clone IMAGE:1519810 3' similar to gb:K02765 |
| 2201 | 14777 | 27350 | 3.39 | 2.1E-01 | BF695073.1 | EST_HUMAN | COMPLEMENT C3 PRECURSOR (HUMAN). |
| 2385 | 14954 | 27526 | 2.01 | 2.1E-01 | 6753235 | NT | 602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5' |
| 2385 | 14954 | 27526 | 2.01 | 2.1E-01 | 6753235 | NT | Mus musculus calcium channel, voltage dependent, alpha2/delta subunit 3 (Ca α 2 δ 3), mRNA |
| 2351 | 15567 | 28041 | 2.53 | 2.1E-01 | 6912445 | NT | Homo sapiens potassium voltage-gated channel, subfamily H (seg-related), member 4 (KCNH4), mRNA |
| 3879 | 16477 | | 6.58 | 2.1E-01 | 6838361 | NT | Beta vulgaris mitochondrion, complete genome |
| 4129 | 16721 | 29176 | 1.22 | 2.1E-01 | P11675 | SWISSPROT | IMMEDIATE-EARLY PROTEIN IE180 |

Table 4

Single Exon Probes Expressed in Fetal Liver

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4129 | 16721 | 29177 | 1.22 | 2.1E-01 | P11675 | SWISSPROT | IMMEDIATE-EARLY PROTEIN IE180 |
| 4338 | 16823 | | 1.38 | 2.1E-01 | AF124528.1 | NT | Orchestria cawiana calcium-binding protein BP23 precursor (BP23) gene, complete cds |
| 4405 | 17051 | | 1.51 | 2.1E-01 | AB033041.1 | NT | Homo sapiens mRNA for KIAA1215 protein, partial cds |
| 4678 | 17258 | 29700 | 1.83 | 2.1E-01 | AB010273.1 | NT | Homo sapiens pshsp47 gene, complete cds |
| 5083 | 17656 | 30097 | 1.83 | 2.1E-01 | U78409.1 | NT | Lycopodium esculentum homeobox 1 protein (THor1) mRNA, partial cds |
| 5434 | 17860 | 30398 | 0.88 | 2.1E-01 | J05082.1 | NT | Vampire bat (D. rotundus) plasminogen activator mRNA, complete cds |
| 5504 | 18138 | 30548 | 6.55 | 2.1E-01 | BF672606.1 | EST_HUMAN | 602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5' |
| 6267 | 18544 | 32368 | 1.16 | 2.1E-01 | AJ223392.1 | NT | Doko fragilis mitochondrial 16S rRNA gene, partial |
| 6978 | 19477 | 32289 | 2.04 | 2.1E-01 | U04642.1 | NT | Human olfactory receptor (OR17-2) gene, partial cds |
| 7438 | 19890 | 32825 | 1.24 | 2.1E-01 | Q01956 | SWISSPROT | VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID) |
| 7438 | 19890 | 32826 | 1.24 | 2.1E-01 | Q01956 | SWISSPROT | VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID) |
| 7447 | 19971 | | 2.17 | 2.1E-01 | AE000972.1 | NT | Archaeoglobus fulgidus section 135 of 172 of the complete genome |
| 7692 | 20201 | 33088 | 2.02 | 2.1E-01 | AF000949.1 | NT | Canis familiaris keratin (KRT9) gene, complete cds |
| 7731 | 20239 | 33130 | 1.14 | 2.1E-01 | AF069887.1 | NT | Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds |
| 7731 | 20239 | 33131 | 1.14 | 2.1E-01 | AF069887.1 | NT | Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds |
| 7765 | 20273 | | 0.88 | 2.1E-01 | T87354.1 | EST_HUMAN | y883b01.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:114783 5' |
| 8017 | 20559 | | 1.19 | 2.1E-01 | 7305030 | NT | Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA |
| 8439 | 20979 | 33894 | 4.93 | 2.1E-01 | U68389.1 | NT | Haemophilus influenzae hmcD, putative haemochrom processing protein (hmcC), putative ABC transporter (hmcB), putative haemochrom structural protein (hmcA), and haemochrom immunity protein (hmcI) genes, complete cds |
| 8732 | 21271 | 34190 | 0.82 | 2.1E-01 | AL040537.1 | EST_HUMAN | DKFZp434H0814_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434H0814 5' |
| 8732 | 21271 | 34191 | 0.82 | 2.1E-01 | AL040537.1 | EST_HUMAN | DKFZp434H0814_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434H0814 5' |
| 8888 | 21428 | | 0.47 | 2.1E-01 | AB022524.1 | NT | Homo sapiens APCL gene, exon 9 |
| 8987 | 21505 | 34428 | 5.93 | 2.1E-01 | Z35786.1 | NT | S. cerevisiae chromosome II reading frame ORF YBL025w |
| 9423 | 21932 | 34890 | 0.6 | 2.1E-01 | N42536.1 | EST_HUMAN | Y11e10.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270654 5' |
| 9423 | 21932 | 34891 | 0.6 | 2.1E-01 | N42536.1 | EST_HUMAN | Y11e10.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270654 5' |
| 9432 | 21958 | 34908 | 2.95 | 2.1E-01 | X97378.1 | NT | A. thaliana mRNA for AFRABP1b protein |
| 9536 | 22036 | 34998 | 1.57 | 2.1E-01 | AB036529.1 | NT | Homo sapiens p53R2 gene for ribonucleotide reductase, exon 8 |
| 10232 | 22727 | 35718 | 1.04 | 2.1E-01 | Z97087.1 | NT | Beta vulgaris mRNA for elongation factor 1-beta |
| 10283 | 22758 | 35745 | 1.96 | 2.1E-01 | P52824 | SWISSPROT | DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) |
| 10289 | 22764 | 35751 | 0.67 | 2.1E-01 | BF574254.1 | EST_HUMAN | (80 KD DIACYLGLYCEROL KINASE) 602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10505 | 22899 | 36007 | 0.5 | 2.1E-01 | AF294296.1 | NT | Anolis lineatopus isolate NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product |
| 11438 | 23898 | | 2.24 | 2.1E-01 | 11038647 | NT | Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA |
| 11451 | 23901 | 36969 | 2.34 | 2.1E-01 | BE180422.1 | EST_HUMAN | RC3-H10822-040500-013-b11 HT0822 Homo sapiens cDNA |
| 11641 | 24602 | | 1.39 | 2.1E-01 | X57624.1 | NT | Drosophila melanogaster ALA-E6 DNA, repeat region |
| 12163 | 24418 | | 1.46 | 2.1E-01 | AF217490.1 | NT | Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds |
| 12465 | 24593 | | 1.72 | 2.1E-01 | BE622149.1 | EST_HUMAN | 601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5' |
| 12607 | 24691 | 30856 | 2.08 | 2.1E-01 | BE672330.1 | EST_HUMAN | 7a56e02x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3223034 3' |
| 12612 | 24695 | 30861 | 1.26 | 2.1E-01 | AJ276505.1 | NT | Mus musculus genomic fragment, 279 Kb, chromosome 7 |
| 214 | 12875 | 25362 | 1.86 | 2.0E-01 | AB017437.1 | NT | Gallus gallus mRNA for avian, complete cds |
| 559 | 13190 | | 2.2 | 2.0E-01 | 7705601 | NT | Homo sapiens CGI-18 protein (LOC51008), mRNA |
| 728 | 13348 | 25940 | 1.24 | 2.0E-01 | MT7085.1 | NT | O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VH2 |
| 843 | 13459 | 25968 | 1.76 | 2.0E-01 | AF027865.1 | NT | Mus musculus Major Histocompatibility Locus class II region |
| 1049 | 13656 | 26167 | 0.72 | 2.0E-01 | D90905.1 | NT | Synschoecis sp. PCC8803 complete genome, 7127, 781449-820916 |
| 1164 | 13766 | 26276 | 3.24 | 2.0E-01 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 1267 | 13891 | 26414 | 1.37 | 2.0E-01 | AJ132695.5 | NT | Homo sapiens rac1 gene |
| 1351 | 13946 | 26470 | 1.22 | 2.0E-01 | AW384637.1 | EST_HUMAN | PM1-HT0422-291290-002-c06 HT0422 Homo sapiens cDNA |
| 1507 | 14089 | | 1.22 | 2.0E-01 | AJ243957.1 | NT | Plum pox virus strain M, complete genome, isolate PS |
| 1534 | 14126 | 26663 | 23.08 | 2.0E-01 | 4503408 | NT | Homo sapiens dystrobrevin, alpha (DTNA), mRNA |
| 1569 | 14191 | 26722 | 3.03 | 2.0E-01 | AB007674.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505 |
| 1604 | 14196 | 26728 | 1.23 | 2.0E-01 | AF260700.1 | NT | Homo sapiens sodium/iodide symporter mRNA, partial cds |
| 1735 | 14326 | 26868 | 1.17 | 2.0E-01 | U22346.1 | NT | Human bradykinin B1 receptor (bradyb1) gene, complete cds |
| 1755 | 14345 | | 1.83 | 2.0E-01 | AF111170.3 | NT | Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene |
| 1795 | 14385 | | 1.99 | 2.0E-01 | U67525.1 | NT | Methanococcus jannaschii section 67 of 150 of the complete genome |
| 1834 | 14518 | 27073 | 1.14 | 2.0E-01 | BE871330.1 | EST_HUMAN | 601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5' |
| 1934 | 14518 | 27074 | 1.14 | 2.0E-01 | BE871330.1 | EST_HUMAN | 601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5' |
| 1837 | 14521 | 27077 | 1 | 2.0E-01 | 8922238 | NT | Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA |
| 2366 | 14955 | | 1.84 | 2.0E-01 | X62877.1 | NT | H. sapiens Nar-D-glucose cotransport regulator gene |
| 2915 | 15532 | | 0.66 | 2.0E-01 | AF074900.1 | NT | Homo sapiens full length insert cDNA YH85A11 |
| 3534 | 16139 | 26621 | 0.7 | 2.0E-01 | P46607 | SWISSPROT | HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10) |
| 3628 | 16229 | | 0.82 | 2.0E-01 | AW238005.1 | EST_HUMAN | xp15602x1 NCI_CGAP_HNB Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element |
| 3768 | 16369 | 26635 | 0.8 | 2.0E-01 | P34641 | SWISSPROT | MER21 repetitive element; CED-11 PROTEIN |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4028 | 16626 | 28068 | 0.78 | 2.0E-01 | Z46806.1 | NT | Sus scrofa |
| 4102 | 16668 | 29152 | 0.68 | 2.0E-01 | X63987.1 | NT | C.parastifica espC gene |
| 4522 | 17108 | 28552 | 0.78 | 2.0E-01 | AF242431.1 | NT | Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-18 |
| 4865 | 17247 | | 8.43 | 2.0E-01 | BE826165.1 | EST_HUMAN | QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA |
| 5192 | 17757 | 30188 | 7.09 | 2.0E-01 | 8922080 | NT | Homo sapiens hypothetical protein ASH1 (ASH1), mRNA |
| 5228 | 16139 | 28821 | 0.62 | 2.0E-01 | P46807 | SWISSPROT | HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10) |
| 5638 | 18285 | 30737 | 2.38 | 2.0E-01 | X56800.1 | NT | Rat SOD-2 gene for manganese-containing superoxide dismutase |
| 5916 | 18538 | 31283 | 2 | 2.0E-01 | 11432540 | NT | Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA |
| 6008 | 18628 | 31361 | 0.69 | 2.0E-01 | X91856.1 | NT | F.rubripes DNA encoding for vely-RNA synthetase |
| 6210 | 18820 | 31591 | 6.48 | 2.0E-01 | U15300.1 | NT | Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds |
| 6321 | 18928 | | 0.71 | 2.0E-01 | M75967.1 | NT | Human hepatocyte growth factor gene, exon 1 |
| 6560 | 19158 | 31855 | 3.94 | 2.0E-01 | X61033.1 | NT | M.aureus mu class glutathione transferase gene |
| 6650 | 19246 | 32049 | 3.63 | 2.0E-01 | AW360865.1 | EST_HUMAN | PM1-CT0247-141098-001-g08 CT0247 Homo sapiens cDNA |
| 7251 | 19780 | 32838 | 0.68 | 2.0E-01 | U93724.1 | NT | Mycoplasma genitalium section 46 of 51 of the complete genome |
| 7336 | 19893 | 32727 | 1.18 | 2.0E-01 | AF260371.1 | NT | Mus musculus phosphofructokinase-1 C isozyme (Pfkc) gene, exons 3 through 7 |
| 7775 | 20284 | 33181 | 1.53 | 2.0E-01 | AK024427.1 | NT | Homo sapiens mRNA for FLJ00016 protein, partial cds |
| 7895 | 20437 | | 8.45 | 2.0E-01 | AF028028.1 | NT | Andes virus strain OI23133 glycoprotein G1 and G2 precursor, gene, partial cds |
| 8142 | 20683 | 33586 | 2.91 | 2.0E-01 | X91151.1 | NT | M.musculus scp2 gene exon 14 |
| 8858 | 21197 | | 0.53 | 2.0E-01 | BE562247.1 | EST_HUMAN | 601344848F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677784 5' |
| 9273 | 21788 | 34749 | 1.03 | 2.0E-01 | U82511.1 | NT | Dictyostelium discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds |
| 9312 | 21828 | 34775 | 0.66 | 2.0E-01 | U71122.1 | NT | Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds |
| 9475 | 21874 | | 4.35 | 2.0E-01 | AE001278.1 | NT | Chlamydia trachomatis section 5 of 87 of the complete genome |
| 9681 | 22160 | 35132 | 0.51 | 2.0E-01 | P11420 | SWISSPROT | DAUGHTERLESS PROTEIN |
| 9681 | 22160 | 35133 | 0.51 | 2.0E-01 | P11420 | SWISSPROT | DAUGHTERLESS PROTEIN |
| 9808 | 22304 | | 1.88 | 2.0E-01 | AF146892.1 | NT | Homo sapiens filamin 2 (FLN2) mRNA, complete cds |
| 9854 | 22449 | 35431 | 1.78 | 2.0E-01 | AF086807.1 | NT | Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds |
| 9854 | 22449 | 35432 | 1.78 | 2.0E-01 | AF086807.1 | NT | Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds |
| 10072 | 22567 | 35562 | 0.53 | 2.0E-01 | AF157814.1 | NT | Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12 |
| 10072 | 22567 | 35563 | 0.53 | 2.0E-01 | AF157814.1 | NT | Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12 |
| 10115 | 22610 | | 0.72 | 2.0E-01 | X78398.1 | NT | D.melanogaster DNA mobile element (hoppe) |
| 10304 | 22788 | 35789 | 0.88 | 2.0E-01 | X97121.1 | NT | R.norvegicus mRNA for NTR2 receptor |
| 10720 | 23248 | 36263 | 2.77 | 2.0E-01 | D88088.1 | NT | Salvelinus pluvius mRNA for transferrin, complete cds |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10720 | 23248 | 30284 | 2.77 | 2.0E-01 | D80888.1 | NT | Sarvelinus pluvius mRNA for transferrin, complete cds |
| 12182 | 24402 | | 1.34 | 2.0E-01 | AF208837.2 | NT | Pimphales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds |
| 12374 | 24887 | | 1.95 | 2.0E-01 | AF302773.1 | NT | Homo sapiens ninhydrin-Lm isoform (nitrin) mRNA, complete cds |
| 12388 | 24807 | 30788 | 2.81 | 2.0E-01 | AW975287.1 | EST_HUMAN | EST387405 IMAGE resequences, MAGN Homo sapiens cDNA |
| 12425 | 24810 | 30888 | 3.97 | 2.0E-01 | A023582.1 | EST_HUMAN | ov80a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3' |
| 12449 | 24584 | | 17.06 | 2.0E-01 | AF078164.2 | NT | Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds |
| 115 | 12786 | | 6.22 | 1.8E-01 | 7548743 | NT | Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA |
| 374 | 13023 | 25509 | 5.4 | 1.8E-01 | AF004353.1 | NT | Mus musculus pelle eer (ep) gene, wild type allele, 3' region, partial cds |
| 684 | 13308 | 25792 | 1.47 | 1.8E-01 | U32581.2 | NT | Homo sapiens lamda10a protein kinase C-interacting protein mRNA, complete cds |
| 684 | 13308 | 25793 | 1.47 | 1.8E-01 | U32581.2 | NT | Homo sapiens lamda10a protein kinase C-interacting protein mRNA, complete cds |
| 691 | 13315 | 25800 | 6.6 | 1.8E-01 | BE070801.1 | EST_HUMAN | RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA |
| 692 | 13315 | 25800 | 6.82 | 1.8E-01 | BE070801.1 | EST_HUMAN | RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA |
| 1023 | 13633 | | 1.92 | 1.8E-01 | 7305180 | NT | Mus musculus intercalin 2 receptor, gamma chain (Il2rg), mRNA |
| 1143 | 13748 | 26258 | 10.04 | 1.8E-01 | A4358813.1 | EST_HUMAN | EST87784 Fetal lung II Homo sapiens cDNA 5' end |
| 1413 | 14006 | 26534 | 2.41 | 1.8E-01 | AF061282.1 | NT | Sorghum bicolor 22 kDa kafirin cluster |
| 1482 | 14075 | | 4.02 | 1.8E-01 | AF184823.1 | NT | Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds |
| 2185 | 14761 | 27331 | 1.29 | 1.8E-01 | AA916482.1 | EST_HUMAN | d44408.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1528369 3' similar to gb:AC03911 |
| 2422 | 14990 | 27563 | 3.27 | 1.8E-01 | 8022533 | NT | GLIA DERIVED NEXIN PRECURSOR (HUMAN); |
| 2849 | 15565 | 28039 | 4.1 | 1.8E-01 | U68068.1 | NT | Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA |
| 2865 | 15580 | | 6.58 | 1.8E-01 | J00822.1 | NT | Sigmoidon hispidus p63 gene, partial cds |
| 3033 | 15649 | 28128 | 1.05 | 1.8E-01 | U25148.1 | NT | Gallus gallus ovalbumin (Y) gene, complete cds |
| 3442 | 16050 | 28528 | 4.19 | 1.8E-01 | D13197.1 | NT | Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds |
| 3528 | 16131 | 28611 | 5.24 | 1.8E-01 | R16467.1 | EST_HUMAN | Mouse gene for immunoglobulin diversity region D1 |
| 3877 | 16475 | 28939 | 0.76 | 1.8E-01 | AF284017.1 | NT | y4210.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5' |
| 4084 | 16681 | 29123 | 3.85 | 1.8E-01 | AB006784.1 | NT | Rattus norvegicus arylacetamide deacetylase gene, complete cds |
| 4157 | 16749 | 29202 | 1.86 | 1.8E-01 | AW754106.1 | EST_HUMAN | Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds |
| 4315 | 16801 | 29345 | 1.17 | 1.8E-01 | BE834943.1 | EST_HUMAN | CM3-CT0315-271189-045-b11 CT0315 Homo sapiens cDNA |
| 4588 | 17161 | 29587 | 0.69 | 1.8E-01 | AL161483.2 | NT | MR1-FN0010-280700-007-d04 FN0010 Homo sapiens cDNA |
| 5153 | 17728 | | 1.11 | 1.8E-01 | AF223842.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5 |
| 5789 | 18414 | | 5.46 | 1.8E-01 | AW130149.1 | EST_HUMAN | Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds |
| 5828 | 18450 | 31173 | 7.81 | 1.8E-01 | AF127837.1 | NT | x728a07.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC |
| 6005 | 18625 | 31360 | 0.73 | 1.8E-01 | AF091216.1 | NT | ACID RECEPTOR ALPHA-1 (HUMAN); |
| | | | | | | | Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a |
| | | | | | | | Mus musculus Wm protein (Wm) gene, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6046 | 18695 | | 2.52 | 1.9E-01 | AU133116.1 | EST_HUMAN | AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5' |
| 6469 | 19070 | 31855 | 1.07 | 1.9E-01 | A1762391.1 | EST_HUMAN | w54h02.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2394098 3' |
| 6623 | 19123 | 31916 | 1.23 | 1.9E-01 | AW148462.1 | EST_HUMAN | xf14c08.x1 NCI_CGAP_K048 Homo sapiens cDNA clone IMAGE:2818030 3' similar to gb:X035559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN); y08a12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element; |
| 7050 | 18068 | 30460 | 1.37 | 1.9E-01 | R43212.1 | EST_HUMAN | Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11 |
| 7072 | 19844 | 32481 | 0.91 | 1.9E-01 | AF034920.1 | NT | Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11 |
| 7072 | 19844 | 32482 | 0.91 | 1.9E-01 | AF034920.1 | NT | Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11 |
| 7503 | 20025 | 32989 | 1.3 | 1.9E-01 | U80822.1 | NT | Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds |
| 7543 | 20083 | 32937 | 2.89 | 1.9E-01 | AF072724.1 | NT | Zea mays starch branching enzyme I (sbe1) gene, complete cds |
| 7827 | 20488 | 33378 | 1.71 | 1.9E-01 | AL161557.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57 |
| 8820 | 21159 | 34074 | 12.12 | 1.9E-01 | AB033024.1 | NT | Homo sapiens mRNA for KIAA1198 protein, partial cds |
| 8875 | 21414 | 34337 | 1.38 | 1.9E-01 | M14588.1 | NT | Marsupial cat beta-globin gene mRNA, partial cds |
| 8875 | 21414 | 34338 | 1.38 | 1.9E-01 | M14588.1 | NT | Marsupial cat beta-globin gene mRNA, partial cds |
| 9789 | 22287 | 35271 | 0.72 | 1.9E-01 | AA912488.1 | EST_HUMAN | cd9g10.s1 NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element |
| 10140 | 22635 | 35628 | 0.71 | 1.9E-01 | BE830553.1 | EST_HUMAN | RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA |
| 10140 | 22635 | 35627 | 0.71 | 1.9E-01 | BE830553.1 | EST_HUMAN | RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA |
| 10523 | 23081 | 36071 | 2.02 | 1.9E-01 | AL161503.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15 |
| 10523 | 23081 | 36072 | 2.02 | 1.9E-01 | AL161503.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15 |
| 10835 | 23187 | 36178 | 2.08 | 1.9E-01 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 11377 | 23828 | 36891 | 1.68 | 1.9E-01 | M22253.1 | NT | Rattus norvegicus sodium channel I mRNA, complete cds |
| 11571 | 24018 | 37088 | 2.68 | 1.9E-01 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 12207 | 24431 | | 1.33 | 1.9E-01 | AF055900.1 | NT | Drosophila melanogaster clathrin light chain mRNA, complete cds |
| 12582 | 24874 | | 3.69 | 1.9E-01 | AF001168.1 | NT | Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds |
| 34 | 12713 | 25172 | 2.56 | 1.8E-01 | U73200.1 | NT | Mus musculus p116Rip mRNA, complete cds |
| 281 | 15412 | 25423 | 1.67 | 1.8E-01 | AB022060.1 | NT | Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds |
| 383 | 13039 | 25530 | 1.76 | 1.8E-01 | 4502532 | NT | Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products |
| 776 | 13396 | 25996 | 0.77 | 1.8E-01 | AB021490.2 | NT | Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds |
| 1018 | 13628 | 26141 | 0.78 | 1.8E-01 | A1912212.1 | EST_HUMAN | wd71102.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3' |
| 1130 | 13732 | 26242 | 1.28 | 1.8E-01 | AF000580.1 | NT | Dicotyledon discoidium plasmid Ddp5, complete genome |
| 1332 | 13928 | 26447 | 6.97 | 1.8E-01 | AL117169.1 | NT | Yersinia pestis plasmid pCD1 |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1551 | 14143 | 28678 | 1.31 | 1.8E-01 | 6753947 | NT | Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA |
| 1551 | 14143 | 28677 | 1.31 | 1.8E-01 | 6753947 | NT | Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA |
| 1887 | 14472 | | 2.79 | 1.8E-01 | 4505038 | NT | Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA |
| 1907 | 14492 | | 2.22 | 1.8E-01 | A1733708.1 | EST_HUMAN | cg22ad10.x6 NCI_CGAP_K143 Homo sapiens cDNA clone IMAGE:1781811 3' similar to TR:O76838 O76838 GAMMA BUTYROBETAINE HYDROXYLASE: |
| 1958 | 14542 | 27088 | 1.52 | 1.8E-01 | AB051897.1 | NT | Mus musculus Scya8, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds |
| 2716 | 15273 | | 2.28 | 1.8E-01 | AW935728.1 | EST_HUMAN | QV3-DT0018-081289-038-p04 DT0018 Homo sapiens cDNA |
| 2923 | 15540 | | 2.36 | 1.8E-01 | AF194589.1 | NT | Jonopsidium aculea LEAFY protein (LEAFY2) gene, partial cds |
| 2828 | 15544 | 28020 | 1.18 | 1.8E-01 | AW182300.1 | EST_HUMAN | x41a03.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2859756 3' |
| 3158 | 15772 | 28238 | 1.31 | 1.8E-01 | AW985178.1 | EST_HUMAN | QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA |
| 3413 | 16021 | 28501 | 0.71 | 1.8E-01 | BF183582.1 | EST_HUMAN | 601809/23R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3' |
| 3683 | 16284 | 28752 | 0.79 | 1.8E-01 | H033389.1 | EST_HUMAN | y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element |
| 3683 | 16284 | 28753 | 0.79 | 1.8E-01 | H033389.1 | EST_HUMAN | y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element |
| 4333 | 16920 | 28382 | 0.78 | 1.8E-01 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 4428 | 17012 | | 4.07 | 1.8E-01 | D37854.1 | NT | Bovine NB25 mRNA for MHC class II (BdA-DQB), complete cds |
| 4654 | 17236 | 28691 | 6.69 | 1.8E-01 | AL161566.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58 |
| 4898 | 17461 | 28914 | 2.51 | 1.8E-01 | AB051897.1 | NT | Mus musculus Scya8, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds |
| 4928 | 17503 | 28950 | 1.03 | 1.8E-01 | X82179.1 | NT | S.tuberosum mRNA for alcohol dehydrogenase |
| 5198 | 17763 | 30188 | 2.18 | 1.8E-01 | AW814270.1 | EST_HUMAN | MR3-ST0203-151289-112-p06 ST0203 Homo sapiens cDNA |
| 5216 | 17781 | 30200 | 1.59 | 1.8E-01 | A1792382.1 | EST_HUMAN | an28g07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5' |
| 5257 | 17820 | 30245 | 1.5 | 1.8E-01 | AF181258.1 | NT | Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds |
| 5281 | 17843 | 30270 | 1.07 | 1.8E-01 | A1439881.1 | EST_HUMAN | 557e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3' |
| 5298 | 17850 | 30276 | 0.59 | 1.8E-01 | AF132115.1 | NT | Arabidopsis thaliana cytochrome b-561 (CYTB561) gene, partial cds |
| 5338 | 17899 | 30314 | 0.78 | 1.8E-01 | AJ132844.1 | NT | Broad bean wilt virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein |
| 5338 | 17899 | 30315 | 0.78 | 1.8E-01 | AJ132844.1 | NT | Broad bean wilt virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein |
| 5398 | 17956 | 30367 | 2.04 | 1.8E-01 | AW809402.1 | EST_HUMAN | MR4-ST0121-041189-019-b01 ST0121 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5976 | 18598 | 31331 | 1 | 1.8E-01 | AL161594.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90 |
| 6082 | 18689 | 31448 | 1.01 | 1.8E-01 | N28829.1 | EST_HUMAN | y438h08.l1 Soares melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:284063 5' |
| 6277 | 18885 | 31653 | 1.1 | 1.8E-01 | 6878428 | NT | Mus musculus Trf receptor-associated factor 6 (Trf6), mRNA |
| 6277 | 18885 | 31654 | 1.1 | 1.8E-01 | 6878428 | NT | Mus musculus Trf receptor-associated factor 6 (Trf6), mRNA |
| 6635 | 19231 | 32035 | 2.03 | 1.8E-01 | Q9QY14 | SWISSPROT | FORKHEAD BOX PROTEIN E3 |
| 6875 | 19271 | | 2.24 | 1.8E-01 | N94893.1 | EST_HUMAN | y62h02.l1 Soares_multiple_sclerosis_2N1bHMSP Homo sapiens cDNA clone IMAGE:278163 5' |
| 7077 | 19649 | 32487 | 1.22 | 1.8E-01 | AB018561.1 | NT | Citellus lateralis mRNA for vsus, complete cds |
| 7077 | 19649 | 32488 | 1.22 | 1.8E-01 | AB018561.1 | NT | Citellus lateralis mRNA for vsus, complete cds |
| 7117 | 19457 | 32272 | 0.71 | 1.8E-01 | BE681853.1 | EST_HUMAN | 601848361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3' |
| 8547 | 21088 | 34009 | 0.47 | 1.8E-01 | AW966118.1 | EST_HUMAN | EST378101 MAGE resequences, MAGI Homo sapiens cDNA |
| 9268 | 21782 | 34741 | 1.13 | 1.8E-01 | MF3258.1 | NT | Human cellular DNA/Human papillomavirus proviral DNA |
| 9298 | 21896 | 34843 | 1.39 | 1.8E-01 | 9626232 | NT | Bacteriophage like, complete genome |
| 9412 | 21921 | | 0.55 | 1.8E-01 | AA463751.1 | EST_HUMAN | h02a05.a1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:949088 similar to contains L1.13 L1 |
| 9494 | 21994 | 34950 | 1.13 | 1.8E-01 | P15272 | SWISSPROT | repetitive element; |
| 9494 | 21994 | 34951 | 1.13 | 1.8E-01 | P15272 | SWISSPROT | AMP NUCLEOSIDASE |
| 9532 | 22032 | 34980 | 0.95 | 1.8E-01 | M26019.1 | NT | AMP NUCLEOSIDASE |
| 9532 | 22032 | 34991 | 0.95 | 1.8E-01 | M26019.1 | NT | S. commune erodine-5'-phosphate decarboxylase (URA1) gene, complete cds |
| 9894 | 22193 | 35168 | 0.62 | 1.8E-01 | P08123 | SWISSPROT | S. commune erodine-5'-phosphate decarboxylase (URA1) gene, complete cds |
| 9898 | 22197 | 35170 | 0.69 | 1.8E-01 | U67548.1 | NT | COLLAGEN ALPHA 2(I) CHAIN PRECURSOR |
| 10039 | 22534 | | 0.64 | 1.8E-01 | AF200262.1 | NT | Methanococcus jannaschii section 90 of 150 of the complete genome |
| 10271 | 22766 | 35753 | 1.22 | 1.8E-01 | X63440.1 | NT | Aquarius encephali cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product |
| 10516 | 23054 | 36068 | 2.37 | 1.8E-01 | X77338.1 | NT | Mus musculus mRNA for P19-protein tyrosine phosphatase |
| 10558 | 23084 | 36106 | 7.47 | 1.8E-01 | U38906.1 | NT | A.thaliana mRNA for ribonucleotide reductase R2 |
| 10615 | 19649 | 32487 | 3.07 | 1.8E-01 | AB018561.1 | NT | Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysis genes, complete cds |
| 10615 | 19649 | 32488 | 3.07 | 1.8E-01 | AB018561.1 | NT | Citellus lateralis mRNA for vsus, complete cds |
| 10618 | 23148 | 36160 | 4.49 | 1.8E-01 | AF019107.1 | NT | Citellus lateralis mRNA for vsus, complete cds |
| 10897 | 23417 | 36434 | 1.84 | 1.8E-01 | M58257.1 | NT | Dictyostelium discoideum unknown (DG1041) gene, complete cds |
| 11337 | 23035 | 36045 | 4.3 | 1.8E-01 | X57033.1 | NT | Human carcinoembryonic antigen (CEA) gene, exon 4 |
| 11589 | 24042 | 37111 | 2.74 | 1.8E-01 | 8394421 | NT | B. taurus mRNA for potassium channel |
| 11626 | 24068 | 37132 | 1.8 | 1.8E-01 | U40487.1 | NT | Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA |
| 11748 | 24148 | | 2.04 | 1.8E-01 | 10086561 | NT | Mycobacterium smegmatis proton antiporter efflux pump (lfrA), complete cds |
| | | | | | | | Bovine ephemeral fever virus, complete genome |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11814 | 24188 | 31032 | 1.41 | 1.8E-01 | BF348823.1 | EST_HUMAN | 602019828F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4155318 5' |
| 12218 | 13828 | 26447 | 1.3 | 1.8E-01 | AL117189.1 | NT | Yersinia pestis plasmid pCD1 |
| 12291 | 24481 | | 5.61 | 1.8E-01 | Q86882 | SWISSPROT | DNA TERMINAL PROTEIN (BELLETTI PROTEIN) (PTP PROTEIN) |
| 12416 | 24689 | | 23.47 | 1.8E-01 | R24494.1 | EST_HUMAN | yH48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5' |
| 12459 | 24590 | | 2.75 | 1.8E-01 | Y11114.1 | NT | E. dispar mRNA for headkinase (hdk1) |
| 12502 | 25045 | 30507 | 1.58 | 1.8E-01 | 8508952 | NT | Rattus norvegicus procollagen C-proteinase enhancer protein (Pcdce), mRNA |
| 603 | 13232 | 25705 | 5.53 | 1.7E-01 | BE385184.1 | EST_HUMAN | 601274804F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815788 5' |
| 838 | 13454 | 25894 | 2.89 | 1.7E-01 | X53330.1 | NT | P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4 |
| 998 | 13608 | | 8.63 | 1.7E-01 | P35816 | SWISSPROT | NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL) |
| 1098 | 13701 | 28210 | 0.87 | 1.7E-01 | AF081810.1 | NT | Lymantia dispar nucleopolydnavirus, complete genome |
| 1098 | 13701 | 28211 | 0.87 | 1.7E-01 | AF081810.1 | NT | Lymantia dispar nucleopolydnavirus, complete genome |
| 1853 | 14441 | 26898 | 0.85 | 1.7E-01 | AL161573.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68 |
| 2025 | 14807 | | 2.84 | 1.7E-01 | AF255051.1 | NT | Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product |
| 2885 | 15503 | 27873 | 1.98 | 1.7E-01 | AF000716.1 | NT | Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds |
| 2885 | 15503 | 27874 | 1.98 | 1.7E-01 | AF000716.1 | NT | Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds |
| 2953 | 15569 | 28044 | 1.53 | 1.7E-01 | AA336808.1 | EST_HUMAN | EST41851 Endometrial tumor Homo sapiens cDNA 5' end |
| 3027 | 15643 | 28121 | 1.9 | 1.7E-01 | AJ238736.1 | NT | Naja naja atra cdx-1 gene, exons 1-3 |
| 3027 | 15643 | 28122 | 1.9 | 1.7E-01 | AJ238736.1 | NT | Naja naja atra cdx-1 gene, exons 1-3 |
| 3139 | 15753 | 28220 | 1.91 | 1.7E-01 | AF081514.1 | NT | Taous canadensis geranylgeranyl diphosphate synthase mRNA, complete cds |
| 3412 | 16020 | 28500 | 1.11 | 1.7E-01 | N55763.1 | EST_HUMAN | J2348F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2348 5' |
| 3494 | 16099 | 28574 | 1.26 | 1.7E-01 | AJ288505.1 | NT | Arabidopsis sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene |
| 4012 | 16610 | 29083 | 4.89 | 1.7E-01 | AJ25377.1 | NT | Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene |
| 4658 | 17240 | | 1.63 | 1.7E-01 | X52836.1 | NT | Schistosoma gregaria alpha repetitive DNA |
| 4877 | 17452 | 28804 | 0.84 | 1.7E-01 | AF217490.1 | NT | Homo sapiens fragile 16D cdc16 reductase (FOR) gene, exons 8, 9, and partial cds |
| 4965 | 17539 | 28981 | 1.07 | 1.7E-01 | AI247635.1 | EST_HUMAN | qH57d08.x1 Soares fetal liver spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element: |
| 5210 | 17775 | | 0.88 | 1.7E-01 | U28376.1 | NT | Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds |
| 5242 | 17808 | 30227 | 1.02 | 1.7E-01 | BF688719.1 | EST_HUMAN | 602186830F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4288848 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5297 | 17959 | | 1.08 | 1.7E-01 | AF072725.1 | NT | Zea mays starch branching enzyme IIb (se) gene, complete cds |
| 5342 | 17903 | 30319 | 0.8 | 1.7E-01 | BF030010.1 | EST_HUMAN | 601557256F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5' |
| 5421 | 17978 | 30388 | 7.82 | 1.7E-01 | J04479.1 | NT | S.pneumoniae DNA polymerase I (polA) gene, complete cds |
| 5604 | 18233 | 30683 | 1.92 | 1.7E-01 | AA470886.1 | EST_HUMAN | ne13a02.s1 NCI_OGAP_Co3 Homo sapiens cDNA clone IMAGE:881068 3' similar to gb:M17888 60S |
| 5804 | 18233 | 30684 | 1.92 | 1.7E-01 | AA470886.1 | EST_HUMAN | ne13a02.s1 NCI_OGAP_Co3 Homo sapiens cDNA clone IMAGE:881068 3' similar to gb:M17888 60S |
| 5779 | 18404 | 31120 | 0.7 | 1.7E-01 | U43599.1 | NT | ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); |
| 6471 | 19072 | 31858 | 20.9 | 1.7E-01 | H72118.1 | EST_HUMAN | Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds |
| 6522 | 19122 | 31913 | 1.33 | 1.7E-01 | A1370978.1 | EST_HUMAN | ys02p08.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:213658 3' |
| 6522 | 19122 | 31914 | 1.33 | 1.7E-01 | A1370978.1 | EST_HUMAN | la20c11.x1 Soares_fetal_lung_NHIL19W Homo sapiens cDNA clone IMAGE:2045492 3' |
| 6837 | 18045 | 30467 | 0.71 | 1.7E-01 | BE300286.1 | EST_HUMAN | la20c11.x1 Soares_fetal_lung_NHIL19W Homo sapiens cDNA clone IMAGE:2045492 3' |
| 6860 | 19537 | | 2.28 | 1.7E-01 | AF028652.3 | NT | 600844007T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860248 3' |
| 7074 | 19848 | | 0.67 | 1.7E-01 | 282910.1 | NT | Mesocricetus auratus oukductin precursor (OVI) gene, complete cds |
| 7272 | 19800 | 32657 | 2.83 | 1.7E-01 | AP000422.1 | NT | Homo sapiens HFE gene |
| 7339 | 19898 | 32730 | 8.92 | 1.7E-01 | BE734179.1 | EST_HUMAN | Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region |
| 7494 | 20017 | 32882 | 1.16 | 1.7E-01 | P16724 | SWISSPROT | 601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5' |
| 7508 | 24784 | 32893 | 0.73 | 1.7E-01 | Q01955 | SWISSPROT | PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN) |
| 7802 | 20345 | 33253 | 1.26 | 1.7E-01 | AF000573.1 | NT | COLLAGEN ALPHA 3(V) CHAIN PRECURSOR |
| 7904 | 20446 | 33352 | 0.54 | 1.7E-01 | AF150689.1 | NT | Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds |
| 8219 | 20760 | 33874 | 6.62 | 1.7E-01 | 7708428 | NT | Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds |
| 8219 | 20760 | 33875 | 6.62 | 1.7E-01 | 7708428 | NT | Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA |
| 8631 | 21170 | 34087 | 0.58 | 1.7E-01 | AW982873.1 | EST_HUMAN | Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA |
| 8682 | 21201 | 34119 | 3.28 | 1.7E-01 | D00394.1 | NT | RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA |
| 8778 | 21317 | 34239 | 0.68 | 1.7E-01 | AF217413.1 | NT | Rat (SHR strain) SX1 gene |
| 8778 | 21317 | 34240 | 0.68 | 1.7E-01 | AF217413.1 | NT | Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced |
| 9095 | 21631 | 34569 | 0.46 | 1.7E-01 | BE253142.1 | EST_HUMAN | Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced |
| 9095 | 21631 | 34570 | 0.46 | 1.7E-01 | BE253142.1 | EST_HUMAN | 601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5' |
| 9509 | 22009 | 34867 | 7.72 | 1.7E-01 | AP001508.1 | NT | 601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5' |
| 9614 | 22114 | 35077 | 0.56 | 1.7E-01 | AW977455.1 | EST_HUMAN | Bacillus halodurans genomic DNA, section 2/14 |
| 9614 | 22114 | 35078 | 0.56 | 1.7E-01 | AW977455.1 | EST_HUMAN | EST388564 IMAGE reassurances, MAGO Homo sapiens cDNA |
| 9631 | 22131 | 35098 | 2.47 | 1.7E-01 | U16288.1 | NT | EST388564 IMAGE reassurances, MAGO Homo sapiens cDNA |
| 9704 | 22203 | 35174 | 1.27 | 1.7E-01 | Z34508.1 | NT | Human class IV alcohol dehydrogenase (ADH7) gene, exon 3 |
| 9704 | 22203 | 35175 | 1.27 | 1.7E-01 | Z34508.1 | NT | Human immunodeficiency virus type 1 (B7.05) env gene (partial) |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9722 | 22220 | 35105 | 0.81 | 1.7E-01 | AJ251749.1 | NT | Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp8 gene) |
| 10132 | 22627 | | 2.24 | 1.7E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 10263 | 22787 | 35777 | 0.99 | 1.7E-01 | 11427203 | NT | Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA |
| 10285 | 22789 | 35779 | 1.72 | 1.7E-01 | AA627972.1 | EST_HUMAN | ng60e07.s1 NCI CGAP_C08 Homo sapiens cDNA clone IMAGE:1148282 3' similar to gbL25081 |
| 10560 | 23098 | 36109 | 9.23 | 1.7E-01 | BE390835.1 | EST_HUMAN | TRANSFORMING PROTEIN RHOC (HUMAN); |
| 10665 | 23215 | 36227 | 2.63 | 1.7E-01 | AA814817.1 | EST_HUMAN | 601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5' |
| 10891 | 23505 | 36536 | 8.7 | 1.7E-01 | 7108300 | NT | d43a03.s1 NCI CGAP_QNS1 Homo sapiens cDNA clone IMAGE:1426924 3' |
| 10891 | 23505 | 36537 | 8.7 | 1.7E-01 | 7106300 | NT | Mus musculus adenomatosis polyposis coli binding protein Ebt1 (Ebt1), mRNA |
| 11598 | 24008 | | 2.18 | 1.7E-01 | P15272 | SWISSPROT | Mus musculus adenomatosis polyposis coli binding protein Ebt1 (Ebt1), mRNA |
| 11643 | 24004 | | 1.45 | 1.7E-01 | AJ272584.1 | NT | AMP NUCLEOSIDASE |
| 11647 | 24079 | 37143 | 4.09 | 1.7E-01 | 11418157 | NT | Blattella aurantiaca mitochondrial partial COII gene for cytochrome c oxidase subunit II |
| 11782 | 25004 | | 1.94 | 1.7E-01 | AL163278.2 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CAGNA1I), mRNA |
| 12333 | 24517 | | 1.38 | 1.7E-01 | N40825.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C078 |
| 12361 | 24548 | 30805 | 12.95 | 1.7E-01 | U01317.1 | NT | yw62c12.r1 Soares_placenta_8to9weeks_2NHIP8a8W Homo sapiens cDNA clone IMAGE:258742 5' |
| 12809 | 24683 | | 1.33 | 1.7E-01 | AJ132510.1 | NT | Human beta globin region on chromosome 11 |
| 131 | 12738 | 25285 | 1.57 | 1.6E-01 | AF217532.1 | NT | Sus scrofa c-fos gene, exons 1-4 |
| 708 | 15388 | 25816 | 1.56 | 1.6E-01 | R31497.1 | EST_HUMAN | Homo sapiens mesonectin kinase gene, exon 6 and 7 |
| 1569 | 14161 | 26862 | 4.35 | 1.6E-01 | AF298117.1 | NT | yh75f12.r1 Soares_placenta_Nb2fP Homo sapiens cDNA clone IMAGE:135589 5' |
| 1868 | 14552 | 27108 | 2.8 | 1.6E-01 | P22063 | SWISSPROT | Homo sapiens homeobox protein OTX2 gene, complete cds |
| 2028 | 14610 | | 1.08 | 1.6E-01 | U10334.1 | NT | AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) |
| 2427 | 15468 | 27569 | 0.98 | 1.6E-01 | X94232.1 | NT | Crossostrea gigas RNA polymerase II largest subunit mRNA, partial cds |
| 2535 | 15089 | 27672 | 1.12 | 1.6E-01 | AB037729.1 | NT | H. sapiens mRNA for novel T-cell activation protein |
| 2917 | 15534 | 28008 | 11.95 | 1.6E-01 | AF185589.1 | NT | Homo sapiens mRNA for KIAA1308 protein, partial cds |
| 2917 | 15534 | 28007 | 11.95 | 1.6E-01 | AF185589.1 | NT | Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region |
| 3041 | 19657 | 28137 | 1.17 | 1.6E-01 | AE001862.1 | NT | Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region |
| 3695 | 16296 | 28785 | 1.35 | 1.6E-01 | AJ003165.1 | NT | Deinoceratops radiodurans R1 section 1 of 2 of the complete chromosome 2 |
| 3695 | 16296 | 28788 | 1.35 | 1.6E-01 | AJ003165.1 | NT | Populus trichocarpa cv. Trichobol AB13 gene |
| 3940 | 16439 | 28901 | 0.71 | 1.6E-01 | AE000962.1 | NT | Populus trichocarpa cv. Trichobol AB13 gene |
| 4072 | 16688 | | 2.65 | 1.6E-01 | AE004413.1 | NT | Archaeoglobus fulgidus section 145 of 172 of the complete genome |
| 4422 | 17007 | 29450 | 11.02 | 1.6E-01 | AF179880.1 | NT | Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome |
| 4554 | 17137 | | 3.42 | 1.6E-01 | AW868601.1 | EST_HUMAN | Homo sapiens apelin gene, complete cds |
| | | | | | | EST_HUMAN | EST1380677 IMAGE resequences, MAGJ Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4563 | 17146 | | 4.68 | 1.6E-01 | 6753319 | NT | Mus musculus chaperonin subunit 3 (gamma) (Cα3), mRNA |
| 5057 | 17630 | 30074 | 0.84 | 1.6E-01 | P40631 | SWISSPROT | MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MCLH) (CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA) |
| 5080 | 17653 | 30083 | 1.45 | 1.6E-01 | AA088343.1 | EST_HUMAN | z84409.s1 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:511381 3' similar to TR:E221865 |
| 5101 | 17673 | 30112 | 1.28 | 1.6E-01 | AJ006356.1 | NT | E221865 38,855 BP SEGMENT OF CHROMOSOME XIV.; |
| 5101 | 17673 | 30113 | 1.28 | 1.6E-01 | AJ006356.1 | NT | Lycopodium obscurum RsaI fragment 2, satellite region |
| 5358 | 17818 | | 1.81 | 1.6E-01 | BF208302.1 | EST_HUMAN | Lycopodium obscurum RsaI fragment 2, satellite region |
| 5359 | 17919 | 30333 | 1.23 | 1.6E-01 | A1874074.1 | EST_HUMAN | 601872523F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4086885 5' |
| 5587 | 18218 | 30688 | 0.76 | 1.6E-01 | L40608.1 | NT | wn48c08.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2439182 3' |
| 5713 | 18339 | 30844 | 2.78 | 1.6E-01 | AW197486.1 | EST_HUMAN | Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds |
| 5713 | 18339 | 30845 | 2.78 | 1.6E-01 | AW197486.1 | EST_HUMAN | xn4301.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75884 O75884 |
| 5725 | 18351 | 31054 | 2.12 | 1.6E-01 | AF034716.1 | NT | HYPOTHETICAL 127.6 KD PROTEIN; |
| 6178 | 18789 | 31558 | 0.84 | 1.6E-01 | BE925803.1 | EST_HUMAN | Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds |
| 6559 | 19157 | 31953 | 2 | 1.6E-01 | AL161588.2 | NT | RC3-BN0034-310800-113-H01 BN0034 Homo sapiens cDNA |
| 6559 | 19157 | 31954 | 2 | 1.6E-01 | AL161588.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84 |
| 7043 | 18083 | 30453 | 3.49 | 1.6E-01 | AW291215.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84 |
| 7753 | 20261 | 33157 | 1.44 | 1.6E-01 | AW248356.1 | EST_HUMAN | U1-H-B12-egl-b-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3' |
| 7770 | 20278 | | 0.75 | 1.6E-01 | AU136525.1 | EST_HUMAN | 2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5' |
| 7810 | 20353 | 33262 | 1.43 | 1.6E-01 | L48349.1 | NT | AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004468 5' |
| 7888 | 20510 | | 0.55 | 1.6E-01 | BE244087.1 | EST_HUMAN | Gorilla gorilla androgen receptor gene, partial exon |
| 8062 | 20604 | 33515 | 0.78 | 1.6E-01 | U38243.1 | NT | TCBAP1E0007 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0807 |
| 8567 | 21106 | 34025 | 0.77 | 1.6E-01 | Z99119.1 | NT | Bacteroides vulgatus beta-lactamase (cbaA) gene, complete cds and mobilization protein (mobA) gene, complete cds |
| 8760 | 21258 | 34220 | 0.65 | 1.6E-01 | R13673.1 | EST_HUMAN | Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410 |
| 8863 | 21402 | | 0.64 | 1.6E-01 | L36861.1 | NT | Yf80h08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5' |
| 8901 | 21439 | 34362 | 1.91 | 1.6E-01 | Z49501.1 | NT | Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds |
| 9039 | 21576 | | 0.8 | 1.6E-01 | AF111167.2 | NT | S.cerevisiae chromosome X reading frame ORF YJF001w |
| 9569 | 22069 | | 1.93 | 1.6E-01 | BF375171.1 | EST_HUMAN | Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene |
| 9572 | 22072 | 35033 | 1.86 | 1.6E-01 | Z49501.1 | NT | RC3-ST0200-041189-011-H01 ST0200 Homo sapiens cDNA |
| | | | | | | | S.cerevisiae chromosome X reading frame ORF YJF001w |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9807 | 22107 | | 1.08 | 1.0E-01 | BE155884.1 | EST_HUMAN | PM2-HT0353-270100-004-F11 HT0353 Homo sapiens cDNA |
| 10536 | 23073 | 36087 | 2.7 | 1.0E-01 | AW850853.1 | EST_HUMAN | IL3-CT0220-111189-028-G01 CT0220 Homo sapiens cDNA |
| 10880 | 23401 | 36418 | 1.55 | 1.0E-01 | BE258849.1 | EST_HUMAN | 601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3181183 5' |
| 10894 | 23508 | | 8.03 | 1.0E-01 | AF100084.1 | NT | Pleurokinase calcium-dependent protein kinase-3 (cdpk3) gene, complete cds |
| 11289 | 23741 | 36798 | 10.88 | 1.0E-01 | 8871552 | NT | Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Aptb1), mRNA |
| 11680 | 25019 | | 1.72 | 1.0E-01 | 8879468 | NT | Mus musculus protein kinase, cGMP-dependent, type II (Ptkg2), mRNA |
| 11784 | 24189 | 36776 | 5.34 | 1.0E-01 | AV719585.1 | EST_HUMAN | AV719585 GLC Homo sapiens cDNA clone GCEMF07 5' |
| 12095 | 24382 | 30868 | 1.55 | 1.0E-01 | L14833.1 | NT | Rat carboxypeptidase PCS mRNA, 5' end |
| 12126 | 24382 | | 1.75 | 1.0E-01 | AW839711.1 | EST_HUMAN | RC1-LT0074-120200-014-F01_1 LT0074 Homo sapiens cDNA |
| 12228 | 24821 | | 11.74 | 1.0E-01 | AB045310.1 | NT | Cucumis sativus KS mRNA for anti-leucine synthase, complete cds |
| 12407 | 24584 | | 5.11 | 1.0E-01 | AK024468.1 | NT | Homo sapiens mRNA for FLJ00104 protein, partial cds |
| 12497 | 24625 | | 3.96 | 1.0E-01 | AF287344.1 | NT | Fuchsioid hybrid cultivar Qiu 84208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product |
| 12521 | 24637 | 30896 | 1.88 | 1.0E-01 | 9506522 | NT | Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA |
| 289 | 12828 | 25412 | 1.76 | 1.5E-01 | BE710087.1 | EST_HUMAN | L3-HT0819-040700-197-E05 HT0819 Homo sapiens cDNA |
| 289 | 12828 | 25413 | 1.76 | 1.5E-01 | BE710087.1 | EST_HUMAN | L3-HT0819-040700-197-E05 HT0819 Homo sapiens cDNA |
| 613 | 15387 | | 2.18 | 1.5E-01 | AV711680.1 | EST_HUMAN | AV711688 DCA Homo sapiens cDNA clone DCAADH08 5' |
| 815 | 13433 | 25038 | 1.04 | 1.5E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 1131 | 13734 | 28244 | 0.84 | 1.5E-01 | AJ009735.1 | NT | Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR |
| 1136 | 13739 | 28248 | 2.28 | 1.5E-01 | AJ251885.1 | NT | Homo sapiens partial SL C22A2 gene for organic cation transporter (OCT2), exon 1 |
| 1152 | 13756 | | 1.61 | 1.5E-01 | L36125.1 | NT | Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end |
| 1258 | 13855 | 28371 | 0.79 | 1.5E-01 | AW195516.1 | EST_HUMAN | xt39d11.xt NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2896085 3' |
| 1318 | 13912 | 28432 | 3.12 | 1.5E-01 | D26535.1 | NT | Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15) |
| 1318 | 13912 | 28433 | 3.12 | 1.5E-01 | D26535.1 | NT | Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15) |
| 1529 | 14121 | 28680 | 1.84 | 1.5E-01 | AF117340.1 | NT | Mus musculus MAP kinase kinase kinase 1 (Meck1) mRNA, complete cds |
| 1851 | 14535 | 27091 | 1.62 | 1.5E-01 | AW444451.1 | EST_HUMAN | UH-HB13-ekb-b-09-0-JL1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3' |
| 2738 | 15291 | 27859 | 1.17 | 1.5E-01 | BF695381.1 | EST_HUMAN | 602083289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5' |
| 2838 | 15554 | | 1.01 | 1.5E-01 | AW572516.1 | EST_HUMAN | hw58a02.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:4247537 5' |
| 3070 | 15885 | 28157 | 0.62 | 1.5E-01 | M81441.1 | NT | THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN); Bos taurus factor V variant 2 (factor V) mRNA, complete cds |
| 3395 | 16003 | 28484 | 6.87 | 1.5E-01 | AA835048.1 | EST_HUMAN | cc88a05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433 |
| 3415 | 16023 | 28504 | 0.65 | 1.5E-01 | Z23104.1 | NT | RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN); L stagnalis mRNA for G protein-coupled receptor |
| 3415 | 16023 | 28505 | 0.65 | 1.5E-01 | Z23104.1 | NT | L stagnalis mRNA for G protein-coupled receptor |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3474 | 16080 | 28553 | 0.89 | 1.5E-01 | AW612237.1 | EST_HUMAN | h2802.x1 NCL_CGAP_JL24 Homo sapiens cDNA clone IMAGE:2858539 3' similar to contains element MER16 repetitive element; |
| 3819 | 16419 | 28881 | 2.13 | 1.5E-01 | U08804.1 | NT | Mus musculus ICR/Swiss glyceralddehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds |
| 3835 | 16434 | 28886 | 0.94 | 1.5E-01 | 7108358 | NT | Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA |
| 3849 | 16447 | 28908 | 0.58 | 1.5E-01 | M97882.1 | NT | XfNA; Thermosaccharibacterium; xfNA; 4182 base-pairs |
| 3894 | 16532 | 28989 | 2.74 | 1.5E-01 | AW685863.1 | EST_HUMAN | H10008.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3' |
| 3951 | 16549 | 29017 | 0.9 | 1.5E-01 | AJ003165.1 | NT | Populus trichocarpa cv. Trichobal ABI3 gene |
| 3951 | 16549 | 29018 | 0.9 | 1.5E-01 | AJ003165.1 | NT | Populus trichocarpa cv. Trichobal ABI3 gene |
| 4124 | 16717 | 29173 | 0.82 | 1.5E-01 | AW388559.1 | EST_HUMAN | RC2-HT0149-191089-012-c09 HT0149 Homo sapiens cDNA |
| 4282 | 16848 | 29298 | 0.62 | 1.5E-01 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 4833 | 17411 | 28884 | 1.29 | 1.5E-01 | BF687885.1 | EST_HUMAN | Homo sapiens cDNA clone IMAGE:4066223 5' |
| 4863 | 15291 | 27659 | 2.03 | 1.5E-01 | BF685381.1 | EST_HUMAN | 602087192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4247537 5' |
| 4906 | 17481 | 28838 | 0.82 | 1.5E-01 | BE173796.1 | EST_HUMAN | GMD-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA |
| 4908 | 17481 | 28839 | 0.82 | 1.5E-01 | BE173796.1 | EST_HUMAN | GMD-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA |
| 5139 | 17711 | 30141 | 1.58 | 1.5E-01 | AL161580.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80 |
| 5481 | 18098 | 30414 | 1.96 | 1.5E-01 | P07896 | SWISSPROT | THROMBOSPONDIN 1 PRECURSOR |
| 5489 | 18123 | 30530 | 0.8 | 1.5E-01 | AF258852.1 | NT | Caiman crocodilus MHC class II beta chain (hclibeta) gene, complete cds |
| 5531 | 18163 | | 5.6 | 1.5E-01 | P15198 | SWISSPROT | SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) |
| 5729 | 18355 | 31059 | 4.68 | 1.5E-01 | AW850764.1 | EST_HUMAN | (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP) |
| 5767 | 18383 | 31108 | 6.97 | 1.5E-01 | U65016.1 | NT | IL3-CT0219-160200-084-F10 CT0219 Homo sapiens cDNA |
| 5767 | 18383 | 31107 | 6.97 | 1.5E-01 | U65016.1 | NT | Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds |
| 6158 | 18788 | 31532 | 1.4 | 1.5E-01 | 6753659 | NT | Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds |
| 6158 | 18788 | 31533 | 1.4 | 1.5E-01 | 6753659 | NT | Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA |
| 6194 | 18804 | 31573 | 1.98 | 1.5E-01 | AJ276505.1 | NT | Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA |
| 6342 | 18948 | 31725 | 3.23 | 1.5E-01 | BE727658.1 | EST_HUMAN | Mus musculus genomic fragment, 279 Kb, chromosome 7 |
| 6394 | 18987 | | 1.86 | 1.5E-01 | 4506398 | NT | 601584322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5' |
| 6484 | 19085 | 31867 | 1.75 | 1.5E-01 | AF134907.1 | NT | Homo sapiens RAD54 (S. cerevisiae)-like (RAD54L) mRNA |
| 6828 | 24765 | 32027 | 1.94 | 1.5E-01 | AE001039.1 | NT | Influenza B virus (B/Nanchang/480/84) NB protein gene, complete cds; and neuraminidase gene, partial cds |
| 6852 | 18248 | 32050 | 4.63 | 1.5E-01 | 11417236 | NT | Archaeoglobus fulgidus section 68 of 172 of the complete genome |
| | | | | | | | Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 6863 | 18259 | 32063 | 1.5 | 1.5E-01 | P48508 | SWISSPROT | GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) |
| 6702 | 18297 | 32101 | 2.16 | 1.5E-01 | Q28462 | SWISSPROT | AMELOGENIN |
| 6786 | 18377 | 32192 | 0.95 | 1.5E-01 | AA714780.1 | EST_HUMAN | nm30410.at NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3' |
| 6813 | 19404 | 32220 | 1.59 | 1.5E-01 | P30143 | SWISSPROT | HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8) |
| 7055 | 18074 | 30484 | 6.39 | 1.5E-01 | AW970265.1 | EST_HUMAN | EST382378 IMAGE resequences, MAGK Homo sapiens cDNA |
| 7268 | 18786 | | 1.9 | 1.5E-01 | AF210842.1 | NT | Homo sapiens HARP (HARP) gene, exon 17 and complete cds |
| 7423 | 18947 | 32813 | 1.5 | 1.5E-01 | AI973157.1 | EST_HUMAN | wf52a08.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2491310 3' |
| 7589 | 20104 | 32979 | 1.02 | 1.5E-01 | AF28073.1 | NT | Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds |
| 7588 | 20104 | 32980 | 1.02 | 1.5E-01 | AF28073.1 | NT | Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds |
| 7596 | 20110 | 32984 | 1.71 | 1.5E-01 | AW500611.1 | EST_HUMAN | UI-HF-BN0-ekk-4-05-0-UL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077408 5' |
| 7596 | 20110 | 32985 | 1.71 | 1.5E-01 | AW500611.1 | EST_HUMAN | UI-HF-BN0-ekk-4-05-0-UL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077408 5' |
| 7722 | 20230 | 33119 | 0.71 | 1.5E-01 | U48580.1 | NT | Saccharomyces cerevisiae weak multicopy suppressor of los1-1 (SOL3) gene, complete cds |
| 8002 | 20544 | 33446 | 1.1 | 1.5E-01 | P21303 | SWISSPROT | MEROZOITE RECEPTOR PK88 PRECURSOR (68 KD PROTECTIVE MINOR SURFACE ANTIGEN) |
| 8161 | 20702 | 33817 | 0.95 | 1.5E-01 | AA970317.1 | EST_HUMAN | cds5g12.at NCI_CGAP_Ki45 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062 |
| 8254 | 20785 | | 1.11 | 1.5E-01 | BE884789.1 | EST_HUMAN | INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN); |
| 8339 | 20880 | | 11.5 | 1.5E-01 | C16800.1 | EST_HUMAN | 601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5' |
| 8372 | 20912 | 33832 | 1.82 | 1.5E-01 | L27835.1 | NT | G16800 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-529H09 5' |
| 8529 | 21068 | 33987 | 2.04 | 1.5E-01 | D64476.1 | NT | Pangasinodon glycos growth hormone (GH) mRNA, complete cds |
| 8550 | 21089 | | 0.86 | 1.5E-01 | P43449 | SWISSPROT | Homo sapiens mRNA for ASK1, complete cds |
| 8772 | 21311 | 34234 | 1.23 | 1.5E-01 | 4501972 | NT | WNT-10A PROTEIN PRECURSOR |
| 9033 | 21570 | 34499 | 2.40 | 1.5E-01 | NT4226.1 | EST_HUMAN | Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA |
| 9121 | 21657 | 34598 | 1.08 | 1.5E-01 | BF585465.1 | EST_HUMAN | z869e08.at Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:206988 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ; |
| 9128 | 21683 | | 2.63 | 1.5E-01 | AV754819.1 | EST_HUMAN | GV0000404 Human Psoriasis Differential Display Homo sapiens cDNA |
| 9326 | 21840 | | 0.94 | 1.5E-01 | AU130007.1 | EST_HUMAN | AV754819 TP Homo sapiens cDNA clone TPAH12 5' |
| 9374 | 20313 | 33215 | 7.21 | 1.5E-01 | U00455.1 | NT | AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5' |
| 9731 | 22229 | 35206 | 0.48 | 1.5E-01 | M77144.1 | NT | Acipenser transmontanus vitellogenin mRNA, partial cds |
| 9835 | 22333 | 35314 | 8.51 | 1.5E-01 | AF007570.1 | NT | Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds |
| 9835 | 22333 | 35315 | 8.61 | 1.5E-01 | AF007570.1 | NT | Aplysia californica carboxypeptidase D mRNA, complete cds |
| 10104 | 22589 | 35591 | 2.54 | 1.5E-01 | X98852.1 | NT | Aplysia californica carboxypeptidase D mRNA, complete cds |
| 10188 | 22683 | | 3.34 | 1.5E-01 | AB027759.1 | NT | P.lentusculus mRNA for integrin beta subunit |
| | | | | | | | Mesocricetus auratus mRNA for collagen type XVII, complete cds |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10210 | 22705 | 35698 | 2.82 | 1.5E-01 | A1814046.1 | EST_HUMAN | wf53h12.x1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN); |
| 10210 | 22705 | 35699 | 2.82 | 1.5E-01 | A1814046.1 | EST_HUMAN | wf53h12.x1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN); |
| 10288 | 22763 | 35775 | 1.75 | 1.5E-01 | U40832.1 | NT | Danio rerio transcription factor Pax6b (Pax6) mRNA, complete cds |
| 10433 | 22827 | 35933 | 1.97 | 1.5E-01 | AJ011984.1 | NT | Claviceps purpurea ps1 gene |
| 10433 | 22827 | 35934 | 1.97 | 1.5E-01 | AJ011984.1 | NT | Claviceps purpurea ps1 gene |
| 10704 | 23233 | 36245 | 5.45 | 1.5E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 10704 | 23233 | 36246 | 5.45 | 1.5E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 10854 | 23469 | 39494 | 1.71 | 1.5E-01 | AW841915.1 | EST_HUMAN | IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA |
| 11045 | 19947 | 32813 | 2.44 | 1.5E-01 | A1973157.1 | EST_HUMAN | wf52c08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3' |
| 11739 | 24875 | | 79.5 | 1.5E-01 | BF700582.1 | EST_HUMAN | 602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5' |
| 12125 | 24381 | | 1.43 | 1.5E-01 | AF030358.2 | NT | Rattus norvegicus chemokine CX3C mRNA, complete cds |
| 12160 | 24899 | | 7.05 | 1.5E-01 | R63077.1 | EST_HUMAN | y987c04.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5' |
| 12288 | 24920 | | 3.12 | 1.5E-01 | AV741272.1 | EST_HUMAN | AV741272 C8 Homo sapiens cDNA clone CBDA004 5' |
| 12408 | 24824 | 30794 | 18.12 | 1.5E-01 | AL136074.2 | NT | Campylobacter jejuni NCTC11168 complete genome; segment 1/8 |
| 12621 | 24699 | 30862 | 3 | 1.5E-01 | Q920Y8 | SWISSPROT | VOLTAGE-DEPENDENT T-TYPE CALCIUM CHANNEL ALPHA-1I SUBUNIT (CAVT.3) |
| 12632 | 24706 | 30865 | 11.33 | 1.5E-01 | AJ276242.1 | NT | Sus scrofa mRNA for sodium iodide symporter |
| 321 | 12975 | | 1.48 | 1.4E-01 | AF009663.1 | NT | Homo sapiens T cell receptor beta locus, TORBV855P to TORBV21S2A2 region |
| 943 | 13556 | | 2.71 | 1.4E-01 | D78638.1 | NT | Xenopus laevis mRNA for DNA (cytosine-5-methyltransferase, complete cds) |
| 1302 | 13606 | | 1.59 | 1.4E-01 | T81864.1 | EST_HUMAN | y454c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3' |
| 1784 | 14374 | | 1.35 | 1.4E-01 | 6876960 | NT | Mus musculus growth differentiation factor 5 (Gdf5), mRNA |
| 1787 | 14377 | 26921 | 1.39 | 1.4E-01 | AE001710.1 | NT | Thermotoga maritima section 22 of 136 of the complete genome |
| 2029 | 14611 | | 10.08 | 1.4E-01 | AA720615.1 | EST_HUMAN | ny72d07.s1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1283821 3' |
| 2614 | 15078 | 27650 | 1.4 | 1.4E-01 | P30708 | SWISSPROT | GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) |
| 2818 | 15370 | 27940 | 4.1 | 1.4E-01 | A1933498.1 | EST_HUMAN | wm74d01.x1 NCI_CGAP_U22 Homo sapiens cDNA clone IMAGE:2441865 3' |
| 4253 | 16841 | 28280 | 10.32 | 1.4E-01 | A1690094.1 | EST_HUMAN | b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3' |
| 4253 | 16841 | 28291 | 10.32 | 1.4E-01 | A1690094.1 | EST_HUMAN | b56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3' |
| 4321 | 16907 | 28349 | 3.71 | 1.4E-01 | AE001710.1 | NT | Thermotoga maritima section 22 of 136 of the complete genome |
| | | | | | | | z50b01.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:453873 3' similar to gb:X01057_maf1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element; |
| 4501 | 17085 | | 0.61 | 1.4E-01 | AA776287.1 | EST_HUMAN | Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA |
| 4784 | 17384 | 28815 | 0.59 | 1.4E-01 | 5453861 | NT | |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5328 | 17890 | | 1.74 | 1.4E-01 | BE910013.1 | EST_HUMAN | 601468056F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900167 5' |
| 5509 | 18142 | 30554 | 4.49 | 1.4E-01 | T80877.1 | EST_HUMAN | ye15c11.s1 Stragene lung (#637210) Homo sapiens cDNA clone IMAGE:117812 3' |
| 5532 | 18164 | 30577 | 4.24 | 1.4E-01 | AB004556.1 | NT | Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds |
| 5532 | 18164 | 30578 | 4.24 | 1.4E-01 | AB004556.1 | NT | Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds |
| 6440 | 18042 | 31830 | 2.7 | 1.4E-01 | BE326801.1 | EST_HUMAN | h167c02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3' |
| 6608 | 19205 | 32012 | 6.4 | 1.4E-01 | AJ1117147.1 | EST_HUMAN | AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000789 5' |
| 6608 | 19205 | 32013 | 6.4 | 1.4E-01 | AJ1117147.1 | EST_HUMAN | AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000789 5' |
| 6686 | 19282 | 32085 | 3.78 | 1.4E-01 | AW082786.1 | EST_HUMAN | xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3' |
| 6686 | 19285 | | 1.53 | 1.4E-01 | BE266538.1 | EST_HUMAN | 601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5' |
| 6718 | 19312 | 32115 | 2.07 | 1.4E-01 | BF378533.1 | EST_HUMAN | QV1-UJ00036-080300-103-009 UM0036 Homo sapiens cDNA |
| 7180 | 19712 | | 0.81 | 1.4E-01 | AL118588.1 | EST_HUMAN | DKFZp761A0910.t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5' |
| 7419 | 18943 | | 1.83 | 1.4E-01 | AW016373.1 | EST_HUMAN | UH-B10-eat-c-09-D.U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3' |
| 7617 | 20130 | 33005 | 1.94 | 1.4E-01 | U85845.1 | NT | Oryctolagus cuniculus fructose 1,6-bisphosphatase (AldB) gene, complete cds |
| 7733 | 20241 | 33132 | 1.77 | 1.4E-01 | AI805192.1 | EST_HUMAN | q180b12.x1 Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:1876563 3' |
| 8410 | 20950 | | 1.28 | 1.4E-01 | AV658047.1 | EST_HUMAN | AV658047 GLC Homo sapiens cDNA clone GLCFSH06 3' |
| 8719 | 21258 | | 0.62 | 1.4E-01 | AI436083.1 | EST_HUMAN | h92b12.x1 Soares_NSF_F9_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:002710 O02710 GAG POLYPEPTIDE. |
| 8844 | 21383 | 34308 | 4.68 | 1.4E-01 | AA307073.1 | EST_HUMAN | EST1178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end |
| 8924 | 21462 | 34379 | 0.62 | 1.4E-01 | AW023636.1 | EST_HUMAN | df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5' |
| 9050 | 21587 | 34518 | 1.21 | 1.4E-01 | R82746.1 | EST_HUMAN | y10h05.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 6' |
| 9050 | 21587 | 34519 | 1.21 | 1.4E-01 | R82746.1 | EST_HUMAN | y10h05.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5' |
| 9114 | 21650 | 34591 | 8.48 | 1.4E-01 | BF310559.1 | EST_HUMAN | 601805465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5' |
| 9199 | 21716 | 34690 | 1.09 | 1.4E-01 | W93411.1 | EST_HUMAN | z084a04.t1 Soares_Fetal_Heart_Nhlh19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element; |
| 9280 | 21806 | 34757 | 1.47 | 1.4E-01 | Y10106.1 | NT | Homo sapiens PHEX gene |
| 9280 | 21806 | 34758 | 1.47 | 1.4E-01 | Y10106.1 | NT | Homo sapiens PHEX gene |
| 9371 | 20310 | 33213 | 1.96 | 1.4E-01 | AF121361.1 | NT | Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase lal (JAL), and zinc finger protein (DNZ1) genes, complete cds |
| 9698 | 22395 | 35371 | 1.18 | 1.4E-01 | AF023813.1 | NT | Macronitrium levatum small ribosomal protein 4 (ps4) gene, chloroplast gene encoding chloroplast protein, partial cds |
| 10000 | 22495 | 35484 | 0.51 | 1.4E-01 | AW021908.1 | EST_HUMAN | df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5' |
| 10000 | 22495 | 35485 | 0.51 | 1.4E-01 | AW021908.1 | EST_HUMAN | df29h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5' |
| 10157 | 22652 | 35645 | 0.72 | 1.4E-01 | BF375285.1 | EST_HUMAN | MF3-ST0218-211289-013-008 S10218 Homo sapiens cDNA |
| 10157 | 22652 | 35646 | 0.72 | 1.4E-01 | BF375285.1 | EST_HUMAN | MF3-ST0218-211289-013-008 S10218 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10360 | 22854 | | 0.73 | 1.4E-01 | T84283.1 | EST_HUMAN | y47d03.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:111365 5' |
| 10489 | 22983 | 35091 | 0.7 | 1.4E-01 | Z06117.1 | NT | Bacillus subtilis complete genome (section 14 of 21): from 2589451 to 2612870 |
| 10587 | 23122 | | 1.89 | 1.4E-01 | AA611480.1 | EST_HUMAN | ca9da03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3' |
| 10722 | 23250 | 36265 | 3.2 | 1.4E-01 | R53400.1 | EST_HUMAN | y170c05.r1 Soares breast 2NtH1Bst Homo sapiens cDNA clone IMAGE:154088 5' |
| 10874 | 23489 | 36519 | 1.66 | 1.4E-01 | P08648 | SWISSPROT | INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E) |
| 11172 | 23679 | 36724 | 1.82 | 1.4E-01 | X66082.1 | NT | C-perfringens ORF for putative membrane transport protein |
| 11210 | 18943 | | 1.96 | 1.4E-01 | AW015373.1 | EST_HUMAN | U1H-BID-est-c-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710288 3' |
| 11344 | 23042 | 36952 | 2.4 | 1.4E-01 | U28780.1 | NT | Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds |
| 12061 | 24344 | 30963 | 4.44 | 1.4E-01 | X74773.1 | NT | P. salina plesid gene secY |
| 12074 | 24352 | | 3.65 | 1.4E-01 | 11968117 | NT | Rattus norvegicus desmin (Des), mRNA |
| 12123 | 25082 | | 1.52 | 1.4E-01 | BE513802.1 | EST_HUMAN | 601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5' |
| 12223 | 24444 | | 9.33 | 1.4E-01 | AF083221.1 | NT | Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transformylase (GART) genes, complete cds |
| 12235 | 24451 | | 1.96 | 1.4E-01 | D84004.1 | NT | Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965 |
| 12315 | 25098 | | 1.77 | 1.4E-01 | P10447 | SWISSPROT | TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL |
| 12340 | 24522 | | 2.01 | 1.4E-01 | AA452305.1 | EST_HUMAN | z330e12.r1 Soares total_fetus_Nt2HF8_9w Homo sapiens cDNA clone IMAGE:788014 5' similar to contains Alu repetitive element. |
| 12545 | 24900 | | 3.55 | 1.4E-01 | D82863.1 | NT | Mus musculus mRNA for prolidase, complete cds |
| 12627 | 24705 | | 1.33 | 1.4E-01 | AW377896.1 | EST_HUMAN | MRO-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA |
| 344 | 12696 | 25481 | 2.28 | 1.3E-01 | 4758467 | NT | Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA |
| 344 | 12696 | 25482 | 2.28 | 1.3E-01 | 4758467 | NT | Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA |
| 555 | 13186 | 25664 | 3.25 | 1.3E-01 | AB013139.1 | NT | Homo sapiens gene for NBS1, complete cds |
| 664 | 13268 | 25769 | 3.03 | 1.3E-01 | AJ277806.1 | NT | Human calicivirus HUJNLV/Girlington/83/AUK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/83/AUK |
| 664 | 13268 | 25770 | 3.03 | 1.3E-01 | AJ277806.1 | NT | Human calicivirus HUJNLV/Girlington/83/AUK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/83/AUK |
| 877 | 13491 | 26009 | 0.78 | 1.3E-01 | X63330.1 | NT | P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4 |
| 927 | 13540 | 26058 | 1.44 | 1.3E-01 | AF139518.1 | NT | Rattus norvegicus A-kinase anchor protein mRNA, complete cds |
| 1064 | 13669 | 26179 | 1.36 | 1.3E-01 | AL117078.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 1166 | 13766 | | 2.03 | 1.3E-01 | AL115285.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 1257 | 13854 | 26370 | 1.36 | 1.3E-01 | AV712467.1 | EST_HUMAN | AV712467 DCA Homo sapiens cDNA clone DCAAF05 5' |
| 1493 | 14085 | | 0.97 | 1.3E-01 | AF146277.1 | NT | Homo sapiens adapter protein CMS mRNA, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2002 | 14584 | 27143 | 2.32 | 1.3E-01 | AL117078.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 2215 | 14790 | | 1.21 | 1.3E-01 | AJ243578.1 | NT | Rhodospseudomonas acidophila pucB5, pucA5, pucB8, pucA8, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151 |
| 2329 | 14900 | | 1.56 | 1.3E-01 | AW812104.1 | EST_HUMAN | RC4-ST0173-191089-032-412 ST0173 Homo sapiens cDNA |
| 2421 | 14988 | | 3.74 | 1.3E-01 | AE001016.1 | NT | Archaeoglobus fulgidus section 81 of 172 of the complete genome |
| 2622 | 15184 | 27750 | 1.55 | 1.3E-01 | M86818.1 | NT | Cerastis auratus keratin type I mRNA, complete cds |
| 3402 | 16011 | 28480 | 0.61 | 1.3E-01 | AF198778.1 | NT | Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α) |
| 3498 | 16103 | 28578 | 0.89 | 1.3E-01 | M21572.1 | NT | Bovine branched chain alpha-keto acid dihydrolylacyl transacylase mRNA, complete cds |
| 3785 | 16385 | 28850 | 1.19 | 1.3E-01 | AP000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7) |
| 3785 | 16385 | 28851 | 1.19 | 1.3E-01 | AP000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7) |
| 3791 | 16391 | 28856 | 0.8 | 1.3E-01 | AB032159.1 | NT | Homo sapiens DD4 gene for dihydrodihydroxydehydrogenase 4 [AKR 1C4], exon 2 |
| 3848 | 16385 | 28850 | 0.62 | 1.3E-01 | AP000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7) |
| 3848 | 16385 | 28851 | 0.62 | 1.3E-01 | AP000001.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7) |
| 3875 | 16473 | 28937 | 0.74 | 1.3E-01 | 6878840 | NT | Rattus norvegicus Fibronectin, gamma polypeptide (Fgg), mRNA |
| 4080 | 16857 | | 1.3 | 1.3E-01 | AL161581.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77 |
| 4125 | 13288 | 25769 | 1.65 | 1.3E-01 | AJ277608.1 | NT | Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK |
| 4125 | 13288 | 25770 | 1.65 | 1.3E-01 | AJ277608.1 | NT | Human calicivirus HUNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83/UK |
| 4218 | 16808 | | 0.95 | 1.3E-01 | AF020713.1 | NT | Bacteriophage SPBc2 complete genome |
| 4238 | 16828 | | 4.04 | 1.3E-01 | AW304341.1 | EST_HUMAN | QV3-DT0018-081289-036-e03 DT0018 Homo sapiens cDNA |
| 4248 | 16834 | 28285 | 2.25 | 1.3E-01 | AF028805.1 | NT | Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds |
| 4265 | 16851 | 28288 | 21.7 | 1.3E-01 | AW273741.1 | EST_HUMAN | sv23f10.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813095 3' |
| 4404 | 16889 | | 1.55 | 1.3E-01 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 4577 | 17160 | 28603 | 0.62 | 1.3E-01 | M21572.1 | NT | Bovine branched chain alpha-keto acid dihydrolylacyl transacylase mRNA, complete cds |
| 4631 | 17214 | 28665 | 2.35 | 1.3E-01 | BE272339.1 | EST_HUMAN | 601128038F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2880063 5' |
| 4698 | 18009 | | 0.94 | 1.3E-01 | BE884017.1 | EST_HUMAN | 601510347F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3911987 5' |
| 5056 | 17629 | 30073 | 1.05 | 1.3E-01 | D78842.1 | EST_HUMAN | HUM520C02B Homo placenta polyA+ (TFujwara) Homo sapiens cDNA clone GEN-520C02 5' |
| 5279 | 17841 | 30288 | 4.06 | 1.3E-01 | AI432531.1 | EST_HUMAN | ff38c10.x1 NC1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562 3' |
| 5366 | 17854 | 30365 | 0.65 | 1.3E-01 | AP000005.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 994001-1166000 nt. position (5/7) |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5444 | 17869 | 30402 | 13.68 | 1.3E-01 | AA981841.1 | EST_HUMAN | α45α07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1]; |
| 5444 | 17869 | 30403 | 13.68 | 1.3E-01 | AA981841.1 | EST_HUMAN | α45α07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1]; |
| 5528 | 18180 | 30575 | 0.69 | 1.3E-01 | AW466888.1 | EST_HUMAN | hα07α08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1 L1 repetitive element; |
| 5565 | 18196 | 30842 | 2.78 | 1.3E-01 | AW804417.1 | EST_HUMAN | QV0-UM0093-100400-189-α08 UM0093 Homo sapiens cDNA |
| 5682 | 18318 | | 0.78 | 1.3E-01 | AF107783.1 | NT | Emaricella nidulans DNA-dependent RNA polymerase II RP8140 (RP82) gene, partial cds |
| 5772 | 18397 | | 0.78 | 1.3E-01 | AF056880.1 | NT | Hepatitis G virus G8_C1.10 genome polypeptide-gene, partial cds |
| 5899 | 18521 | 31246 | 0.89 | 1.3E-01 | BF210920.1 | EST_HUMAN | 601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5' |
| 6009 | 18206 | 32014 | 15.81 | 1.3E-01 | AB031328.1 | NT | Schizosaccharomyces pombe gene for Alp41, complete cds |
| 6884 | 18280 | 32083 | 2.07 | 1.3E-01 | X68891.1 | NT | C.jacchus intron 4 of visual pigment gene (red allele) |
| 6883 | 19818 | | 0.82 | 1.3E-01 | W26367.1 | EST_HUMAN | 26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 7305 | 19833 | | 1.94 | 1.3E-01 | H48684.1 | EST_HUMAN | y333α02.L1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:207075 5' |
| 7900 | 20442 | | 0.67 | 1.3E-01 | BE272338.1 | EST_HUMAN | 601126095F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5' |
| 7914 | 20456 | 33362 | 1.62 | 1.3E-01 | 11423294 | NT | Homo sapiens PRO0811 protein (PRO0811), mRNA |
| 7945 | 20487 | 33397 | 0.98 | 1.3E-01 | BF690522.1 | EST_HUMAN | 602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4286074 3' |
| 8180 | 20721 | | 0.47 | 1.3E-01 | BE582528.1 | EST_HUMAN | 601333829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3688634 5' |
| 8286 | 20827 | | 4.81 | 1.3E-01 | Z74102.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL054c |
| 8325 | 20868 | | 3.78 | 1.3E-01 | 8823919 | NT | Homo sapiens core histone macrα2α2.2 (MACROH2A2), mRNA |
| 8465 | 21005 | 33823 | 1.05 | 1.3E-01 | BF690522.1 | EST_HUMAN | 602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4286074 3' |
| 8878 | 21416 | 34339 | 0.52 | 1.3E-01 | R11172.1 | EST_HUMAN | y339g11.L1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:128284 5' similar to SP:RL2B_RAT P28316 60S RIBOSOMAL PROTEIN ; |
| 8878 | 21416 | | 0.52 | 1.3E-01 | R11172.1 | EST_HUMAN | y339g11.L1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:128284 5' similar to SP:RL2B_RAT P28316 60S RIBOSOMAL PROTEIN ; |
| 8146 | 21681 | 34625 | 1.94 | 1.3E-01 | 11068003 | NT | Plutella xylostella granulovirus, complete genome |
| 8146 | 21681 | 34626 | 1.94 | 1.3E-01 | 11068003 | NT | Plutella xylostella granulovirus, complete genome |
| 8393 | 21816 | 34766 | 5.08 | 1.3E-01 | AF023128.1 | NT | Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds |
| 9896 | 22185 | | 0.8 | 1.3E-01 | N86348.1 | EST_HUMAN | J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 28 |
| 9894 | 22459 | | 0.8 | 1.3E-01 | 8393940 | NT | Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA |
| 10036 | 22531 | 35526 | 0.83 | 1.3E-01 | AW851589.1 | EST_HUMAN | MR2-CT0222-201089-001-α01 CT0222 Homo sapiens cDNA |

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|---|
| 10282 | 24797 | 35776 | 0.9 | 1.3E-01 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 10417 | 22911 | 35911 | 0.82 | 1.3E-01 | AU121237.1 | EST_HUMAN | AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5' |
| 10511 | 23049 | | 3.33 | 1.3E-01 | BF330999.1 | EST_HUMAN | MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA |
| 10975 | 23460 | 36520 | 1.58 | 1.3E-01 | AF119117.1 | NT | Homo sapiens dopamine transporter (SLC8A3) gene, complete cds |
| 11130 | 23638 | | 5.15 | 1.3E-01 | 6671745 | NT | Mus musculus cofillin 2, muscle (Cif2), mRNA |
| 11468 | 23918 | 36984 | 3.61 | 1.3E-01 | BE279449.1 | EST_HUMAN | 601159052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5' |
| 11802 | 24241 | 31007 | 1.64 | 1.3E-01 | BE618346.1 | EST_HUMAN | 601462741F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3686003 5' |
| 12048 | 24332 | | 3.27 | 1.3E-01 | AJ242790.1 | NT | Gallus gallus sox1 gene for lymphoblastin, exons 1-3 |
| 12466 | 24594 | | 1.63 | 1.3E-01 | AW001114.1 | EST_HUMAN | wu24009.x1 Soares_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to |
| 12647 | 24721 | | 1.84 | 1.3E-01 | BE958903.1 | EST_HUMAN | TR-O60287 O60287 KIAA0539 PROTEIN. ; |
| 406 | 13061 | 25573 | 10.81 | 1.2E-01 | AI421744.1 | EST_HUMAN | 601644622R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928860 3' |
| 449 | 12678 | | 1.43 | 1.2E-01 | U68912.1 | NT | ANNEXIN V (HUMAN); |
| 573 | 13203 | | 2.58 | 1.2E-01 | AF039442.1 | NT | Dichytalium discoidum ORF DG1016 gene, partial cds |
| 1419 | 14012 | 26541 | 2.31 | 1.2E-01 | AU149148.1 | EST_HUMAN | Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds |
| 1419 | 14012 | 26542 | 2.31 | 1.2E-01 | AU149148.1 | EST_HUMAN | AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3' |
| 1428 | 14019 | | 3.26 | 1.2E-01 | AV735249.1 | EST_HUMAN | AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3' |
| 1431 | 14023 | | 6.69 | 1.2E-01 | AL445066.1 | NT | AV735249 cda Homo sapiens cDNA clone cdAAJB11 5' |
| 1554 | 14146 | | 1.19 | 1.2E-01 | AA897474.1 | EST_HUMAN | Thermoplasma acidophilum complete genome; segment 4/5 |
| 1673 | 14285 | 26709 | 1.48 | 1.2E-01 | Q14634 | SWISSPROT | 644609.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TRCQ16871 |
| 1691 | 14283 | 26819 | 2.77 | 1.2E-01 | AI285402.1 | EST_HUMAN | Q16871 ANTH-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ; |
| 1805 | 14395 | | 21.02 | 1.2E-01 | X89211.1 | NT | NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3) |
| 1884 | 14548 | | 2.23 | 1.2E-01 | AW448388.1 | EST_HUMAN | q66109.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3' |
| 2228 | 14801 | 27373 | 1.31 | 1.2E-01 | BF248480.1 | EST_HUMAN | H. sapiens DNA for endogenous retroviral like element |
| 2325 | 14898 | 27470 | 1.08 | 1.2E-01 | AL163213.2 | NT | UH-HB13-ek-e-10-0-JL.s1 NCI_CGAP_Su65 Homo sapiens cDNA clone IMAGE:2734554 3' |
| 2416 | 14884 | | 1.05 | 1.2E-01 | Z31405.1 | EST_HUMAN | 601621657F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5' |
| 2625 | 15167 | 27754 | 1.36 | 1.2E-01 | AW686556.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C013 |
| | | | | 1.05 | Z31405.1 | EST_HUMAN | HSAAAEZBT1 TEST1, Human adult Testis tissue Homo sapiens cDNA |
| | | | | 1.36 | 1.2E-01 | EST_HUMAN | QV3-BND046-220300-126-f10 BN0048 Homo sapiens cDNA |
| | | | | | | EST_HUMAN | 1s18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228888 3' similar to TRCQ14048 Q14048 |
| 2754 | 15309 | 27675 | 1.11 | 1.2E-01 | AI623388.1 | EST_HUMAN | COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] ; contains element PTR5 repetitive element ; |
| 2868 | 15486 | 27659 | 1.22 | 1.2E-01 | U18018.1 | NT | Human E1A enhancer binding protein (E1A-F) mRNA, partial cds |

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2827 | 15543 | 28019 | 2.37 | 1.2E-01 | A1720470.1 | EST_HUMAN | ss80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb1.050895 |
| 2861 | 15577 | 28056 | 3.28 | 1.2E-01 | M16384.1 | NT | 60S RIBOSOMAL PROTEIN L30 (HUMAN); |
| 3037 | 15653 | 28132 | 0.83 | 1.2E-01 | X56882.1 | NT | Human creatine kinase-B mRNA, complete cds |
| 3267 | 15678 | 28382 | 2.08 | 1.2E-01 | AW370688.1 | EST_HUMAN | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3288 | 15807 | | 1.19 | 1.2E-01 | U67800.1 | NT | QV1-BT0259-281089-021-405 BT0259 Homo sapiens cDNA |
| 3525 | 16130 | | 0.62 | 1.2E-01 | Z89118.1 | NT | Methanococcus jannaschii section 142 of 150 of the complete genome |
| 3573 | 16177 | 28659 | 0.82 | 1.2E-01 | X56882.1 | NT | Bacillus subtilis complete genome (section 15 of 21); from 2706131 to 3013540 |
| 3573 | 16177 | 28660 | 0.82 | 1.2E-01 | X56882.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3688 | 16130 | | 1.08 | 1.2E-01 | Z89118.1 | NT | Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA) |
| 3833 | 16432 | | 0.64 | 1.2E-01 | BF128551.1 | EST_HUMAN | Bacillus subtilis complete genome (section 15 of 21); from 2706131 to 3013540 |
| 4261 | 16847 | 29294 | 1.98 | 1.2E-01 | Z54255.1 | NT | 601810788R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053688 3' |
| 4261 | 16847 | 29295 | 1.98 | 1.2E-01 | Z54255.1 | NT | P. clarid mRNA; repeat region (ID 2MR17) |
| 4402 | 16867 | 29431 | 0.6 | 1.2E-01 | M15861.1 | NT | P. clarid mRNA; repeat region (ID 2MR17) |
| 4830 | 17408 | 29882 | 0.98 | 1.2E-01 | Z48183.1 | NT | Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19 |
| | | | | | | NT | L. esculentum mRNA for glycylase-1 |
| | | | | | | NT | Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced |
| 4809 | 17484 | | 2.93 | 1.2E-01 | AF221633.1 | NT | |
| 5183 | 17732 | 30159 | 1.06 | 1.2E-01 | BF577357.1 | EST_HUMAN | 602135185F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4280185 5' |
| 5275 | 17836 | 30262 | 10.23 | 1.2E-01 | AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 5275 | 17836 | 30263 | 10.23 | 1.2E-01 | AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 5423 | 17880 | | 1.99 | 1.2E-01 | AL162757.2 | NT | Neisseria meningitidis serogroup A strain Z2481 complete genome, segment 677 |
| 5457 | 18082 | 30408 | 0.71 | 1.2E-01 | AA744369.1 | EST_HUMAN | ny63c04.e1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282650 3' |
| | | | | | | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 5503 | 18137 | 30547 | 1.13 | 1.2E-01 | AF223391.1 | NT | |
| 5513 | 18146 | 30557 | 2.28 | 1.2E-01 | W33035.1 | EST_HUMAN | z008002.1 Soares_papillary_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:321689 5' |
| 5571 | 18202 | 30652 | 2.3 | 1.2E-01 | Z98268.1 | NT | Homo sapiens gene encoding pleckstrin (exons 1-13) |
| 5686 | 18322 | 30822 | 0.89 | 1.2E-01 | Z48234.1 | NT | Madame de la Roche, Granary Smith adh mRNA for alcohol dehydrogenase |
| 6347 | 18662 | 31731 | 1.81 | 1.2E-01 | BE620945.1 | EST_HUMAN | 601483518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5' |
| 6395 | 18698 | 31777 | 0.81 | 1.2E-01 | P10842 | SWISSPROT | MATING-TYPE P-SPECIFIC POLYPEPTIDE P1 |
| 6441 | 18043 | 31831 | 2.38 | 1.2E-01 | AW845275.1 | EST_HUMAN | IL0-CT0031-221089-113-e04 CT0031 Homo sapiens cDNA |
| 6502 | 19102 | 31887 | 1.59 | 1.2E-01 | M26925.1 | NT | Mouse galactosyltransferase mRNA, complete cds |
| 6755 | 18348 | 32157 | 0.88 | 1.2E-01 | BF347985.1 | EST_HUMAN | 602023112F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156388 5' |
| 7833 | 20375 | | 1.31 | 1.2E-01 | BE007072.1 | EST_HUMAN | PM3-BIN0137-280300-002-109 BN0137 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7903 | 20445 | 33351 | 3.58 | 1.2E-01 | A1913753.1 | EST_HUMAN | wc98g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW:GST2_HUMAN |
| 7950 | 20492 | 33401 | 0.72 | 1.2E-01 | Q02389 | SWISSPROT | Q89735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II: |
| 8251 | 20792 | 33709 | 0.9 | 1.2E-01 | A1832681.1 | EST_HUMAN | NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22) |
| 8335 | 20876 | | 9.03 | 1.2E-01 | AW083652.1 | EST_HUMAN | at71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3' |
| | | | | | | | xc49db07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN); |
| 8355 | 20895 | | 4.17 | 1.2E-01 | AF053772.1 | NT | Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds |
| 8392 | 20832 | 33852 | 0.92 | 1.2E-01 | J03956.1 | NT | N crassa vacuolar ATPase 67-Kd subunit (vma-2) gene, complete cds |
| 8392 | 20832 | 33853 | 0.92 | 1.2E-01 | J03956.1 | NT | N crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds |
| 8337 | 21076 | | 0.83 | 1.2E-01 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 272 |
| 8623 | 21182 | | 2.14 | 1.2E-01 | U32714.1 | NT | Haemophilus influenzae Rd section 29 of 163 of the complete genome |
| 8657 | 21186 | | 0.85 | 1.2E-01 | X15181.1 | NT | M. musculus DNA fragment of Apolipoprotein B gene |
| 9491 | 21947 | 34896 | 2.66 | 1.2E-01 | X77961.1 | NT | S. cerevisiae HXT5 gene |
| 9918 | 22414 | 35389 | 2.65 | 1.2E-01 | AF710857.1 | EST_HUMAN | AV710857 Cu Homo sapiens cDNA clone QUAKE08 5' |
| 10155 | 22650 | 35844 | 0.48 | 1.2E-01 | AJ718396.1 | EST_HUMAN | as58g09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2333056 3' |
| 10798 | 23290 | | 3.58 | 1.2E-01 | D28184.1 | NT | Yeast MPT5 gene for suppressor protein, complete cds |
| 10944 | 23460 | | 3.87 | 1.2E-01 | BE962324.2 | EST_HUMAN | 601855578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3' |
| 11026 | 23540 | | 1.62 | 1.2E-01 | BF314481.1 | EST_HUMAN | 601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5' |
| 11134 | 23642 | 36682 | 2.87 | 1.2E-01 | AF190463.1 | NT | Homo sapiens dynein intermediate chain DNAL1 (DNAL1) gene, exon 17 |
| 11193 | 23698 | 36748 | 1.57 | 1.2E-01 | R40246.1 | EST_HUMAN | yf80cd2.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:28880 3' |
| 11382 | 23834 | | 1.8 | 1.2E-01 | M65108.1 | NT | Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds |
| 11667 | 24090 | | 4.22 | 1.2E-01 | AV658033.1 | EST_HUMAN | AV658033 GLC Homo sapiens cDNA clone GLCFB12 3' |
| 12029 | 24319 | | 4.43 | 1.2E-01 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 272 |
| 12109 | 25038 | 30503 | 3.9 | 1.2E-01 | Q04912 | SWISSPROT | MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN) |
| 12228 | 24447 | | 1.95 | 1.2E-01 | AF188992.1 | NT | Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntactin gene, partial cds |
| 12230 | 13203 | | 17.94 | 1.2E-01 | AF039442.1 | NT | Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds |
| 12345 | 24528 | | 1.81 | 1.2E-01 | X53981.1 | NT | R. norvegicus NIF68 gene for 68kDa neurofilament |
| 12440 | 24577 | 30915 | 8.5 | 1.2E-01 | AJ299903.1 | EST_HUMAN | qp20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3' |
| 12463 | 24591 | | 2.19 | 1.2E-01 | L10187.1 | NT | Xenopus laevis Integrin alpha 3 subunit mRNA, partial cds |
| 12468 | 24972 | | 9.71 | 1.2E-01 | O98433 | SWISSPROT | CYCLIN T |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12648 | 16130 | | 1.65 | 1.2E-01 | Z09118.1 | NT | Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540 |
| 590 | 13220 | 25698 | 0.8 | 1.1E-01 | AI691003.1 | EST_HUMAN | h18d08.x1 NC1_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3' |
| 643 | 13268 | 25743 | 2.98 | 1.1E-01 | AA568006.1 | EST_HUMAN | nm008g11.s1 NC1_CGAP_Cof10 Homo sapiens cDNA clone IMAGE:1058620 3' similar to gb:X06985_mel1 |
| 1082 | 13697 | 26207 | 1.54 | 1.1E-01 | BF697308.1 | EST_HUMAN | HEME OXYGENASE 1 (HUMAN); |
| 1124 | 13727 | | 1.48 | 1.1E-01 | AL161560.2 | NT | 602123847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5' |
| 1201 | 15435 | 26314 | 3.68 | 1.1E-01 | AW972158.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60 |
| 1292 | 13687 | 26411 | 1.89 | 1.1E-01 | D64004.1 | NT | EST384142 IMAGE: resseques, MAGL Homo sapiens cDNA |
| 1568 | 14160 | 26691 | 2.94 | 1.1E-01 | AU140363.1 | EST_HUMAN | Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002865 |
| 2353 | 14924 | | 3.72 | 1.1E-01 | 6755215 | NT | AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5' |
| 2578 | 15401 | | 1.24 | 1.1E-01 | 6978678 | NT | Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA |
| 2802 | 15164 | | 1.06 | 1.1E-01 | AW821908.1 | EST_HUMAN | Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA |
| 2880 | 15498 | 27968 | 1.17 | 1.1E-01 | S82418.1 | NT | RCO-ST0378-210100-032-g04 ST0378 Homo sapiens cDNA |
| 3068 | 15883 | 28165 | 0.78 | 1.1E-01 | F03285.1 | EST_HUMAN | Interleukin-12 p35 subunit [Homo sapiens, Genomic, 700 nt, segment 4 of 5] |
| 3385 | 15994 | | 1.87 | 1.1E-01 | 6753231 | NT | HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3' |
| 3468 | 16075 | 28548 | 2.27 | 1.1E-01 | BE383186.1 | EST_HUMAN | Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA |
| 3489 | 16104 | 28579 | 1.59 | 1.1E-01 | X82135.1 | NT | 601308678F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3827088 5' |
| 3538 | 16143 | 28628 | 0.59 | 1.1E-01 | R68948.1 | EST_HUMAN | C.reinhardtii nuclear gene on linkage group XX |
| 3642 | 16245 | 28720 | 0.8 | 1.1E-01 | Y07695.1 | NT | yq62g08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains |
| 3783 | 16364 | | 1.35 | 1.1E-01 | P07394 | SWISSPROT | Alu repetitive element; |
| 3771 | 16372 | 28837 | 1.61 | 1.1E-01 | X52708.1 | NT | A.immerus gene for transposase |
| 4188 | 16778 | 29223 | 1.61 | 1.1E-01 | AW819412.1 | EST_HUMAN | ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50) |
| 4188 | 16778 | 29224 | 1.61 | 1.1E-01 | AW819412.1 | EST_HUMAN | G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5 |
| 4339 | 16928 | | 12.27 | 1.1E-01 | AF157088.1 | NT | MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA |
| 4374 | 16961 | 29407 | 0.63 | 1.1E-01 | AW802056.1 | EST_HUMAN | MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA |
| 4745 | 17328 | 29768 | 1.11 | 1.1E-01 | S44957.1 | NT | Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds |
| 4858 | 17533 | 29875 | 1.21 | 1.1E-01 | Y07695.1 | NT | IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA |
| | | | | | | | Tape-1=Integral membrane protein TAPA-1 [mouse, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7] |
| | | | | | | | A.immerus gene for transposase |
| | | | | | | | Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; |
| 5169 | 16784 | | 0.78 | 1.1E-01 | AF030001.1 | NT | Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), |
| 5431 | 17988 | 30392 | 4.82 | 1.1E-01 | AV730569.1 | EST_HUMAN | CREB-RP, and tenascin X (TNX) genes, complete |
| 5431 | 17988 | 30393 | 4.82 | 1.1E-01 | AV730569.1 | EST_HUMAN | AV730569 HTF Homo sapiens cDNA clone HTFAAC12 5' |
| | | | | | | | AV730569 HTF Homo sapiens cDNA clone HTFAAC12 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5435 | 16245 | 28720 | 0.57 | 1.1E-01 | Y07695.1 | NT | A.immerus gene for transposase |
| 5850 | 18474 | | 4.49 | 1.1E-01 | AA747218.1 | EST_HUMAN | nc76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element; |
| 5914 | 18536 | 31261 | 1.17 | 1.1E-01 | AF020927.1 | NT | 6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 8 |
| 5974 | 18594 | 31328 | 0.84 | 1.1E-01 | BF339519.1 | EST_HUMAN | 602039178F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5' |
| 5974 | 18594 | 31328 | 0.84 | 1.1E-01 | BF339519.1 | EST_HUMAN | 602039178F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5' |
| 6001 | 18621 | 31356 | 2 | 1.1E-01 | X68951.1 | NT | S.pombe ste8 gene encoding protein kinase |
| 6031 | 18650 | 31391 | 5.02 | 1.1E-01 | M86533.1 | NT | Providencia rettgeri penicillin G amidase gene |
| 6177 | 18787 | 31555 | 1.75 | 1.1E-01 | AJ007079.1 | NT | Homo sapiens LGMD2B gene |
| 6197 | 18807 | 31576 | 1.6 | 1.1E-01 | BE769152.1 | EST_HUMAN | PM3-F10024-130600-004-f12 FT0024 Homo sapiens cDNA |
| 6216 | 18826 | 31586 | 7.81 | 1.1E-01 | AW853699.1 | EST_HUMAN | RC3-CT0254-280869-011-e01 CT0254 Homo sapiens cDNA |
| 6582 | 19180 | 31958 | 1.38 | 1.1E-01 | AF035748.1 | EST_HUMAN | AF035748 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43 |
| 6598 | 19186 | 32001 | 0.84 | 1.1E-01 | AI216307.1 | EST_HUMAN | gg76806.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:1841099 3' |
| 6721 | 19315 | 32118 | 3.92 | 1.1E-01 | O68635 | SWISSPROT | ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME) |
| 6805 | 19396 | | 3.07 | 1.1E-01 | AF032922.1 | NT | Homo sapiens syntrophin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds |
| 6888 | 19623 | 32458 | 2.36 | 1.1E-01 | 11432372 | NT | Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA |
| 7238 | 25119 | | 0.97 | 1.1E-01 | BF382758.1 | EST_HUMAN | 601816524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4050653 5' |
| 7345 | 24780 | 32737 | 0.92 | 1.1E-01 | AP000008.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt. position (877) |
| 7542 | 20062 | 32835 | 7.24 | 1.1E-01 | BF684628.1 | EST_HUMAN | 602140978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5' |
| 7542 | 20062 | 32836 | 7.24 | 1.1E-01 | BF684628.1 | EST_HUMAN | 602140978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5' |
| 7651 | 20163 | 33051 | 1.85 | 1.1E-01 | P41067 | SWISSPROT | TRAB PROTEIN |
| 7682 | 20163 | | 0.7 | 1.1E-01 | Z14098.1 | NT | B. subtilis gene encoding hypothetical polypeptide synthase |
| 7683 | 20194 | 33082 | 3.53 | 1.1E-01 | AA788784.1 | EST_HUMAN | ah31506.s1 Soares_parathyroid_tumor_NhiHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483 |
| 7809 | 20451 | 33358 | 1.41 | 1.1E-01 | U67482.1 | NT | CHROMOGRANIN A PRECURSOR (HUMAN); |
| 8149 | 20690 | 33603 | 1.6 | 1.1E-01 | AA483574.1 | EST_HUMAN | Methanococcus jannaschii section 34 of 150 of the complete genome |
| 8149 | 20690 | 33604 | 1.6 | 1.1E-01 | AA483574.1 | EST_HUMAN | nt04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943382 |
| 8197 | 20738 | 33650 | 1.18 | 1.1E-01 | X01233.1 | NT | nt04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943382 |
| 8235 | 20776 | | 1.15 | 1.1E-01 | AW817818.1 | EST_HUMAN | H.sapiens IL15 gene |
| 8292 | 20833 | 33755 | 1.54 | 1.1E-01 | AL134349.1 | EST_HUMAN | PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA |
| 8752 | 21291 | 34211 | 8.48 | 1.1E-01 | U02482.1 | NT | DKFZp547P194.1 547 (synonym: hfb1) Homo sapiens cDNA clone DKFZp547P194 5' |
| 8843 | 21382 | 34307 | 0.87 | 1.1E-01 | A1807474.1 | EST_HUMAN | Pedicrococcus acitilactici H plasmid pSMB74 pediocin Aclt production (pap) gene cluster papA, papB, papC and papD genes, complete cds |
| | | | | | | | wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element |

Table 4

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8838 | 21476 | 34397 | 0.48 | 1.1E-01 | AF050061.1 | NT | Homo sapiens C16orf3 large protein mRNA, complete cds |
| 8873 | 21511 | 34433 | 2.22 | 1.1E-01 | AA182153.1 | EST_HUMAN | z983b12.11 Stratiogene muscle 837208 Homo sapiens cDNA clone IMAGE:827743 5' |
| 8873 | 21511 | 34434 | 2.22 | 1.1E-01 | AA182153.1 | EST_HUMAN | z983b12.11 Stratiogene muscle 837209 Homo sapiens cDNA clone IMAGE:827743 5' |
| 8882 | 21588 | 34528 | 0.82 | 1.1E-01 | Y12727.1 | NT | P.fluitosus paraf dph5 gene and argF gene |
| 9082 | 21828 | 34585 | 2.28 | 1.1E-01 | T72875.1 | EST_HUMAN | y418f03.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN); |
| 9119 | 21655 | | 0.67 | 1.1E-01 | BE883260.1 | EST_HUMAN | 801438872F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3822048 5' |
| 9343 | 21857 | | 1.13 | 1.1E-01 | BE142305.1 | EST_HUMAN | CM3-HT0142-271088-028-g11 HT0142 Homo sapiens cDNA |
| 9417 | 21928 | | 2.2 | 1.1E-01 | BF085149.1 | EST_HUMAN | MR2-GN0027-040800-005-408 GN0027 Homo sapiens cDNA |
| 9824 | 22322 | | 0.5 | 1.1E-01 | AL161543.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43 |
| 10107 | 22602 | | 1.03 | 1.1E-01 | R80590.1 | EST_HUMAN | y68a09.s1 Soares placenta Nb2f-IP Homo sapiens cDNA clone IMAGE:147084 3' |
| 10240 | 22735 | 35727 | 0.88 | 1.1E-01 | U60529.1 | NT | Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds |
| 10554 | 23080 | 36104 | 1.6 | 1.1E-01 | AF245277.1 | NT | Dichostelium discoideum kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds |
| 10884 | 15683 | 28155 | 2.12 | 1.1E-01 | F03265.1 | EST_HUMAN | HSCIRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3' |
| 10882 | 23325 | | 3.23 | 1.1E-01 | AF168032.1 | NT | Carassius auratus actinin beta A precursor, mRNA, complete cds |
| 10823 | 23442 | 38483 | 3.76 | 1.1E-01 | R23708.1 | EST_HUMAN | y435f12.11 Soares placenta Nb2f-IP Homo sapiens cDNA clone IMAGE:131768 5' similar to contains Alu repetitive element; contains TAR1 repetitive element ; |
| 10931 | 23449 | 38470 | 1.85 | 1.1E-01 | 8881351 | NT | Rattus norvegicus Phosphofructokinase, liver, B-type (Pfkf), mRNA |
| 10947 | 18587 | 31288 | 1.56 | 1.1E-01 | AL110985.1 | NT | Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 11060 | 23572 | 36809 | 1.74 | 1.1E-01 | X70058.1 | NT | MLmusculus cytokine gene |
| 11085 | 23597 | 36833 | 3.35 | 1.1E-01 | Z11810.1 | NT | Z.mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase |
| 11085 | 23597 | 36834 | 3.35 | 1.1E-01 | Z11810.1 | NT | Z.mobilis tgf and lig genes encoding RNA guanine transglycosylase and DNA ligase |
| 11188 | 23691 | 36738 | 2.99 | 1.1E-01 | P17437 | SWISSPROT | SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN) |
| 11884 | 24231 | | 4.01 | 1.1E-01 | BE767023.1 | EST_HUMAN | RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA |
| 12143 | 24835 | | 3.29 | 1.1E-01 | BE974568.1 | EST_HUMAN | 601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850804 3' |
| 12587 | 24884 | 30880 | 1.98 | 1.1E-01 | BF239753.1 | EST_HUMAN | 601680350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5' |
| 1243 | 13841 | | 2.35 | 1.0E-01 | O62855 | SWISSPROT | DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) |
| 1315 | 13809 | 28429 | 1.92 | 1.0E-01 | A085499.1 | EST_HUMAN | ws08d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13 |
| 1436 | 14028 | 28557 | 2.23 | 1.0E-01 | AL161504.2 | NT | MER7 repetitive element ; |
| 2531 | 15095 | 27867 | 0.97 | 1.0E-01 | AW451365.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18 |
| 3563 | 16167 | 28849 | 1.04 | 1.0E-01 | BF033891.1 | EST_HUMAN | UHF-B13-abc-d-07-Q-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738420 3' |
| 3782 | 16382 | 28847 | 0.82 | 1.0E-01 | BF239818.1 | EST_HUMAN | 601456301F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3858849 5' |
| 3804 | 16503 | 28884 | 1.41 | 1.0E-01 | AF287081.1 | NT | 601606488F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5' |
| | | | | | | | Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3904 | 16503 | 28985 | 1.41 | 1.0E-01 | AF297061.1 | NT | Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes |
| 4027 | 16625 | 29097 | 2.82 | 1.0E-01 | BF365703.1 | EST_HUMAN | QV2-NT0048-160800-310-605 NT0048 Homo sapiens cDNA |
| 4498 | 17080 | 29529 | 1.82 | 1.0E-01 | AE002265.2 | NT | Chlamydia pneumoniae AF39, section 91 of 94 of the complete genome |
| 4653 | 17235 | | 0.97 | 1.0E-01 | AI782349.1 | EST_HUMAN | an32a04.y6 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5' |
| 4822 | 17400 | 29853 | 1.8 | 1.0E-01 | U50450.1 | NT | Drosophila melanogaster tyrosine kinase p45 isoform (ter) mRNA, complete cds |
| 4920 | 17495 | 29946 | 0.96 | 1.0E-01 | AA765434.1 | EST_HUMAN | ca05H03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304117 3' |
| 5050 | 17623 | 30068 | 2.12 | 1.0E-01 | AW952344.1 | EST_HUMAN | EST384414 IMAGE resequences, MAGB Homo sapiens cDNA |
| 5408 | 17865 | 30375 | 1.06 | 1.0E-01 | AV721471.1 | EST_HUMAN | AV721471 HTB Homo sapiens cDNA clone HTBBQE10 5' |
| 5415 | 17872 | | 0.88 | 1.0E-01 | AV763960.1 | EST_HUMAN | AV763960 MDS Homo sapiens cDNA clone MDSBQB11 5' |
| 5524 | 18159 | | 8.57 | 1.0E-01 | W88490.1 | EST_HUMAN | zh62H04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3' |
| 6040 | 18659 | | 0.95 | 1.0E-01 | AK024472.1 | NT | Homo sapiens mRNA for FLJ000065 protein, partial cds |
| 6175 | 18788 | 31554 | 11.01 | 1.0E-01 | AF274875.1 | NT | Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds |
| 6477 | 18078 | 31861 | 0.98 | 1.0E-01 | AA481879.1 | EST_HUMAN | z441g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:743002 3' |
| 6489 | 18080 | 31873 | 0.82 | 1.0E-01 | AA406039.1 | EST_HUMAN | L1.L3 L1 repetitive element; |
| 7091 | 19682 | | 1.71 | 1.0E-01 | R23821.1 | EST_HUMAN | z467c12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu |
| 7717 | 20225 | | 2.33 | 1.0E-01 | Y12488.1 | NT | y434h08.r1 Soares_placenta Nb2-IP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element |
| 7874 | 20418 | 33324 | 0.53 | 1.0E-01 | AA861081.1 | EST_HUMAN | M.musculus wtn gene |
| 8107 | 20648 | | 0.8 | 1.0E-01 | 4758365 | NT | ak32g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407698 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN); |
| 8429 | 20869 | | 0.83 | 1.0E-01 | AW189797.1 | EST_HUMAN | Homo sapiens fibroblast growth factor 13 (FGF13) mRNA |
| 9113 | 21649 | 34590 | 1.08 | 1.0E-01 | AF102855.2 | NT | z408a01.x1 NCI_CGAP_UH4 Homo sapiens cDNA clone IMAGE:2876889 3' similar to gb:X17208 40S |
| 9416 | 21825 | 34873 | 0.49 | 1.0E-01 | R44693.1 | EST_HUMAN | RIBOSOMAL PROTEIN S4 (HUMAN);contains TAR1.3 TAR1 repetitive element; |
| 9426 | 21835 | | 2.05 | 1.0E-01 | M79729.1 | NT | Rattus norvegicus synaptic SAPAP-interacting protein Synapman mRNA, complete cds |
| 9469 | 21868 | | 2.67 | 1.0E-01 | AE001801.1 | NT | Human pro-alpha-1(V) collagen mRNA, complete cds |
| 9483 | 21840 | 34888 | 0.71 | 1.0E-01 | W01855.1 | EST_HUMAN | Helicobacter pylori, strain J99 section 62 of 132 of the complete genome |
| 9735 | 22233 | 35211 | 1.67 | 1.0E-01 | BF240154.1 | EST_HUMAN | z468c10.s1 Soares_fetal_liver_NbH19W Homo sapiens cDNA clone IMAGE:327282 3' |
| 9848 | 22346 | 35327 | 8.17 | 1.0E-01 | AB046799.1 | NT | 601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5' |
| 9848 | 22346 | 35328 | 8.17 | 1.0E-01 | AB046799.1 | NT | Homo sapiens mRNA for KIAA1579 protein, partial cds |
| 10048 | 22543 | | 2.05 | 1.0E-01 | AW957425.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1579 protein, partial cds |
| 10053 | 22548 | 35542 | 0.61 | 1.0E-01 | T51952.1 | EST_HUMAN | EST369815 IMAGE resequences, MAGB Homo sapiens cDNA |
| | | | | | | | y428a06.s1 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10234 | 22728 | 35720 | 1.08 | 1.0E-01 | BE782750.1 | EST_HUMAN | 601594604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939098 5' |
| 10537 | 23074 | | 2.11 | 1.0E-01 | AU159127.1 | EST_HUMAN | AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3' |
| 10910 | 23428 | 38448 | 3.33 | 1.0E-01 | BF242948.1 | EST_HUMAN | 601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5' |
| 10910 | 23428 | 38448 | 3.33 | 1.0E-01 | BF242946.1 | EST_HUMAN | 601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5' |
| 11278 | 23731 | 36788 | 5.03 | 1.0E-01 | BE780543.1 | EST_HUMAN | 601592558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939734 5' |
| 11870 | 24581 | | 3.49 | 1.0E-01 | BE537719.1 | EST_HUMAN | 601055534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5' |
| 12104 | 24388 | | 1.74 | 1.0E-01 | 7862165 | NT | Homo sapiens KIAA0514 gene product (KIAA0514), mRNA |
| 12122 | 24380 | | 1.36 | 1.0E-01 | X00854.1 | NT | Drosophila melanogaster fcz gene |
| 12338 | 24519 | | 2.27 | 1.0E-01 | AA737081.1 | EST_HUMAN | ntx11c08.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255760 3' |
| 12413 | 25031 | | 4.74 | 1.0E-01 | U52891.1 | NT | Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds |
| 12445 | 24581 | | 2.17 | 1.0E-01 | BE537719.1 | EST_HUMAN | 601055534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5' |
| 12495 | 24623 | | 1.83 | 1.0E-01 | BE158805.1 | EST_HUMAN | QV4-H10401-211289-084-g03 HT0401 Homo sapiens cDNA |
| 12511 | 25001 | | 41.15 | 1.0E-01 | U66834.1 | NT | Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds |
| 12578 | 24674 | | 7.73 | 1.0E-01 | AF001507.1 | NT | Bacillus halodurans genomic DNA, section 1/14 |
| 2808 | 15358 | 27825 | 0.83 | 9.8E-02 | AF274008.1 | NT | Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pkc-R11) mRNA, complete cds |
| 2813 | 15385 | 27834 | 1.95 | 9.8E-02 | BE545554.1 | EST_HUMAN | 601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5' |
| 2813 | 15385 | 27835 | 1.95 | 9.8E-02 | BE545554.1 | EST_HUMAN | 601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5' |
| 3305 | 15916 | 28383 | 1.86 | 9.8E-02 | AF088810.1 | NT | Homo sapiens neuridin III-alpha gene, partial cds |
| 4025 | 16823 | 29095 | 0.64 | 9.8E-02 | AB21637.1 | EST_HUMAN | zu45c03.58 Scores ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740832 3' |
| 7049 | 18088 | 30459 | 9.12 | 9.8E-02 | D83710.1 | NT | Aspergillus terreus BSD mRNA for blebsidin S deaminase, complete cds |
| 7858 | 20398 | 33304 | 0.65 | 9.8E-02 | AW103088.1 | EST_HUMAN | xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2586528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ; |
| 7858 | 20398 | 33305 | 0.65 | 9.8E-02 | AW103088.1 | EST_HUMAN | xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2586528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ; |
| 9181 | 21758 | 34704 | 1.1 | 9.8E-02 | 6755111 | NT | Mus musculus phospholipid transfer protein (Pltp), mRNA |
| 589 | 13219 | | 1.48 | 9.8E-02 | X56338.1 | NT | O. sativa RAmYG gene for alpha-amylase |
| 3179 | 15792 | 28263 | 4.23 | 9.8E-02 | AF184274.1 | NT | Daucus carota leucanthyocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds |
| 4308 | 16804 | 28337 | 8.69 | 9.8E-02 | AF257329.1 | NT | Leptospira maculans beta-tubulin mRNA, complete cds |
| 4308 | 16804 | 28338 | 8.69 | 9.8E-02 | AF257329.1 | NT | Leptospira maculans beta-tubulin mRNA, complete cds |
| 7495 | 20018 | | 0.99 | 9.8E-02 | X54133.1 | NT | Human HIP1P delta mRNA for protein tyrosine phosphatase delta |
| 9178 | 21755 | | 1.05 | 9.8E-02 | M61943.1 | NT | Human laminin B1 chain gene, exon 26 |
| 11334 | 23032 | 36041 | 2.27 | 9.8E-02 | BF037421.1 | EST_HUMAN | 601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3884287 5' |
| 11840 | 24203 | | 1.46 | 9.8E-02 | 8383751 | NT | Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1304 | 13988 | 28516 | 1.24 | 9.7E-02 | AB005808.1 | NT | Aloe arborescens mRNA for NADP-malic enzyme, complete cds |
| 1628 | 14221 | | 1.75 | 9.7E-02 | 4503710 | NT | Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA |
| 2301 | 14874 | 27450 | 2.11 | 9.7E-02 | BE168680.1 | EST_HUMAN | QV1-HT0516-070300-085-a04 HT0516 Homo sapiens cDNA |
| 4055 | 18652 | | 4.76 | 9.7E-02 | Q08795 | SWISSPROT | CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33) |
| 5548 | 18180 | 30594 | 1.01 | 9.7E-02 | AF089189.1 | NT | Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds |
| 5548 | 18180 | 30595 | 1.01 | 9.7E-02 | AF089189.1 | NT | Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds |
| 6165 | 18777 | 31541 | 1.29 | 9.7E-02 | AW954476.1 | EST_HUMAN | EST368546 IMAGE resequences, MAGC Homo sapiens cDNA |
| 7340 | 19867 | 32731 | 3.28 | 9.7E-02 | Z89119.1 | NT | Bacillus subtilis complete genome (section 16 of 21); from 2897771 to 3213410 |
| 7824 | 20468 | 33374 | 1.29 | 9.7E-02 | N22798.1 | EST_HUMAN | yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3' |
| 7824 | 20468 | 33375 | 1.29 | 9.7E-02 | N22798.1 | EST_HUMAN | yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3' |
| 8783 | 21322 | 34246 | 1.47 | 9.7E-02 | AB93984.1 | EST_HUMAN | wx78808.x1 NCI_QGAP_Ox88 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:V52851_mart1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); |
| 11076 | 23588 | | 2.34 | 9.7E-02 | U69337.1 | NT | Mus musculus ligatin (Lgtn) mRNA, partial cds |
| 2080 | 14640 | 27213 | 1.33 | 9.6E-02 | AD80721.1 | EST_HUMAN | aa47d11.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878485 3' |
| 2080 | 14640 | 27214 | 1.33 | 9.6E-02 | AD80721.1 | EST_HUMAN | aa47d11.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878485 3' |
| 4437 | 17023 | 28463 | 7.64 | 9.6E-02 | Z32686.2 | NT | Proteus mirabilis fibrinolytic operon, strain H14320 |
| 5142 | 17713 | 30144 | 1.03 | 9.6E-02 | AW968250.1 | EST_HUMAN | EST378303 IMAGE resequences, MAGI Homo sapiens cDNA |
| 6254 | 18863 | | 2.74 | 9.6E-02 | BE910039.1 | EST_HUMAN | 601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3800165 5' |
| 8317 | 20858 | | 0.61 | 9.6E-02 | AU137084.1 | EST_HUMAN | AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5' |
| 9463 | 21888 | 34944 | 1.34 | 9.6E-02 | AV987888.1 | EST_HUMAN | AV987888 GKC Homo sapiens cDNA clone GKCAH02 5' |
| 9786 | 22284 | | 1.35 | 9.6E-02 | BE984895.1 | EST_HUMAN | 601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918363 5' |
| 9852 | 22447 | 35429 | 1.21 | 9.6E-02 | AJ243211.1 | NT | Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55 |
| 9852 | 22447 | 35430 | 1.21 | 9.6E-02 | AJ243211.1 | NT | Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55 |
| 10055 | 22550 | 35544 | 1.26 | 9.6E-02 | AB013985.1 | NT | Antitritrion majus transposon Tam3 pseudogene for transposase (in S-5 copy) |
| 10055 | 22550 | 35545 | 1.26 | 9.6E-02 | AB013985.1 | NT | Antitritrion majus transposon Tam3 pseudogene for transposase (in S-5 copy) |
| 10159 | 22854 | 35849 | 3.43 | 9.6E-02 | P08174 | SWISSPROT | COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55) |
| 10621 | 23153 | 36165 | 7.28 | 9.6E-02 | Z78702.1 | NT | Mycobacterium tuberculosis H37Rv complete genome; segment 102/162 |
| 11588 | 24013 | 37082 | 1.81 | 9.6E-02 | AA625755.1 | EST_HUMAN | z091g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745382 3' |
| 12486 | 24817 | | 1.55 | 9.6E-02 | H14589.1 | EST_HUMAN | ym19H03.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3' |
| 4177 | 16768 | 28217 | 2.24 | 9.5E-02 | AW982395.1 | EST_HUMAN | CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA |
| 5286 | 17848 | 30274 | 1.12 | 9.5E-02 | U63374.1 | NT | Lycopodium obscurum polygalacturonase isoenzyme 1 beta subunit gene, complete cds |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5846 | 18470 | 31186 | 0.82 | 9.5E-02 | P51854 | SWISSPROT | TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN) |
| 7344 | 18871 | 32736 | 4.47 | 9.5E-02 | AB003473.1 | NT | <i>Trimeresurus flavoviridis</i> DNA for phospholipase A2 inhibitor, complete cds |
| 7569 | 20088 | 32963 | 6.95 | 9.5E-02 | AL161538.2 | NT | <i>Arabidopsis thaliana</i> DNA chromosome 4, contig fragment No. 38 |
| 7885 | 18470 | 31186 | 0.9 | 9.5E-02 | P51854 | SWISSPROT | TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN) |
| 7821 | 20363 | 33271 | 2.04 | 9.5E-02 | BF035861.1 | EST_HUMAN | 601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 7821 | 20363 | 33272 | 2.04 | 9.5E-02 | BF035861.1 | EST_HUMAN | 601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 10559 | 23095 | 38107 | 3.19 | 9.5E-02 | BF035861.1 | EST_HUMAN | 601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 10559 | 23095 | 38108 | 3.19 | 9.5E-02 | BF035861.1 | EST_HUMAN | 601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5' |
| 12557 | 24658 | | 2.4 | 9.5E-02 | AF272732.1 | NT | <i>Arabidopsis thaliana</i> putative transcription factor (MYB110) mRNA, complete cds |
| 1873 | 14458 | 27015 | 3.67 | 9.4E-02 | BF071063.1 | EST_HUMAN | 602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5' |
| 1804 | 14489 | 27050 | 1.36 | 9.4E-02 | U55944.1 | NT | <i>Cavia porcellus</i> 3beta-hydroxysteroid sulfotransferase mRNA, complete cds |
| 1804 | 14489 | 27051 | 1.36 | 9.4E-02 | U55944.1 | NT | <i>Cavia porcellus</i> 3beta-hydroxysteroid sulfotransferase mRNA, complete cds |
| 3949 | 16547 | 28015 | 5.59 | 9.4E-02 | Z33058.1 | NT | <i>M. capricolum</i> DNA for CONTIG MC073 |
| 5383 | 17942 | | 0.83 | 9.4E-02 | X98106.1 | NT | <i>Lactobacillus bacteriophage phig1</i> e complete genomic DNA |
| 6459 | 19060 | 31846 | 0.73 | 9.4E-02 | AF097363.1 | NT | <i>Triticum aestivum</i> heat shock protein 101 (Hsp101a) mRNA, complete cds |
| 8536 | 21075 | | 2.32 | 9.4E-02 | Z46863.1 | NT | <i>Acinetobacter</i> sp. cysD, cdbQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes |
| 10813 | 20107 | 32982 | 2.33 | 9.4E-02 | L78833.1 | NT | Human BRCA1, Rho7 and vcl genes, complete cds, and tp35 gene, partial cds |
| 11722 | 24834 | | 6.48 | 9.4E-02 | U31815.1 | NT | Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds |
| 12945 | 24719 | 30869 | 3.54 | 9.4E-02 | U27699.1 | NT | Human pepBGT-1 betaine-GABA transporter mRNA, complete cds |
| 3018 | 15834 | | 1.68 | 9.3E-02 | 4809280 | NT | Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA |
| 3083 | 15879 | | 7.31 | 9.3E-02 | 6912525 | NT | Homo sapiens nescopharyngeal epithelium specific protein 1 (NESG1), mRNA |
| 3285 | 15906 | 28387 | 2.05 | 9.3E-02 | BF575511.1 | EST_HUMAN | 602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288289 5' |
| 4232 | 16820 | 28269 | 4.11 | 9.3E-02 | BE391943.1 | EST_HUMAN | 601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607853 5' |
| 4232 | 16820 | 28270 | 4.11 | 9.3E-02 | BE391943.1 | EST_HUMAN | 601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607853 5' |
| 4840 | 17418 | | 1.28 | 9.3E-02 | AV732224.1 | EST_HUMAN | AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5' |
| 5843 | 18467 | | 0.73 | 9.3E-02 | AP001507.1 | NT | <i>Bacillus halodurans</i> genomic DNA, section 1/14 |
| 8160 | 20731 | 33843 | 0.52 | 9.3E-02 | AW568007.1 | EST_HUMAN | EST189 Human Fetal Brain MATCHMAKER cDNA Library/Homo sapiens cDNA |
| 9052 | 21589 | | 0.5 | 9.3E-02 | AL113179.1 | NT | <i>Borhyia cinerea</i> strain T4 cDNA library under conditions of nitrogen deprivation |
| 9828 | 22126 | 35060 | 2.1 | 9.3E-02 | BE962631.2 | EST_HUMAN | 601655898F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855861 3' |
| 10094 | 22589 | 35581 | 3.16 | 9.3E-02 | Q15034 | SWISSPROT | HYPOTHEITICAL PROTEIN KIAA0032 |
| 10094 | 22589 | 35582 | 3.16 | 9.3E-02 | Q15034 | SWISSPROT | HYPOTHEITICAL PROTEIN KIAA0032 |
| 10222 | 22717 | | 3.82 | 9.3E-02 | AW206117.1 | EST_HUMAN | UHH-B11-efx-h-05-0-UJ.s1 NCI_OGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3' |
| 11992 | 24854 | | 2.27 | 9.3E-02 | AJ248650.1 | NT | <i>Photobacterium damsela</i> subsp. <i>damsela</i> partial gyrB gene for DNA gyrase B subunit |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12378 | 24886 | | 16.03 | 9.3E-02 | AW468650.1 | EST_HUMAN | hd28h12.1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3' |
| 12589 | 24933 | | 3.18 | 9.3E-02 | AF100956.1 | NT | Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bln1 (BING-1), leucine (leucine), RafGOS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr |
| 249 | 12809 | 25390 | 5.24 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 249 | 12809 | 25391 | 5.24 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 249 | 12809 | 25392 | 5.24 | 9.2E-02 | U60315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 2269 | 14843 | | 1.58 | 9.2E-02 | RS4158.1 | EST_HUMAN | yg8907.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5' |
| 3213 | 15825 | 28302 | 3.92 | 9.2E-02 | Q28631 | SWISSPROT | MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20) |
| 3345 | 15855 | 28430 | 0.86 | 9.2E-02 | AA534354.1 | EST_HUMAN | nt79e01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:826138 3' |
| 3646 | 16249 | | 1.16 | 9.2E-02 | 6755215 | NT | Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA |
| 4322 | 16808 | | 1.42 | 9.2E-02 | U62048.1 | NT | Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region |
| 4396 | 16861 | | 0.65 | 9.2E-02 | BE298722.1 | EST_HUMAN | 600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5' |
| 4744 | 17325 | 28787 | 1.44 | 9.2E-02 | X96402.1 | NT | G. gallus Mla-CK gene |
| 7861 | 20463 | 33402 | 1.75 | 9.2E-02 | T46920.1 | EST_HUMAN | yg8908.11 Stratagene placenta (4637225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:XS8009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN) |
| 8117 | 20658 | 33567 | 2.11 | 9.2E-02 | X95256.1 | NT | H. vulgare xylose isomerase gene |
| 12656 | 24930 | | 2.09 | 9.2E-02 | Z22150.1 | NT | S. dysgalactiae fbaA gene |
| 448 | 12877 | 25134 | 2.83 | 9.1E-02 | X77866.1 | NT | O. cuniculus K12 keratin gene |
| 3733 | 16334 | | 0.85 | 9.1E-02 | AW372568.1 | EST_HUMAN | PM2-BT0349-161269-001-f02 BT0349 Homo sapiens cDNA |
| 4562 | 17165 | 28608 | 1.55 | 9.1E-02 | AL161554.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54 |
| 5905 | 18527 | 31253 | 1.5 | 9.1E-02 | AF128756.1 | NT | Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH1, G86, G8c, G8d, G8e, G8f, BAT5, G5b, GSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds |
| 7420 | 19944 | 32809 | 11.98 | 9.1E-02 | AW160658.1 | EST_HUMAN | au74605.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781988 5' |
| 7698 | 20180 | 33067 | 0.89 | 9.1E-02 | AF000081.1 | NT | Aeropyrum pernix genomic DNA, section 47 |
| 7695 | 20204 | 33097 | 0.68 | 9.1E-02 | U38073.1 | NT | Mus musculus thymopolein zeta mRNA, complete cds |
| 8855 | 21394 | 34317 | 1.05 | 9.1E-02 | Y14378.1 | NT | Homo sapiens gamma actin gene, exon 9 |
| 10325 | 22819 | | 1.39 | 9.1E-02 | T02884.1 | EST_HUMAN | FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end |
| 10354 | 22848 | 35842 | 1.52 | 9.1E-02 | S74059.1 | NT | Tg616-Cy4 actin (Tritonastes gratilae=sea urchins, embryos, Genomic, 5275 nt) |
| 10380 | 22874 | 35867 | 0.73 | 9.1E-02 | Y11187.1 | NT | A. thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes |
| 11656 | 24083 | | 2.35 | 9.1E-02 | 8633494 | NT | Bacteriophage Mu, complete genome |
| 11898 | 25036 | | 1.62 | 9.1E-02 | AA179901.1 | EST_HUMAN | zp38h12.s1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA : |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11978 | 24289 | | 2.21 | 9.1E-02 | AF052696.1 | NT | Rattus norvegicus cell cycle protein p55CDC gene, complete cds |
| 12467 | 24877 | | 17.53 | 9.1E-02 | AJ281390.1 | NT | Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11 |
| 12672 | 24740 | | 1.6 | 9.1E-02 | AF226888.1 | NT | Bombyx mori fibroin heavy chain Fib-H (fib-H) gene, complete cds |
| 774 | 13393 | 26893 | 3.92 | 9.0E-02 | P15328 | SWISSPROT | FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP) |
| 1876 | 14268 | 26801 | 6.34 | 9.0E-02 | BE220482.1 | EST_HUMAN | h09g10.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176842 3' similar to contains Alu repetitive element; |
| 2829 | 15381 | 27061 | 1.76 | 9.0E-02 | AF138522.1 | NT | HIV-1 p8c085-08 from USA envelope glycoprotein (env) gene, partial cds |
| 2829 | 15381 | 27852 | 1.76 | 9.0E-02 | AF138522.1 | NT | HIV-1 p8c085-08 from USA envelope glycoprotein (env) gene, partial cds |
| 3380 | 15889 | 28488 | 0.83 | 9.0E-02 | AF279135.1 | NT | Dicotyledonum discoidium spore coat structural protein SP05 (cotE) gene, complete cds |
| 4367 | 16873 | 29422 | 0.58 | 9.0E-02 | S68757.1 | NT | corticosteroid-binding globulin [Saimiri sciureus=squirrel monkey, liver, mRNA, 1474 nt] |
| 4367 | 16873 | 29423 | 0.59 | 9.0E-02 | S68757.1 | NT | corticosteroid-binding globulin [Saimiri sciureus=squirrel monkey, liver, mRNA, 1474 nt] |
| 4775 | 17356 | 28808 | 1.68 | 9.0E-02 | X65740.2 | NT | Plasmodium falciparum P-type ATPase 3 gene |
| 5401 | 17859 | 30370 | 1.12 | 9.0E-02 | Q24597 | SWISSPROT | REGULATORY PROTEIN ZESTE |
| 6146 | 18780 | 31519 | 18.48 | 9.0E-02 | W58037.1 | EST_HUMAN | za68a12.r1 Soares_fetal_lung_NhrL19W Homo sapiens cDNA clone IMAGE:297894 5' similar to PIR:S52171 S52171 small G protein - human ; |
| 6830 | 19410 | | 1.1 | 9.0E-02 | BF062851.1 | EST_HUMAN | 7h63d03.x1 NC1_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element; |
| 6864 | 19598 | 32428 | 0.77 | 9.0E-02 | R62805.1 | EST_HUMAN | y11508.s1 Soares_placenta_Nhr2HP Homo sapiens cDNA clone IMAGE:138903 3' |
| 12300 | 24497 | | | | | | Escherichia coli strain E2349/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tr (tr), OrfU (orfU), > |
| 1486 | 14079 | 28817 | 2.42 | 9.0E-02 | AF022236.1 | NT | 602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5' |
| 1486 | 14079 | 28818 | 1.46 | 9.0E-02 | BF701593.1 | EST_HUMAN | 602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5' |
| 2430 | 14867 | 27571 | 9.68 | 9.0E-02 | BE153572.1 | EST_HUMAN | PM0-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA |
| 4277 | 16863 | | 1.79 | 9.0E-02 | AF286055.1 | NT | Atrichum angustatum AtranFla2 protein (AtranFla2) gene, partial cds |
| 4741 | 17322 | 29762 | 1.91 | 9.0E-02 | AA424887.1 | EST_HUMAN | zw03db04.s1 Soares_NhrIMPu_S1 Homo sapiens cDNA clone IMAGE:768199 3' |
| 6014 | 18634 | 31370 | 3.35 | 9.0E-02 | AW452122.1 | EST_HUMAN | UIH-B13-alo-f08-0-U1.s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3' |
| 6014 | 18634 | 31371 | 3.35 | 9.0E-02 | AW452122.1 | EST_HUMAN | UIH-B13-alo-f08-0-U1.s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3' |
| 6028 | 18845 | 31387 | 3.24 | 9.0E-02 | 11433478 | NT | Homo sapiens similar to endoglycan (H. sapiens) (LOC33107), mRNA |
| 7244 | 19773 | 32630 | 1.76 | 9.0E-02 | P47259 | SWISSPROT | FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE ; METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE] |
| 7559 | 20077 | | 2.15 | 9.0E-02 | Z78021.1 | NT | H.sapiens flow-sorted chromosome 8 HindIII fragment, SC8pA20f8 |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7994 | 20536 | 33439 | 0.99 | 8.9E-02 | P29475 | SWISSPROT | NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS) |
| 8072 | 20614 | 33628 | 0.98 | 8.9E-02 | BF701665.1 | EST_HUMAN | 60212911F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5' |
| 8072 | 20614 | 33528 | 0.98 | 8.9E-02 | BF701665.1 | EST_HUMAN | 60212911F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5' |
| 8534 | 21073 | 33983 | 4.81 | 8.9E-02 | AA306319.1 | EST_HUMAN | EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end |
| 9538 | 22038 | 34698 | 0.83 | 8.9E-02 | AI285827.1 | EST_HUMAN | qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 |
| 9538 | 22038 | 34699 | 0.83 | 8.9E-02 | AI285827.1 | EST_HUMAN | qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1 |
| 9848 | 22147 | 35118 | 0.95 | 8.9E-02 | AA330356.1 | EST_HUMAN | MER10 repetitive element |
| 11721 | 24884 | | 2.61 | 8.9E-02 | P18524 | SWISSPROT | EST44454 Fetal brain 1 Homo sapiens cDNA 5' end |
| 11872 | 24224 | | 4.82 | 8.9E-02 | BF68918.1 | EST_HUMAN | MYOSIN-2 ISOFORM |
| 12044 | 24330 | | 3.07 | 8.9E-02 | 6980220 | NT | 602128882F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4288180 5' |
| 12307 | 25104 | | 1.57 | 8.9E-02 | U40493.1 | NT | Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA |
| 1416 | 14009 | 28538 | 1.36 | 8.9E-02 | Q27474 | SWISSPROT | Ceratitis capitata mariner transposon transposase gene, complete cds |
| 3971 | 16569 | 29038 | 1.08 | 8.9E-02 | AA289128.1 | EST_HUMAN | PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP]) |
| 4106 | 16700 | | 4.3 | 8.9E-02 | O00268 | SWISSPROT | EST11595 Uterus Homo sapiens cDNA 5' end |
| 4390 | 16976 | | 0.98 | 8.9E-02 | 4580423 | NT | TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130) |
| 8918 | 21458 | 34376 | 1.18 | 8.9E-02 | AA151872.1 | EST_HUMAN | Homo sapiens paired box gene 8 (entiridia, keratitis) (PAX8), isoform b, mRNA |
| 10997 | 23511 | 36543 | 3.11 | 8.9E-02 | BE284455.1 | EST_HUMAN | 2789a05.s1 Stratagene colon (#637204) Homo sapiens cDNA clone IMAGE:588288 3' |
| 10997 | 23511 | 36544 | 3.11 | 8.9E-02 | BE284455.1 | EST_HUMAN | 601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5' |
| 11142 | 23650 | 36892 | 10.91 | 8.9E-02 | AL040129.1 | EST_HUMAN | 601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5' |
| 11948 | 24277 | 31019 | 1.73 | 8.9E-02 | Z71501.1 | NT | DKFZp434D1313_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5' |
| 3756 | 16357 | 28826 | 3.9 | 8.7E-02 | U82895.2 | NT | S. cerevisiae chromosome XIV reading frame ORF YNL285w |
| 3756 | 16357 | 28827 | 3.9 | 8.7E-02 | U82895.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xp28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 4816 | 17394 | 28847 | 1.42 | 8.7E-02 | AF178838.1 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xp28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 5284 | 17828 | | 1.2 | 8.7E-02 | AE000895.1 | NT | Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds |
| 5517 | 18149 | 30561 | 5.18 | 8.7E-02 | AA288875.1 | EST_HUMAN | Methanobacterium thermoautotrophicum from bases 1176181 to 1189408 (section 101 of 148) of the complete genome |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5517 | 18149 | 30562 | 5.18 | 8.7E-02 | AA268875.1 | EST_HUMAN | z55g08.s1 NCI_QGAP_GC81 Homo sapiens cDNA clone IMAGE:701438 3' |
| 6831 | 18580 | 32421 | 0.75 | 8.7E-02 | AJ271885.2 | NT | Mus musculus partial Kcna1 gene for potassium channel protein, exons 10-14 |
| 6831 | 18580 | 32422 | 0.75 | 8.7E-02 | AJ271885.2 | NT | Mus musculus partial Kcna1 gene for potassium channel protein, exons 10-14 |
| 7803 | 20346 | 33910 | 0.46 | 8.7E-02 | AA284532.1 | EST_HUMAN | z20e03.s1 Soares ovary tumor NB-HOT Homo sapiens cDNA clone IMAGE:713892 3' |
| 8452 | 20892 | 33910 | 0.64 | 8.7E-02 | AE004787.1 | NT | Pseudomonas aeruginosa PA01, section 348 of 528 of the complete genome |
| 8452 | 20892 | 33911 | 0.64 | 8.7E-02 | AE004787.1 | NT | Pseudomonas aeruginosa PA01, section 348 of 528 of the complete genome |
| 10580 | 23125 | | 2.71 | 8.7E-02 | L04758.1 | NT | Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end |
| 11191 | 23898 | 36745 | 1.77 | 8.7E-02 | AJ007763.1 | NT | Glucobacter oxydans tRNA-Ile and tRNA-Ala genes |
| 11835 | 24268 | | 2.35 | 8.7E-02 | X17116.1 | NT | Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease |
| 12142 | 24388 | | 2.72 | 8.7E-02 | 6878057 | NT | Mus musculus nidogen 2 (Nid2), mRNA |
| 1285 | 13889 | 28412 | 0.51 | 8.6E-02 | AJ271798.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 2286 | 14880 | 27435 | 2.47 | 8.6E-02 | BE408887.1 | EST_HUMAN | 601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3838843 5' |
| 3222 | 15834 | 28312 | 2.42 | 8.6E-02 | L05468.1 | NT | Trichomonas vaginalis beta-tubulin (tub1) gene, complete cds |
| 3708 | 16307 | | 4.02 | 8.6E-02 | AF153382.1 | NT | Dicystotellium discoideum adenyl cyclase (acrA) gene, complete cds |
| 4584 | 17187 | 28610 | 0.58 | 8.6E-02 | U68178.1 | NT | Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region |
| 6244 | 18853 | 31624 | 5.78 | 8.6E-02 | J10826.1 | NT | Homo sapiens LCN1b gene |
| 6512 | 19112 | 31800 | 1.56 | 8.6E-02 | J00440.1 | NT | Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a) |
| 6512 | 19112 | 31800 | 1.56 | 8.6E-02 | J00440.1 | NT | Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a) |
| 7581 | 20086 | 32974 | 1.14 | 8.6E-02 | P14618 | SWISSPROT | INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR) |
| 7871 | 20413 | 33319 | 1.23 | 8.6E-02 | 5730088 | NT | Homo sapiens Srf2-related CBP activator protein (SRCAP) mRNA |
| 7871 | 20413 | 33320 | 1.23 | 8.6E-02 | 5730088 | NT | Homo sapiens Srf2-related CBP activator protein (SRCAP) mRNA |
| 8015 | 20557 | 33480 | 0.76 | 8.6E-02 | 11427428 | NT | Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA |
| 8073 | 20615 | | 0.65 | 8.6E-02 | U60188.1 | NT | Dicystotellium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds |
| 8652 | 22151 | 35121 | 1.18 | 8.6E-02 | AF111170.3 | NT | Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene |
| 8688 | 22187 | | 1.27 | 8.6E-02 | AW652153.1 | EST_HUMAN | H20c08.x1 NCI_QGAP_GU1 Homo sapiens cDNA clone IMAGE:2872846 3' |
| 10057 | 22552 | 35547 | 0.74 | 8.6E-02 | AF026504.1 | NT | Rattus norvegicus SPA-1 like protein p1284 mRNA, complete cds |
| 10824 | 23345 | 36360 | 1.68 | 8.6E-02 | AF206551.1 | NT | Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product |
| 10824 | 23345 | 36361 | 1.68 | 8.6E-02 | AF206551.1 | NT | Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product |
| 11128 | 23636 | 36877 | 4.74 | 8.6E-02 | BF305808.1 | EST_HUMAN | 601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5' |
| 11128 | 23636 | 36878 | 4.74 | 8.6E-02 | BF305808.1 | EST_HUMAN | 601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5' |
| 11315 | 23013 | 36022 | 7.58 | 8.6E-02 | AE001073.1 | NT | Archaeoglobus fulgidus section 34 of 172 of the complete genome |
| 2440 | 15007 | 27578 | 2.52 | 8.5E-02 | AE000852.1 | NT | Helicobacter pylori 26695 section 130 of 134 of the complete genome |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5885 | 18507 | | 1.91 | 8.5E-02 | P08089 | SWISSPROT | M PROTEIN, SEROTYPE 6 PRECURSOR |
| 6162 | 18775 | 31537 | 5.64 | 8.5E-02 | AF233885.1 | NT | Mus musculus phospholipase C-like protein mRNA, partial cds |
| 8542 | 21081 | 34002 | 1.76 | 8.5E-02 | 8754779 | NT | Mus musculus myosin XV (Myo15), mRNA |
| 9750 | 22248 | 35230 | 3.08 | 8.5E-02 | BE833054.1 | EST_HUMAN | RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA |
| 9750 | 22248 | 35231 | 3.08 | 8.5E-02 | BE833054.1 | EST_HUMAN | RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA |
| 10379 | 22873 | 35888 | 0.92 | 8.5E-02 | 11418108 | NT | Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA |
| 11035 | 23549 | | 12.56 | 8.5E-02 | AF155510.1 | NT | Homo sapiens heparanase precursor, mRNA, complete cds |
| 11050 | 23563 | 38598 | 4.42 | 8.5E-02 | AB001582.1 | NT | Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds |
| 12354 | 24614 | | 5.89 | 8.5E-02 | AJ005588.1 | NT | Anthrax toxin mRNA for MYB-related transcription factor |
| 12358 | 24647 | | 2.27 | 8.5E-02 | AA362834.1 | EST_HUMAN | EST172736 Ovary II Homo sapiens cDNA 5' end |
| 2690 | 15474 | 27816 | 3.71 | 8.4E-02 | W68330.1 | EST_HUMAN | zid44e11.1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:343532 5' |
| 5200 | 17765 | | 1 | 8.4E-02 | X01472.1 | NT | Drosophila melanogaster copia-like element 17.6 |
| 5369 | 17829 | 30343 | 0.88 | 8.4E-02 | 5453817 | NT | Homo sapiens nucleobindin 1 (NUCB1), mRNA |
| 5515 | 18147 | 30559 | 8.48 | 8.4E-02 | BE267153.1 | EST_HUMAN | 601180436F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3534393 5' |
| 6791 | 19382 | 32197 | 1.67 | 8.4E-02 | AK024458.1 | NT | Homo sapiens mRNA for FLJ00050 protein, partial cds |
| 7972 | 20514 | 33421 | 7.35 | 8.4E-02 | BE085074.1 | EST_HUMAN | CM3-B10790-280400-162-005 B10790 Homo sapiens cDNA |
| 8776 | 21315 | 34237 | 1.13 | 8.4E-02 | AF218880.1 | NT | Homo sapiens atrial precursor (ATRN) gene, exon 2 |
| 10285 | 22760 | 35747 | 1.61 | 8.4E-02 | A1795184.1 | EST_HUMAN | ss88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312 |
| 11858 | 24217 | 31042 | 1.92 | 8.4E-02 | R79408.1 | EST_HUMAN | O88312 G08-4.; |
| 2056 | 14637 | 27208 | 2.06 | 8.3E-02 | 5835680 | NT | y63h12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5' |
| 2056 | 14637 | 27208 | 2.06 | 8.3E-02 | 5835680 | NT | boddes hexagonus mitochondrion, complete genome |
| 3652 | 16255 | 28728 | 8.98 | 8.3E-02 | P75334 | SWISSPROT | boddes hexagonus mitochondrion, complete genome |
| 3680 | 16281 | 28748 | 0.68 | 8.3E-02 | AA36797.1 | EST_HUMAN | HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR |
| 3680 | 16281 | 28749 | 0.68 | 8.3E-02 | AA36797.1 | EST_HUMAN | th82g08.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3' |
| 5418 | 17873 | | 1.71 | 8.3E-02 | AW802857.1 | EST_HUMAN | th82g08.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3' |
| 6408 | 19009 | 31791 | 0.89 | 8.3E-02 | AB42338.1 | EST_HUMAN | QV3-NIN1025-030500-179-e04 NN1025 Homo sapiens cDNA |
| 6504 | 19104 | 31889 | 3.05 | 8.3E-02 | AF052883.1 | EST_HUMAN | w078f11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3' |
| 7822 | 20464 | 33371 | 3.57 | 8.3E-02 | AF195787.1 | NT | Homo sapiens protocadherin 43 gene, exon 1 |
| 7855 | 20497 | | 1.31 | 8.3E-02 | AA865285.1 | EST_HUMAN | Rattus norvegicus dysophrin-related protein 2 A-form splice variant (Dnp2) mRNA, complete cds |
| 8241 | 20782 | | 4.14 | 8.3E-02 | AA987873.1 | EST_HUMAN | cg81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3' |
| 9457 | 21883 | 34935 | 1.55 | 8.3E-02 | AW583503.1 | EST_HUMAN | la05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE.; |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9470 | 21868 | | 1.84 | 8.3E-02 | AL161565.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91 |
| 10244 | 22739 | | 0.56 | 8.3E-02 | AF020409.1 | NT | Dicotyledonum discoidium Doca (doca) mRNA, complete cds |
| 11550 | 23998 | 37070 | 1.7 | 8.3E-02 | AA700756.1 | EST_HUMAN | z63d04.s1 Sources_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435367 3' similar to contains element MER22 repetitive element: |
| 11953 | 25040 | | 1.36 | 8.3E-02 | BE958458.1 | EST_HUMAN | 601644770F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3828893 5' |
| 1421 | 14014 | | 9.32 | 8.2E-02 | Y08170.2 | NT | Gallus gallus mRNA for for OBCAM protein gamma isoform |
| 1542 | 14134 | 26868 | 1.79 | 8.2E-02 | AF167077.2 | NT | Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds |
| 3109 | 15724 | | 2.23 | 8.2E-02 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 3874 | 16472 | | 1.88 | 8.2E-02 | AL161498.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10 |
| 4079 | 16875 | 28136 | 1.29 | 8.2E-02 | AL163206.2 | NT | Homo sapiens chromosome 21 segment HS21C006 |
| 4371 | 16958 | 29400 | 7.76 | 8.2E-02 | P48860 | SWISSPROT | LEUCOCYTE ANTIGEN CD97 PRECURSOR |
| 4371 | 16958 | 29401 | 7.76 | 8.2E-02 | P48860 | SWISSPROT | LEUCOCYTE ANTIGEN CD97 PRECURSOR |
| 4371 | 16958 | 29402 | 7.76 | 8.2E-02 | P48860 | SWISSPROT | LEUCOCYTE ANTIGEN CD97 PRECURSOR |
| 5240 | 17804 | 30225 | 3.53 | 8.2E-02 | U76009.1 | NT | Mus musculus zinc transporter (ZnT-3) gene, complete cds |
| 5400 | 17958 | 30369 | 0.9 | 8.2E-02 | AU119830.1 | EST_HUMAN | AU119830 HEMBA1 Homo sapiens cDNA clone HEMBA1006744 5' |
| 5538 | 18170 | 30585 | 1.62 | 8.2E-02 | BE987030.1 | EST_HUMAN | 601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3824523 5' |
| 7092 | 18693 | 32502 | 3.11 | 8.2E-02 | AF308555.1 | NT | Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds |
| 8707 | 21248 | 34169 | 2.98 | 8.2E-02 | AW875126.1 | EST_HUMAN | RC2-PT0004-031289-011-405 PT0004 Homo sapiens cDNA |
| 9517 | 22017 | 34974 | 4.88 | 8.2E-02 | X04197.1 | NT | Beet necrotic yellow vein virus RNA-2 |
| 9678 | 22177 | 35152 | 2.2 | 8.2E-02 | BE294318.1 | EST_HUMAN | 60115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355596 5' |
| 11959 | 24281 | 31023 | 5.69 | 8.2E-02 | AE002246.2 | NT | Chlamydia pneumoniae AF38, section 73 of 94 of the complete genome |
| 12383 | 24906 | | 4.6 | 8.2E-02 | AF275366.1 | NT | Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced |
| 5929 | 18531 | 31278 | 1.08 | 8.1E-02 | AE004006.1 | NT | Xylella fastidiosa, section 152 of 229 of the complete genome |
| 6516 | 19116 | 31808 | 0.97 | 8.1E-02 | T11532.1 | EST_HUMAN | A1484F Heart Homo sapiens cDNA clone A1484 |
| 7248 | 19777 | | 0.72 | 8.1E-02 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 7582 | 20097 | | 1.03 | 8.1E-02 | A169268.1 | EST_HUMAN | w838608.X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3' |
| 8281 | 20822 | 33741 | 0.62 | 8.1E-02 | 11428974 | NT | Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA |
| 8281 | 20822 | 33742 | 0.62 | 8.1E-02 | 11428974 | NT | Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA |
| 9628 | 22324 | | 1.7 | 8.1E-02 | AY005150.1 | NT | Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds |
| 11371 | 23823 | 36886 | 1.87 | 8.1E-02 | AL163202.2 | NT | Homo sapiens chromosome 21 segment HS21C002 |
| 6 | 15405 | 25143 | 9.1 | 8.0E-02 | AW854653.1 | EST_HUMAN | EST368723 IMAGE resequencing, MAGC Homo sapiens cDNA |
| 971 | 13582 | 26095 | 1.13 | 8.0E-02 | U80315.1 | NT | Molluscum contagiosum virus subtype 1, complete genome |
| 1736 | 15449 | 26889 | 10.86 | 8.0E-02 | D26535.1 | NT | Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15) |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1736 | 15449 | 26870 | 10.86 | 8.0E-02 | D26835.1 | NT | Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15) |
| 1947 | 14531 | 27087 | 3.32 | 8.0E-02 | BE067219.1 | EST_HUMAN | PM3-BT0347-170200-001-808 BT0347 Homo sapiens cDNA |
| 2413 | 14981 | 27556 | 1.14 | 8.0E-02 | D80915.1 | NT | Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2287259 |
| 2413 | 14981 | 27557 | 1.14 | 8.0E-02 | D80915.1 | NT | Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2287259 |
| 2509 | 15073 | | 4.88 | 8.0E-02 | BF246744.1 | EST_HUMAN | 601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5' |
| 2847 | 13733 | 28243 | 0.87 | 8.0E-02 | M23448.1 | NT | Dichoselium discoidum cyclic nucleotide phosphodiesterase gene, complete cds |
| 2925 | 15541 | 28016 | 0.84 | 8.0E-02 | AL445087.1 | NT | Thermoplasma acidophilum complete genome; segment 5/5 |
| 3898 | 16487 | 28948 | 0.59 | 8.0E-02 | AW988118.1 | EST_HUMAN | EST378191 MAGE sequences, MAGI Homo sapiens cDNA |
| 4146 | 16738 | | 0.95 | 8.0E-02 | 4503034 | NT | Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA |
| 4890 | 17465 | 28920 | 2.26 | 8.0E-02 | AK34202.1 | EST_HUMAN | 831g02.x1 NCJ_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114 3' |
| 4939 | 17514 | | 5.81 | 8.0E-02 | X72794.1 | NT | M. musculus gene for gelatinase B |
| 6051 | 18669 | 31408 | 3.07 | 8.0E-02 | AF278948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 7232 | 18669 | 31408 | 1.42 | 8.0E-02 | AF278948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 8089 | 20811 | 33524 | 3.68 | 8.0E-02 | AL114983.1 | NT | Bethyis cinerea strain T4 cDNA library under conditions of nitrogen deprivation |
| 9311 | 21825 | 34773 | 1.22 | 8.0E-02 | X74208.1 | NT | H. sapiens AGT gene, intron 4 |
| 9311 | 21825 | 34774 | 1.22 | 8.0E-02 | X74208.1 | NT | H. sapiens AGT gene, intron 4 |
| 10063 | 22558 | | 0.57 | 8.0E-02 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 10671 | 23203 | 36216 | 3.69 | 8.0E-02 | AF217786.1 | NT | Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds |
| 11993 | 24302 | 30888 | 3.6 | 8.0E-02 | AJ005375.1 | NT | Drosophila oreana hunchback region |
| 12595 | 16738 | | 3.88 | 8.0E-02 | 4503034 | NT | Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA |
| 2218 | 14793 | 27366 | 4.15 | 7.9E-02 | BE250008.1 | EST_HUMAN | 600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5' |
| 3007 | 15623 | 28101 | 11.7 | 7.9E-02 | AI582028.1 | EST_HUMAN | ar88c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173846 3' similar to gb:226878 |
| | | | | | | | 60S RIBOSOMAL PROTEIN L38 (HUMAN); |
| 3895 | 16463 | 28827 | | | | | Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG9 (cg9), CG1 (cg1), CG8 (cg8), CG2 (cg2), and CG7 (cg7) genes, complete cds |
| 3917 | 16515 | 28878 | 0.82 | 7.9E-02 | AF030894.2 | NT | Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA |
| 3917 | 16515 | 28879 | 3 | 7.9E-02 | 8681044 | NT | Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA |
| 4834 | 17509 | | 1.36 | 7.9E-02 | AB008018.1 | NT | Arabidopsis thaliana RXW24L mRNA, partial cds |
| 5390 | 17948 | 30360 | 0.58 | 7.9E-02 | AF035672.1 | NT | Mus musculus MHC class I related protein 1 (MR1) gene, complete cds |
| 5390 | 17948 | 30361 | 0.58 | 7.9E-02 | AF035672.1 | NT | Mus musculus MHC class I related protein 1 (MR1) gene, complete cds |
| 6798 | 18389 | | 1.08 | 7.9E-02 | BF368016.1 | EST_HUMAN | RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA |
| 7875 | 20517 | 33424 | 3.32 | 7.9E-02 | U27832.1 | NT | Saccharomyces cerevisiae suppressor of Mif2 Smt4p (SMT4) gene, complete cds |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8941 | 22436 | 35412 | 4.71 | 7.9E-02 | A081644.1 | EST_HUMAN | ou33b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA IMAGE:1632465 3' similar to WP:C37A2.2 |
| 8941 | 22436 | 35413 | 4.71 | 7.9E-02 | A081644.1 | EST_HUMAN | CE086111 |
| 12478 | 24613 | | 1.42 | 7.9E-02 | A1781639.1 | EST_HUMAN | ou33b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA IMAGE:1632465 3' similar to WP:C37A2.2 |
| 1252 | 13849 | 26365 | 1.36 | 7.8E-02 | A1783275.1 | EST_HUMAN | CE086111 |
| 1252 | 13849 | 26366 | 1.36 | 7.8E-02 | A1783275.1 | EST_HUMAN | wg88h01.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3' |
| 4812 | 17487 | 28943 | 0.87 | 7.8E-02 | BE836331.1 | EST_HUMAN | ou33b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA IMAGE:1570467 5' similar to contains L1.13 L1 |
| 5247 | 18412 | | 2.77 | 7.8E-02 | BE250048.1 | EST_HUMAN | repetitive element ; |
| | | | | | | | ou33b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA IMAGE:1570467 5' similar to contains L1.13 L1 |
| | | | | | | | repetitive element ; |
| | | | | | | | PM3-FND058-140700-005-609 FN0058 Homo sapiens cDNA |
| | | | | | | | 600843059F1 NIH_MGC_15 Homo sapiens cDNA IMAGE:2859883 5' |
| 7136 | 19475 | 32287 | 1.34 | 7.8E-02 | U82685.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 7136 | 19475 | 32288 | 1.34 | 7.8E-02 | U82685.2 | NT | Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 8720 | 21250 | 34179 | 1.46 | 7.8E-02 | BE897847.1 | EST_HUMAN | 601440439F1 NIH_MGC_72 Homo sapiens cDNA IMAGE:3925449 5' |
| 8813 | 21352 | 34274 | 0.8 | 7.8E-02 | X78344.1 | NT | S.cerevisiae CAT8 gene |
| 8883 | 21521 | 34447 | 0.83 | 7.8E-02 | AF233437.1 | NT | Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds |
| 8883 | 21521 | 34448 | 0.83 | 7.8E-02 | AF233437.1 | NT | Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds |
| 9283 | 21883 | 34828 | 1.08 | 7.8E-02 | AA468354.1 | EST_HUMAN | nc88b06.t1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:771731 |
| 9717 | 22215 | 35180 | 0.5 | 7.8E-02 | Z09124.1 | NT | Bacillus subtilis complete genome (section 21 of 21); from 3989281 to 4214814 |
| 10544 | 23081 | 36094 | 1.87 | 7.8E-02 | U32323.1 | NT | Human Interleukin-11 receptor alpha chain gene, complete cds |
| 12394 | 24550 | 30806 | 1.95 | 7.8E-02 | U72847.1 | NT | Homo sapiens envelopin (EVPL) gene, exons 16 through 18 |
| 1444 | 15442 | 28568 | 0.91 | 7.7E-02 | AF181897.1 | NT | Homo sapiens WRN (WRN) gene, complete cds |
| 3647 | 18250 | | 2.82 | 7.7E-02 | AJ238083.1 | NT | Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements |
| 5128 | 17701 | 30135 | 0.92 | 7.7E-02 | AL161501.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13 |
| 7850 | 20392 | 33295 | 5.56 | 7.7E-02 | AA402949.1 | EST_HUMAN | zu33d11.t1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to |
| 9748 | 22247 | 35228 | 5.97 | 7.7E-02 | F38080 | SWISSPROT | TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN. ; |
| | | | | | | | PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10037 | 22532 | 35527 | 0.75 | 7.7E-02 | A1318682.1 | EST_HUMAN | ts80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:20503359 3' similar to gb:Z26878 60S |
| 10037 | 22532 | 35528 | 0.75 | 7.7E-02 | A1318682.1 | EST_HUMAN | RIBOSOMAL PROTEIN L38 (HUMAN); |
| 10889 | 23410 | 36428 | 4.97 | 7.7E-02 | 11422757 | NT | ts80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:20503359 3' similar to gb:Z26878 60S |
| 12194 | 24894 | | 1.81 | 7.7E-02 | 11438858 | NT | RIBOSOMAL PROTEIN L38 (HUMAN); |
| 3434 | 18042 | 28523 | 3.08 | 7.8E-02 | BE514432.1 | EST_HUMAN | Homo sapiens KIAA0628 gene product (KIAA0628), mRNA |
| 3455 | 18062 | 28537 | 0.87 | 7.8E-02 | AA286447.1 | EST_HUMAN | Homo sapiens interferon regulatory factor 7 (IRF7), mRNA |
| 3615 | 18218 | 28697 | 0.87 | 7.8E-02 | AJ400877.1 | NT | 601318428F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5' |
| 4993 | 17567 | | 2.04 | 7.8E-02 | AW898844.1 | EST_HUMAN | EST112214 Carabellum II Homo sapiens cDNA 5' end similar to protodactherin 43 |
| 6247 | 18858 | 31627 | 0.7 | 7.8E-02 | A081275.1 | EST_HUMAN | Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 |
| 6497 | 19088 | 31882 | 0.83 | 7.8E-02 | BE379328.1 | EST_HUMAN | gene |
| 9292 | 21882 | 34839 | 1.24 | 7.8E-02 | AJ131018.1 | NT | RC3-CT0347-110300-014-05 CT0347 Homo sapiens cDNA |
| 9811 | 22309 | | 1.7 | 7.8E-02 | AL139078.2 | NT | an2502.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1689730 3' |
| 10120 | 22815 | 35605 | 0.52 | 7.8E-02 | BE78002.1 | EST_HUMAN | 601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5' |
| 10251 | 22746 | | 0.49 | 7.8E-02 | BE956038.2 | EST_HUMAN | Homo sapiens SCL gene locus |
| 10480 | 22974 | 35981 | 0.72 | 7.8E-02 | X92656.1 | NT | Campylobacter jejuni NCTC11168 complete genome; segment 5/8 |
| 10480 | 22974 | 35982 | 0.72 | 7.8E-02 | X92656.1 | NT | RC1-HT0545-020800-017-008 HT0545 Homo sapiens cDNA |
| 11526 | 23874 | 37044 | 2.58 | 7.8E-02 | AW898845.1 | EST_HUMAN | 601854915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3639810 3' |
| 817 | 13435 | 25940 | 1.18 | 7.5E-02 | | NT | L. esculentum mRNA for those phosphate translocator |
| 817 | 13435 | 25941 | 1.18 | 7.5E-02 | | NT | L. esculentum mRNA for those phosphate translocator |
| 4608 | 17189 | 28636 | 0.57 | 7.5E-02 | AB015081.1 | NT | QV3-BN0046-150400-151-004 BN0046 Homo sapiens cDNA |
| 8280 | 20821 | 33740 | 1.15 | 7.5E-02 | A1884387.1 | EST_HUMAN | Homo sapiens solute carrier family 8 (neurotransmitter transporter, glycine), member 9 (SLC8A9), mRNA |
| 8444 | 20984 | 33899 | 1.18 | 7.5E-02 | AU116913.1 | EST_HUMAN | Homo sapiens solute carrier family 8 (neurotransmitter transporter, glycine), member 9 (SLC8A9), mRNA |
| 9945 | 22440 | | 0.5 | 7.5E-02 | BF221730.1 | EST_HUMAN | Homo sapiens IL-18 gene for Interleukin-18, intron 1 and exon 2 |
| 10387 | 22881 | 35975 | 0.9 | 7.5E-02 | BF206808.1 | EST_HUMAN | ts80b08.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA |
| 10481 | 22975 | 35983 | 0.71 | 7.5E-02 | X79460.1 | NT | ENOLASE (HUMAN); |
| 503 | 13135 | 25623 | 1.23 | 7.4E-02 | AW839547.1 | EST_HUMAN | AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5' |
| 1509 | 14101 | | 0.97 | 7.4E-02 | AF030027.1 | NT | 7c61c05.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element |
| | | | | | | | MER27 repetitive element; |
| | | | | | | | 601870203F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5' |
| | | | | | | | C.fiml DSM 20113 16S rDNA |
| | | | | | | | RC5-LT0054-280100-011-H09 LT0054 Homo sapiens cDNA |
| | | | | | | | Equine herpesvirus 4 strain NS80587, complete genome |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2816 | 15178 | | 1.04 | 7.4E-02 | 6755069 | NT | Mus musculus paired-like homeodomain transcription factor 1 (Pitd1), mRNA |
| 3654 | 16257 | 28729 | 0.84 | 7.4E-02 | AI807885.1 | EST_HUMAN | wf43d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3' |
| 4814 | 17382 | 28844 | 1.33 | 7.4E-02 | L78810.1 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 4911 | 17486 | 28942 | 2.82 | 7.4E-02 | 6978442 | NT | Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA |
| 5052 | 17625 | | 1.65 | 7.4E-02 | AE000898.1 | NT | Methanobacterium thermoautotrophicum from bases 1076134 to 1086763 (section 92 of 148) of the complete genome |
| 5076 | 17649 | 30090 | 1.67 | 7.4E-02 | 6678492 | NT | Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrp), mRNA |
| 5303 | 17951 | 30384 | 0.93 | 7.4E-02 | AJ012489.1 | NT | Caenorhabditis elegans mRNA for DYS-1 protein, partial |
| 6821 | 18218 | | 1.84 | 7.4E-02 | R17477.1 | EST_HUMAN | ig14g08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5' |
| 7485 | 20008 | 32874 | 0.88 | 7.4E-02 | AA605132.1 | EST_HUMAN | no71d02.e1 NCJ_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3' |
| 7842 | 20384 | 33288 | 1.23 | 7.4E-02 | BE880112.1 | EST_HUMAN | 601493369F-1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885284 5' |
| 8438 | 20878 | 33853 | 1.2 | 7.4E-02 | U56089.1 | NT | Human periodic tyrosophen protein 2 (PWP2) gene, exons 15 to 21, and complete cds |
| 9063 | 21629 | 34566 | 0.92 | 7.4E-02 | AW62805.1 | EST_HUMAN | h67d11.y1 NCJ_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN |
| 9083 | 21629 | 34567 | 0.92 | 7.4E-02 | AW62805.1 | EST_HUMAN | h67d11.y1 NCJ_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN |
| 9360 | 20269 | 33197 | 0.72 | 7.4E-02 | A672839.1 | EST_HUMAN | O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ; |
| 9360 | 20269 | 33198 | 0.72 | 7.4E-02 | A672839.1 | EST_HUMAN | we74d02.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3' |
| 9728 | 22226 | 35203 | 0.85 | 7.4E-02 | U62283.1 | NT | we74d02.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3' |
| 11600 | 24043 | | 1.57 | 7.4E-02 | U89282.1 | NT | Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds |
| 11912 | 24250 | | 1.29 | 7.4E-02 | 11525893 | NT | Rattus norvegicus telomerase protein component 1 (TLP1) mRNA, complete cds |
| 12187 | 25015 | | 4.44 | 7.4E-02 | AW370431.1 | EST_HUMAN | Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA |
| 12351 | 24531 | 30826 | 2.8 | 7.4E-02 | BF035098.1 | EST_HUMAN | CMA-HT0243-Q81198-037-411 HT0243 Homo sapiens cDNA |
| 12381 | 24535 | 30801 | 1.37 | 7.4E-02 | AJ223459.2 | NT | 601453813F-1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857738 5' |
| 494 | 13127 | 25613 | 1.42 | 7.3E-02 | BE964961.2 | EST_HUMAN | Aspergillus nidulans prnD, prnX, prnA genes |
| 494 | 13127 | 25614 | 1.42 | 7.3E-02 | BE964961.2 | EST_HUMAN | 601658738F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3886209 3' |
| 713 | 13334 | 25820 | 2.89 | 7.3E-02 | AE001788.1 | NT | 601658738F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3886209 3' |
| 1528 | 15444 | 26859 | 4.47 | 7.3E-02 | AW900281.1 | EST_HUMAN | Thermotoga maritima section 101 of 130 of the complete genome |
| 1885 | 15453 | | 16.16 | 7.3E-02 | AL183302.2 | NT | CMM-NN1004-130300-284-908 NN1004 Homo sapiens cDNA |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C102 |
| | | | | | | | Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, |
| | | | | | | | TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, |
| 3838 | 18437 | | 0.59 | 7.3E-02 | U66059.1 | NT | TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, |
| 5137 | 17709 | | 1.11 | 7.3E-02 | U12283.1 | NT | TCRBV13S9A1SS> |
| | | | | | | | Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6680 | 19178 | 31978 | 1.56 | 7.3E-02 | AA779977.1 | EST_HUMAN | 224602.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:102428 26S PROTEASE SUBUNIT 4 (HUMAN); |
| 7484 | 20007 | 32872 | 4.36 | 7.3E-02 | P05143 | SWISSPROT | PROLINE-RICH PROTEIN MP-3 |
| 7484 | 20007 | 32873 | 4.36 | 7.3E-02 | P05143 | SWISSPROT | PROLINE-RICH PROTEIN MP-3 |
| 8109 | 20650 | | 1.06 | 7.3E-02 | 7662107 | NT | Homo sapiens KIAA0424 protein (KIAA0424), mRNA |
| 9137 | 21672 | | 1.38 | 7.3E-02 | AB011060.1 | NT | Homo sapiens mRNA for KIAA0518 protein, partial cds |
| 11095 | 19178 | 31978 | 3.07 | 7.3E-02 | AA779977.1 | EST_HUMAN | 224602.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:102428 26S PROTEASE SUBUNIT 4 (HUMAN); |
| 125 | 12784 | 25279 | 1.38 | 7.2E-02 | AE000882.1 | NT | Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome |
| 125 | 12784 | 25280 | 1.38 | 7.2E-02 | AE000882.1 | NT | Methanobacterium thermoautotrophicum from bases 1029155 to 1039834 (section 88 of 148) of the complete genome |
| 1524 | 14116 | 26652 | 2.11 | 7.2E-02 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 1524 | 14116 | 26653 | 2.11 | 7.2E-02 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |
| 2585 | 15148 | | 2.76 | 7.2E-02 | U14794.1 | NT | Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds |
| 3954 | 16552 | 26021 | 0.59 | 7.2E-02 | AW28322.1 | EST_HUMAN | U14794.1 U14794.1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2732049 3' |
| 4438 | 17024 | 29464 | 3.65 | 7.2E-02 | BF572307.1 | EST_HUMAN | 602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251850 5' |
| 5223 | 17768 | 30207 | 0.89 | 7.2E-02 | AB001562.1 | NT | Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds |
| 5491 | 18125 | 30533 | 2.8 | 7.2E-02 | U67531.1 | NT | Methanococcus jannaschii section 73 of 150 of the complete genome |
| 5492 | 18126 | 30534 | 8.6 | 7.2E-02 | P11120 | SWISSPROT | CALMODULIN |
| 6265 | 18873 | | 0.83 | 7.2E-02 | BF217698.1 | EST_HUMAN | 601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5' |
| 7220 | 19751 | 32007 | 1.27 | 7.2E-02 | BF216088.1 | EST_HUMAN | 601883568F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5' |
| 7261 | 19789 | | 1.54 | 7.2E-02 | 5834897 | NT | Strongylocentrotus purpuratus mitochondrion, complete genome |
| 8128 | 20669 | 33578 | 0.69 | 7.2E-02 | P05143 | SWISSPROT | PROLINE-RICH PROTEIN MP-3 |
| 8128 | 20668 | 33579 | 0.69 | 7.2E-02 | P05143 | SWISSPROT | PROLINE-RICH PROTEIN MP-3 |
| 8994 | 21532 | | 0.5 | 7.2E-02 | Y17217.1 | NT | Lactococcus lactis cspE gene |
| 9495 | 21995 | | 0.57 | 7.2E-02 | X16349.1 | NT | Human gene for sex hormone-binding globulin (SHBG) |
| 9529 | 22028 | 34988 | 2.28 | 7.2E-02 | AV712452.1 | EST_HUMAN | AV712452 DCA Homo sapiens cDNA clone DCAUG01 5' |
| 9674 | 22173 | 35149 | 4.69 | 7.2E-02 | L14581.1 | NT | Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds |
| 9628 | 22328 | 35307 | 1.01 | 7.2E-02 | BF125398.1 | EST_HUMAN | 601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028438 5' |
| 9814 | 22410 | 35386 | 2.73 | 7.2E-02 | AW873187.1 | EST_HUMAN | h24411.x1 NCI CGAP_Ad1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q82340 Q82340 ATYPICAL PKC SPECIFIC BINDING PROTEIN.; |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| | | | | | | | Homo sapiens zinc finger protein 82 (ZFP82), expressed-Xq28:TS protein (XQ28:ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds |
| 10254 | 22749 | 35737 | 2.11 | 7.2E-02 | U82885.2 | NT | |
| 10370 | 22884 | 35857 | 6.88 | 7.2E-02 | BE585003.1 | EST_HUMAN | 601343928F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5' |
| 10382 | 22886 | | 3.22 | 7.2E-02 | BE589214.1 | EST_HUMAN | 601066184F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5' |
| 10782 | 23315 | 36324 | 6.18 | 7.2E-02 | AF049874.1 | NT | Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds |
| 11822 | 24182 | 31033 | 1.54 | 7.2E-02 | AA773696.1 | EST_HUMAN | af81a04.f1 Soares_NIH-MIPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5' |
| 11857 | 24216 | | 4.88 | 7.2E-02 | AJ230796.1 | EST_HUMAN | AJ230798 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3' |
| 11914 | 24252 | | 2.01 | 7.2E-02 | AA584465.1 | EST_HUMAN | nc05h08.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1088839 3' |
| 11979 | 24280 | | 3.59 | 7.2E-02 | U82828.1 | NT | Homo sapiens ataxia telangiectasia (ATM) gene, complete cds |
| 11886 | 24858 | | 7.52 | 7.2E-02 | AW800862.1 | EST_HUMAN | CNA-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA |
| 12514 | 24633 | | 1.85 | 7.2E-02 | AA401779.1 | EST_HUMAN | z57c12.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728454 5' |
| 1948 | 14532 | 27088 | 1.42 | 7.1E-02 | L02280.1 | NT | Human Immunodeficiency virus type 1 (D6) proviral structural capsid protein (gag) gene, partial cds |
| 2331 | 14802 | 27473 | 4.53 | 7.1E-02 | BF208602.1 | EST_HUMAN | 601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082881 5' |
| 7848 | 20390 | 33282 | 0.84 | 7.1E-02 | A125284.1 | EST_HUMAN | q82a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736822 3' |
| 11700 | 24113 | | 6.04 | 7.1E-02 | BE304784.1 | EST_HUMAN | 601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5' |
| 554 | 13185 | 25663 | 0.97 | 7.0E-02 | Q07082 | SWISSPROT | COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR |
| 1547 | 14139 | | 1.43 | 7.0E-02 | X98877.1 | NT | M. arbutus Mitc-1 gene |
| 1788 | 14388 | 26833 | 0.94 | 7.0E-02 | AA056343.1 | EST_HUMAN | z6804.s1 Strategene colon (#637204) Homo sapiens cDNA clone IMAGE:509599 3' |
| 3004 | 15680 | 28153 | 2.03 | 7.0E-02 | AW138152.1 | EST_HUMAN | U1-H-B11-acy-c-07-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718020 3' |
| 3688 | 16584 | 28033 | 1.71 | 7.0E-02 | AA816438.1 | EST_HUMAN | af85a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S |
| 4118 | 16712 | 28186 | 1.11 | 7.0E-02 | BE070284.1 | EST_HUMAN | RIBOSOMAL PROTEIN L32 (HUMAN); |
| 4219 | 16807 | | 1.11 | 7.0E-02 | AW782862.1 | EST_HUMAN | QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA |
| 4284 | 16880 | 28327 | 1.28 | 7.0E-02 | AF077821.1 | NT | CNO-UM0001-080300-270-e12 UM0001 Homo sapiens cDNA |
| 5003 | 17638 | 30079 | 9.58 | 7.0E-02 | BF381887.1 | EST_HUMAN | Genes familiars inducible ribic acids synthase mRNA, complete cds |
| 5380 | 18211 | | 0.84 | 7.0E-02 | Y09143.2 | NT | 601818291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5' |
| 7431 | 18665 | 32820 | 0.88 | 7.0E-02 | AV880285.1 | EST_HUMAN | Lumbricus rubellus mRNA for cyclophilin B |
| 9027 | 21584 | 34493 | 1.41 | 7.0E-02 | 8628113 | NT | AV880285 GK Homo sapiens cDNA clone GKCAED6 5' |
| 9515 | 22015 | 34973 | 1.25 | 7.0E-02 | K02001.1 | NT | African swine fever virus, complete genome |
| 8883 | 22360 | 35340 | 0.73 | 7.0E-02 | U27286.1 | NT | Rat Ig gamma epsilon H-chain gene C-region, 3' end |
| 11251 | 23781 | 36837 | 2.88 | 7.0E-02 | AA724295.1 | EST_HUMAN | Human myosin binding protein H (MyBP-H) gene, complete cds |
| | | | | | | | af89a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837 |
| | | | | | | | TIGHT JUNCTION PROTEIN ZO-1 (HUMAN); |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 540 | 13171 | 25849 | 11.84 | 6.9E-02 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 540 | 13171 | 25850 | 11.84 | 6.9E-02 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 1378 | 13971 | | 1.34 | 6.9E-02 | 4507888 | NT | Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products |
| 3660 | 16458 | 28921 | 1.16 | 6.9E-02 | Q06364 | SWISSPROT | 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) |
| 3660 | 16458 | 28922 | 1.16 | 6.9E-02 | Q06364 | SWISSPROT | 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) |
| | | | | | | | Enterococcus faecium cysteine aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB (bglB), beta-glucosidase specific transport protein (bglS), transcription antiterminator (bglR), enterocin B precursor (entB), enterocin B immunity protease |
| 5361 | 17840 | 30354 | 3.59 | 6.9E-02 | AF121254.1 | NT | Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds |
| 7966 | 20538 | | 1.13 | 6.9E-02 | U12022.1 | NT | 601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5' |
| 8488 | 21027 | 33944 | 1.1 | 6.9E-02 | BE567435.1 | EST_HUMAN | 601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5' |
| 8488 | 21027 | 33945 | 1.1 | 6.9E-02 | BE567435.1 | EST_HUMAN | 601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5' |
| 8048 | 21585 | 34516 | 0.61 | 6.9E-02 | U22987.1 | NT | Barbican duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds |
| 11853 | 24213 | | 17.91 | 6.9E-02 | X74315.1 | NT | Xlaevis XFD2 mRNA for fork head protein |
| 12031 | 24321 | | 1.96 | 6.9E-02 | P44821 | SWISSPROT | PROTEIN TRANSPORT PROTEIN HOFH HOMOLOG |
| 12568 | 24468 | | 3.68 | 6.9E-02 | AF195863.1 | NT | Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds |
| 1828 | 14511 | 27065 | 1.83 | 6.8E-02 | AA496759.1 | EST_HUMAN | ee30f02.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 |
| 1828 | 14511 | 27068 | 1.83 | 6.8E-02 | AA496759.1 | EST_HUMAN | MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN); |
| 1650 | 14634 | 27060 | 3.09 | 6.8E-02 | AF156873.1 | NT | ee30f02.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 |
| 2023 | 14605 | 27170 | 1.68 | 6.8E-02 | BE263781.1 | EST_HUMAN | MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN); |
| 4651 | 17233 | | 0.66 | 6.8E-02 | BE141076.1 | EST_HUMAN | Homo sapiens putative hepatic transcription factor (WBCSR14) gene, complete cds |
| 6980 | 19478 | | 4.63 | 6.8E-02 | BE061890.1 | EST_HUMAN | 601194141F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537708 5' |
| 7324 | 19851 | 32713 | 8.08 | 6.8E-02 | AL163288.2 | NT | MRO-HT00689-071089-001-c05 HT00689 Homo sapiens cDNA |
| 8230 | 20771 | 33680 | 5.36 | 6.8E-02 | AJ248287.1 | NT | RC1-BT0254-080300-017-409 BT0254 Homo sapiens cDNA |
| 8230 | 20771 | 33691 | 5.36 | 6.8E-02 | AJ248287.1 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 11846 | 25064 | | 2.48 | 6.8E-02 | T03214.1 | EST_HUMAN | Pyrococcus abyssi complete genome, segment 56 |
| 11763 | 24168 | | 2.42 | 6.8E-02 | AA758014.1 | EST_HUMAN | Pyrococcus abyssi complete genome, segment 56 |
| 12380 | 24547 | | 1.37 | 6.8E-02 | AW975838.1 | EST_HUMAN | FB4A8 Fetal brain, Stratiogene Homo sapiens cDNA clone FB4A8 3' and similar to LINE-1 |
| 12444 | 24580 | | 2.87 | 6.8E-02 | | EST_HUMAN | af678015.81 Soares testis_NHT Homo sapiens cDNA clone 1320705 3' |
| 12650 | 25008 | 30614 | 1.54 | 6.8E-02 | | NT | EST387848 MAGe resequences, MAGN Homo sapiens cDNA |
| 1576 | 14169 | | 1.51 | 6.7E-02 | AF115536.1 | NT | Mus musculus latent TGF beta binding protein (Tgfb), mRNA |
| 1838 | 14522 | 27078 | 3.82 | 6.7E-02 | AJ220285.1 | EST_HUMAN | Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA |
| | | | | | | | Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP101 allele, complete cds |
| | | | | | | | qg78e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3780 | 16380 | 28844 | 4.61 | 6.7E-02 | P17278 | SWISSPROT | HOMEOBOX PROTEIN HOXD4 (CHOX-A) |
| 4942 | 17420 | 28873 | 3.51 | 6.7E-02 | AP001514.1 | NT | Bacillus halodurans genomic DNA, section 8/14 |
| 7792 | 20335 | 33241 | 0.63 | 6.7E-02 | X62895.1 | NT | H.sapiens DNA for cGMP phosphodiesterase (exons 4-22) |
| 7792 | 20335 | 33242 | 0.63 | 6.7E-02 | X62895.1 | NT | H.sapiens DNA for cGMP phosphodiesterase (exons 4-22) |
| 9518 | 22018 | 34975 | 0.75 | 6.7E-02 | AW137359.1 | EST_HUMAN | UIH-B11-acr-g-01-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3' |
| 9518 | 22018 | 34976 | 0.75 | 6.7E-02 | AW137359.1 | EST_HUMAN | UIH-B11-acr-g-01-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3' |
| 2225 | 14800 | 27372 | 3 | 6.6E-02 | AJ288241.1 | NT | Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts |
| 3510 | 16115 | 28594 | 9.7 | 6.6E-02 | R64308.1 | EST_HUMAN | y18b10.s1 Soares placenta N62-IP Homo sapiens cDNA clone IMAGE:138578 3' |
| 3524 | 16129 | 28609 | 3.24 | 6.6E-02 | 7108357 | NT | Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA |
| 3524 | 16129 | 28610 | 3.24 | 6.6E-02 | 7108357 | NT | Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA |
| 4154 | 16748 | 28200 | 1.83 | 6.6E-02 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 5114 | 17898 | 30122 | 11.2 | 6.6E-02 | Q61703 | SWISSPROT | INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2) |
| 5114 | 17898 | 30123 | 11.2 | 6.6E-02 | Q61703 | SWISSPROT | INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2) |
| 5164 | 17733 | 30160 | 0.57 | 6.6E-02 | AA383244.1 | EST_HUMAN | z74807.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:U4270 TUMOR |
| 5164 | 17733 | 30161 | 0.57 | 6.6E-02 | AA383244.1 | EST_HUMAN | NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN); |
| 6698 | 19294 | 32099 | 4.11 | 6.6E-02 | X08411.1 | NT | NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN); |
| 7898 | 20430 | 33338 | 1.58 | 6.6E-02 | AF052572.1 | NT | NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN); |
| 8408 | 20849 | 33868 | 0.72 | 6.6E-02 | AF06055.1 | NT | P.vulgaris mRNA for chalcone synthase |
| 8714 | 21253 | | 0.49 | 6.6E-02 | O60873 | SWISSPROT | Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds |
| 8852 | 21391 | 34312 | 0.52 | 6.6E-02 | 9629188 | NT | Dicotyledon discodermidum darlin (dsar) gene, complete cds |
| 8852 | 21391 | 34313 | 0.52 | 6.6E-02 | 9629188 | NT | DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3) |
| 8802 | 22359 | 35339 | 0.59 | 6.6E-02 | A1458752.1 | EST_HUMAN | Human respiratory syncytial virus, complete genome |
| 8959 | 22494 | 35483 | 1.54 | 6.6E-02 | Y07848.1 | NT | Human respiratory syncytial virus, complete genome |
| 10028 | 22524 | | 0.53 | 6.6E-02 | 11430559 | NT | Human respiratory syncytial virus, complete genome |
| 10842 | 23363 | 36378 | 7.09 | 6.6E-02 | BF374248.1 | EST_HUMAN | Human respiratory syncytial virus, complete genome |
| 12251 | 24462 | | 2.87 | 6.6E-02 | 9837891 | NT | Human respiratory syncytial virus, complete genome |
| 12585 | 24678 | | 1.38 | 6.6E-02 | AF167430.1 | NT | Human respiratory syncytial virus, complete genome |
| 608 | 13236 | 25710 | 1.65 | 6.6E-02 | BF072639.1 | EST_HUMAN | Human respiratory syncytial virus, complete genome |
| 1024 | 13635 | 26151 | 2.61 | 6.6E-02 | 7706068 | NT | Human respiratory syncytial virus, complete genome |
| 1435 | 14028 | 28556 | 3.4 | 6.6E-02 | U47824.1 | NT | Human respiratory syncytial virus, complete genome |
| 1770 | 14360 | 28905 | 1.42 | 6.6E-02 | AE000764.1 | NT | Human respiratory syncytial virus, complete genome |
| 5349 | 17909 | 30324 | 0.88 | 6.6E-02 | D45898.1 | NT | Human respiratory syncytial virus, complete genome |

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Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5747 | 18373 | 31081 | 1.70 | 6.5E-02 | AA443991.1 | EST_HUMAN | z46h12.s1 Soares ovary tumor NIDHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M28038 |
| 6864 | 18260 | 32094 | 0.89 | 6.5E-02 | BF685340.1 | EST_HUMAN | HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN); |
| 7051 | 18070 | 30461 | 0.90 | 6.5E-02 | U22861.1 | NT | 602118687F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276029 5' |
| 6854 | 22352 | 35332 | 0.65 | 6.5E-02 | BE963200.2 | EST_HUMAN | Azobacter vinelandii ATCC 8048 negative regulator MucB (mucB) gene, partial cds |
| 6854 | 22352 | 35333 | 0.66 | 6.5E-02 | BE963200.2 | EST_HUMAN | 601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3' |
| 10303 | 22857 | 35848 | 0.59 | 6.5E-02 | BF106300.1 | EST_HUMAN | 601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3' |
| 10518 | 23058 | 36067 | 5.86 | 6.5E-02 | AA195648.1 | EST_HUMAN | 601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5' |
| 11688 | 24091 | | 5.28 | 6.5E-02 | M21498.1 | NT | z132g05.s1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:965144 3' |
| 12040 | 24327 | | 3.84 | 6.5E-02 | AF102883.1 | NT | Rabbit microsomal epoxide hydrolase |
| 801 | 13230 | 25703 | 1.74 | 6.4E-02 | X94548.1 | NT | Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds |
| 5841 | 18270 | 30743 | 1.21 | 6.4E-02 | A191956.1 | EST_HUMAN | A carterae precursor of peridinin-chlorophyll-protein (PCP) gene |
| 6261 | 18669 | 31639 | 5.4 | 6.4E-02 | AF052733.1 | NT | qe07b01.x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 |
| 6261 | 18669 | 31640 | 5.4 | 6.4E-02 | AF052733.1 | NT | LTR8 repetitive element |
| 6534 | 19134 | 31827 | 0.68 | 6.4E-02 | A872896.1 | EST_HUMAN | Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds |
| 6807 | 19841 | 32477 | 4.7 | 6.4E-02 | BE974448.1 | EST_HUMAN | Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds |
| 8278 | 20819 | | 2.68 | 6.4E-02 | 8753323 | NT | we73g12.x1 Soares_Deckgraeffe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2346780 3' |
| 8568 | 21138 | 34052 | 3.59 | 6.4E-02 | AA983305.1 | EST_HUMAN | 801680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3' |
| 9055 | 21582 | 34522 | 0.85 | 6.4E-02 | AF150185.1 | EST_HUMAN | Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA |
| 9506 | 22008 | | 0.61 | 6.4E-02 | BE834083.1 | EST_HUMAN | kt419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5' |
| 9633 | 22133 | 35088 | 1.79 | 6.4E-02 | A8011128.1 | NT | AF150185 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone C8DAIA10 |
| 10182 | 22657 | 35652 | 0.68 | 6.4E-02 | AF087150.1 | NT | RC1-OT0083-150800-014-g08 OT0083 Homo sapiens cDNA |
| 10182 | 22657 | 35653 | 0.68 | 6.4E-02 | AF087150.1 | NT | Homo sapiens mRNA for KIAA0554 protein, partial cds |
| | | | | | | | Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18 |
| | | | | | | | Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18 |
| | | | | | | | |
| 11554 | 24002 | 37074 | 2.05 | 6.4E-02 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 11554 | 24002 | 37075 | 2.05 | 6.4E-02 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 11931 | 24971 | | 4.88 | 6.4E-02 | AF107890.1 | NT | Homo sapiens mucin 5B (MUC5B) gene, partial cds |
| 11988 | 24298 | 30883 | 2.89 | 6.4E-02 | AJ277174.1 | NT | Drosophila melanogaster mRNA for mod(modg4)51.4 protein |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1791 | 14361 | 26828 | 3.03 | 6.3E-02 | AF106905.1 | NT | Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; snRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes |
| 3684 | 16286 | | 2.41 | 6.3E-02 | P37082 | SWISSPROT | HEAT SHOCK PROTEIN 70 HOMOLOG |
| 6285 | 18893 | 31692 | 1.1 | 6.3E-02 | BF210736.1 | EST_HUMAN | 601873316F1 NIH_MGC_94 Homo sapiens cDNA clone IMAGE:4087469 5' |
| 7291 | 19819 | | 1.05 | 6.3E-02 | X97869.1 | NT | H. sapiens gene encoding La subunit |
| 9215 | 21732 | 34675 | 0.96 | 6.3E-02 | AJ243916.1 | NT | Drosophila melanogaster Domain gene, exons 1-3 |
| 9827 | 22423 | 35397 | 2.88 | 6.3E-02 | AB010162.1 | NT | Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152 |
| 10172 | 22687 | | 0.87 | 6.3E-02 | AV698070.1 | EST_HUMAN | AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5' |
| 10594 | 18893 | 31692 | 3.9 | 6.3E-02 | BF210736.1 | EST_HUMAN | 601873316F1 NIH_MGC_94 Homo sapiens cDNA clone IMAGE:4087469 5' |
| 4337 | 16824 | 26365 | 3.3 | 6.2E-02 | AL161572.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68 |
| 4431 | 17017 | | 1.04 | 6.2E-02 | AF271235.1 | NT | Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNP1) mRNA, complete cds |
| 4682 | 17264 | | 6.75 | 6.2E-02 | Q82191 | SWISSPROT | 52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52) |
| 6899 | 19624 | 32459 | 0.76 | 6.2E-02 | D49530.1 | NT | Spirulina platensis DNA for adenylate cyclase, complete cds |
| 7623 | 20136 | 33014 | 0.78 | 6.2E-02 | U41453.1 | NT | Rattus norvegicus PKC binding protein and substrate mRNA, complete cds |
| 8877 | 25123 | | 0.81 | 6.2E-02 | M61101.1 | NT | Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds |
| 9267 | 21783 | 34742 | 0.5 | 6.2E-02 | AA778450.1 | EST_HUMAN | af20506 s1 Soares, total Fetus_Nb24-F8_9w Homo sapiens cDNA clone IMAGE:1032178 3' |
| 9401 | 21910 | 34859 | 1.05 | 6.2E-02 | 6877898 | NT | Mus musculus chromosomal cell derived factor receptor 2 (Sdr2), mRNA |
| 11027 | 23541 | 36576 | 1.74 | 6.2E-02 | AF217490.1 | NT | Homo sapiens fragile 160 oxidoreductase (FOR) gene, exons 8, 9, and partial cds |
| 11228 | 23757 | 36814 | 1.89 | 6.2E-02 | AJ242735.1 | NT | Metarhizium anisopliae mRNA for Chymotrypsin (chy1 gene) |
| 11770 | 25097 | | 6.34 | 6.2E-02 | AE000750.1 | NT | Aquifex aeolicus section 82 of 109 of the complete genome |
| 12200 | 24426 | 30951 | 3.58 | 6.2E-02 | BF112038.1 | EST_HUMAN | 73708.x1 Soares_NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q8Y4S9 Q8Y4S8 HYPOTHETICAL 30.3 KD PROTEIN. [1]; |
| 277 | 12934 | 25420 | 4.8 | 6.1E-02 | D18471.1 | NT | Human mRNA, Xq terminal portion |
| 4063 | 16680 | | 2.78 | 6.1E-02 | U73325.1 | NT | Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds |
| 4768 | 17340 | 28786 | 1.09 | 6.1E-02 | AF119413.1 | NT | Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds |
| 4768 | 17340 | 28787 | 1.09 | 6.1E-02 | AF119413.1 | NT | Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds |
| 6262 | 18870 | | 1.42 | 6.1E-02 | 4507070 | NT | Homo sapiens SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA |
| 8207 | 20748 | 33681 | 3.31 | 6.1E-02 | X99288.1 | NT | H. sapiens mRNA for B-HLH DNA binding protein |
| 8595 | 21134 | 34048 | 0.95 | 6.1E-02 | BE971853.1 | EST_HUMAN | 601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3' |
| 8595 | 21134 | 34049 | 0.95 | 6.1E-02 | BE971853.1 | EST_HUMAN | 601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3' |
| 10608 | 23142 | 36153 | 6.34 | 6.1E-02 | BE178543.1 | EST_HUMAN | IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11728 | 25009 | | 23.38 | 6.1E-02 | X70588.1 | NT | S japonicum mRNA for serine-enzyme |
| 12317 | 24880 | | 1.39 | 6.1E-02 | AI888611.1 | EST_HUMAN | U5907.X1 NC1_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2282801 3' |
| 12484 | 24592 | | 7.98 | 6.1E-02 | AL183207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 1305 | 13889 | 28419 | 1.01 | 6.0E-02 | AE001777.1 | NT | Thermotoga maritima section 89 of 138 of the complete genome |
| 2700 | 15257 | 27825 | 1.16 | 6.0E-02 | AW988848.1 | EST_HUMAN | EST380924 IMAGE: ressequences, MAGJ Homo sapiens cDNA |
| 2801 | 15353 | | 1.58 | 6.0E-02 | AB031288.1 | NT | Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, rRNA-Gln, rRNA-Phe, rRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2 |
| 2803 | 12777 | 25259 | 1.09 | 6.0E-02 | AA188730.1 | EST_HUMAN | zp78c04.r1 Stratagene HeLa cell c3 937218 Homo sapiens cDNA clone IMAGE:626310 5' |
| 2803 | 12777 | 25260 | 1.09 | 6.0E-02 | AA188730.1 | EST_HUMAN | zp78c04.r1 Stratagene HeLa cell c3 937218 Homo sapiens cDNA clone IMAGE:626310 5' |
| 3266 | 15878 | 28380 | 1.24 | 6.0E-02 | AA372378.1 | EST_HUMAN | EST84288 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein |
| 3266 | 15878 | 28381 | 1.24 | 6.0E-02 | AA372378.1 | EST_HUMAN | EST84288 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein |
| 3697 | 16298 | | 1.01 | 6.0E-02 | BE964443.2 | EST_HUMAN | 601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876080 3' |
| 5104 | 17878 | 30118 | 0.85 | 6.0E-02 | Z67738.2 | NT | Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA |
| 5595 | 18225 | | 1.89 | 6.0E-02 | AW370211.1 | EST_HUMAN | RC3-BT02633-011199-013-b04 BT0253 Homo sapiens cDNA |
| 6384 | 18088 | 31748 | 1.43 | 6.0E-02 | AB07537.1 | EST_HUMAN | W48H05.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.1 L1 L1 repetitive element; |
| 7063 | 18082 | 30438 | 2.73 | 6.0E-02 | 5174688 | NT | Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA |
| 7063 | 18082 | 30439 | 2.73 | 6.0E-02 | 5174688 | NT | Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA |
| 7239 | 19768 | 32624 | 2.17 | 6.0E-02 | BF382348.1 | EST_HUMAN | 601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049228 5' |
| 7672 | 20184 | 33072 | 1.94 | 6.0E-02 | AI204275.1 | EST_HUMAN | qf58c08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754189 3' |
| 8361 | 20901 | | 0.57 | 6.0E-02 | 11488495 | NT | Reclinomonas americana mitochondrion, complete genome |
| 9186 | 21713 | 34656 | 1.12 | 6.0E-02 | AI823167.1 | EST_HUMAN | ts78a08.x1 NC1_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2237982 3' |
| 9186 | 21713 | 34657 | 1.12 | 6.0E-02 | AI823167.1 | EST_HUMAN | ts78a08.x1 NC1_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2237982 3' |
| 9327 | 21841 | 34782 | 2 | 6.0E-02 | AJ245365.1 | NT | Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2 |
| 9327 | 21841 | 34783 | 2 | 6.0E-02 | AJ245365.1 | NT | Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2 |
| 9819 | 22317 | 35288 | 0.51 | 6.0E-02 | AA309797.1 | EST_HUMAN | EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like |
| 9819 | 22317 | 35300 | 0.51 | 6.0E-02 | AA309797.1 | EST_HUMAN | EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like |
| 11214 | 23717 | | 2.13 | 6.0E-02 | AA128386.1 | EST_HUMAN | zp87c08.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:585168 5' similar to gb-X89181 60S RIBOSOMAL PROTEIN L31 (HUMAN); |
| 11985 | 24295 | 30982 | 1.43 | 6.0E-02 | 11431702 | NT | Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA |
| 12394 | 24554 | | 6.04 | 6.0E-02 | AJ809273.1 | EST_HUMAN | Wf88h03.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR-O60298 O60298 KIAA0551 PROTEIN; |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 260 | 12910 | 25393 | 4.78 | 5.8E-02 | AW834719.1 | EST_HUMAN | RC1-DT0001-280100-012-910 DT0001 Homo sapiens cDNA |
| 3012 | 15828 | 28107 | 2.75 | 5.8E-02 | AF180289.1 | NT | Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced |
| 4768 | 17349 | 29789 | 0.97 | 5.8E-02 | AL191535.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35 |
| 4768 | 17349 | 29800 | 0.97 | 5.8E-02 | AL191535.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35 |
| 4852 | 17430 | | 0.8 | 5.8E-02 | AF168111.1 | NT | Duck parvovirus strain 90-2183 capsid protein (VP3) gene, partial cds |
| 4888 | 17570 | 30014 | 0.96 | 5.8E-02 | AF006304.1 | NT | Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds |
| 6873 | 24774 | 32374 | 0.67 | 5.8E-02 | AF145880.1 | NT | Drosophila melanogaster LD23107 sting (sting) mRNA, complete cds |
| 8552 | 21091 | 34011 | 1.98 | 5.8E-02 | 9055249 | NT | Mus musculus inoquids related homeobox 5 (Drosophila) (In5), mRNA |
| 8072 | 20311 | | 0.82 | 5.8E-02 | BF242748.1 | EST_HUMAN | 601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105894 5' |
| 10884 | 23198 | | 3.41 | 5.8E-02 | 6878870 | NT | Mus musculus folistatin-like (Fsl), mRNA |
| 10889 | 23419 | 38438 | 2.35 | 5.8E-02 | 11433336 | NT | Homo sapiens ninein (LOC51189), mRNA |
| 11429 | 23880 | | 1.83 | 5.8E-02 | AJ240793.1 | NT | Gallus gallus HIKC9 telomere junction |
| 968 | 13579 | | 5.2 | 5.8E-02 | D80110.1 | NT | Thiobacillus ferrooxidans marC, marA genes and URF-1 |
| 1700 | 14293 | 26828 | 1 | 5.8E-02 | Q61768 | SWISSPROT | KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) |
| 2888 | 15504 | | 0.88 | 5.8E-02 | AJ223821.1 | NT | Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5 |
| 3725 | 16326 | 28793 | 1.35 | 5.8E-02 | AE001775.1 | NT | Thermotoga maritima section 87 of 138 of the complete genome |
| 4448 | 17032 | 29473 | 5.29 | 5.8E-02 | AW051827.1 | EST_HUMAN | wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3' |
| 4448 | 17032 | 29474 | 5.28 | 5.8E-02 | AW051827.1 | EST_HUMAN | wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3' |
| 4845 | 17227 | 29682 | 5.04 | 5.8E-02 | AJ247505.1 | EST_HUMAN | qh58f01.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); |
| 4845 | 17227 | 29683 | 5.04 | 5.8E-02 | AJ247505.1 | EST_HUMAN | qh58f01.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); |
| 4874 | 17256 | | 1.98 | 5.8E-02 | AF086264.1 | NT | Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds |
| 5294 | 17856 | 30282 | 0.57 | 5.8E-02 | AF275398.1 | NT | Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced |
| 5294 | 17856 | 30283 | 0.57 | 5.8E-02 | AF275398.1 | NT | Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced |
| 6088 | 18685 | 31428 | 1.52 | 5.8E-02 | AA190694.1 | EST_HUMAN | zp86a11.s1 Stratagene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:627088 3' |
| 7670 | 20182 | 33068 | 2.73 | 5.8E-02 | M89150.1 | NT | Human polymorphic microsatellite DNA |
| 7670 | 20182 | 33070 | 2.73 | 5.8E-02 | M89150.1 | NT | Human polymorphic microsatellite DNA |
| 8601 | 21140 | 34054 | 0.76 | 5.8E-02 | AF163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 11871 | 24223 | | 2.86 | 5.8E-02 | AF122017.1 | NT | Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds |
| 12177 | 25085 | | 6.45 | 5.8E-02 | AA604288.1 | EST_HUMAN | no75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3083 | 15708 | 28179 | 1.13 | 5.7E-02 | AI081844.1 | EST_HUMAN | ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 |
| 3107 | 15722 | 28183 | 1.6 | 5.7E-02 | AF119117.1 | NT | CE08811: |
| 3769 | 16370 | | 0.98 | 5.7E-02 | AF001292.1 | NT | Homo sapiens dopamine transporter (SLC8A3) gene, complete cds |
| 3871 | 16469 | 28632 | 2.44 | 5.7E-02 | AW868791.1 | EST_HUMAN | Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XI (ctt-12) and globin XI (ctt-11) genes, complete cds |
| 4795 | 17373 | | 1.08 | 5.7E-02 | MF5089.1 | NT | EST378865 IMAGE resequences, MAGI Homo sapiens cDNA |
| 5334 | 17895 | 30310 | 0.89 | 5.7E-02 | AJ251973.1 | NT | Bos taurus lysozyme gene (cow 3), complete cds |
| 6039 | 18658 | | 0.9 | 5.7E-02 | AF275948.1 | NT | Homo sapiens partial steath-1 gene |
| 8086 | 20637 | 33548 | 1.48 | 5.7E-02 | AJ28080.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 9794 | 22282 | 35245 | 0.65 | 5.7E-02 | 6681280 | NT | Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene) |
| 11087 | 23579 | 30617 | 4.17 | 5.7E-02 | AF52885.1 | EST_HUMAN | Mus musculus ec2 oncogene (Ec2), mRNA |
| 11087 | 23579 | 30618 | 4.17 | 5.7E-02 | AF52885.1 | EST_HUMAN | cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random |
| 11227 | 23738 | | 1.58 | 5.7E-02 | AL163303.2 | NT | cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random |
| 12085 | 24891 | | 12.98 | 5.7E-02 | D50320.1 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 12257 | 24467 | | 1.71 | 5.7E-02 | AJ271735.1 | NT | Pig DNA for SPAL-2, complete cds |
| 12334 | 24985 | | 3.31 | 5.7E-02 | AF217490.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 12483 | 25074 | | 8.94 | 5.7E-02 | AF261280.1 | NT | Homo sapiens fragile 16D oddo reductase (FOR) gene, exons 8, 9, and partial cds |
| 12622 | 24700 | 30863 | 1.58 | 5.7E-02 | R48513.1 | EST_HUMAN | Pan troglodytes apolipoprotein-E gene, complete cds |
| 1574 | 14167 | 26638 | 1.2 | 5.6E-02 | AF094455.1 | NT | y684d10.s1 Soares breast 2NtHtBst Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1 repetitive element: |
| 4746 | 17327 | 28789 | 1.21 | 5.6E-02 | AB013100.1 | NT | Hydrocotyle radundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product |
| 4806 | 17384 | 29834 | 1.2 | 5.6E-02 | AA280588.1 | EST_HUMAN | Lycopodium esculentum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds |
| 6766 | 19359 | 32168 | 5.98 | 5.6E-02 | AW172708.1 | EST_HUMAN | z945c01.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:700418 3' |
| 6871 | 19548 | 32372 | 0.9 | 5.6E-02 | AA868182.1 | EST_HUMAN | y02e10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2650050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN: |
| 7205 | 19736 | 32588 | 3.1 | 5.6E-02 | BE008001.1 | EST_HUMAN | cd47712.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element: |
| 8737 | 21276 | 34188 | 2.2 | 5.6E-02 | BE542883.1 | EST_HUMAN | QV0-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA |
| 8737 | 21276 | 34189 | 2.2 | 5.6E-02 | BE542883.1 | EST_HUMAN | 601087159F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5' |
| | | | | | | | 601087159F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9728 | 22224 | 35201 | 1.07 | 5.6E-02 | AA482864.1 | EST_HUMAN | n40407.s1 NCL_CGAP_Av1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G768859 G768859 |
| 11439 | 23888 | | 2.33 | 5.6E-02 | AF260225.1 | NT | LAMINA ASSOCIATED POLYPEPTIDE 1C.; |
| 2879 | 15237 | 27804 | 6.14 | 5.5E-02 | X97868.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 3251 | 15863 | 28345 | 3.83 | 5.6E-02 | 6755501 | NT | H. sapiens gene encoding La autoantigen |
| 4296 | 16882 | 28328 | 1.12 | 5.5E-02 | L41581.1 | NT | Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA |
| 5940 | 18464 | 31188 | 3.19 | 5.5E-02 | Q01174 | SWISSPROT | Galid herpesvirus mRNA fragment |
| 6176 | 18484 | 31188 | 3.86 | 5.5E-02 | Q01174 | SWISSPROT | TROPOMYOSIN ALPHA CHAIN, NON MUSCLE |
| 7412 | 19837 | 32802 | 1.77 | 5.5E-02 | 6755902 | NT | TROPOMYOSIN ALPHA CHAIN, NON MUSCLE |
| 8063 | 20605 | 33516 | 0.77 | 5.5E-02 | AF170911.1 | NT | Mus musculus tufalin 1 (Tuf1), mRNA |
| 8063 | 20605 | 33517 | 0.77 | 5.5E-02 | AF170911.1 | NT | Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds |
| 8573 | 22073 | 35034 | 0.61 | 5.5E-02 | 10947034 | NT | Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds |
| 9573 | 22073 | 35035 | 0.61 | 5.5E-02 | 10947034 | NT | Homo sapiens eIF4E-transporter (4E-T), mRNA |
| 9864 | 22163 | 35136 | 1.26 | 5.5E-02 | U89492.1 | NT | Homo sapiens eIF4E-transporter (4E-T), mRNA |
| | | | | | | | Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2 |
| 10898 | 23418 | 36435 | 11.52 | 5.5E-02 | U09771.1 | NT | Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB);> |
| 3054 | 15670 | | 0.85 | 5.4E-02 | AJ277488.1 | NT | Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor |
| 3489 | 18013 | | 6.27 | 5.4E-02 | BE073488.1 | EST_HUMAN | RC8-BT0559-140200-012-Q03 BT0559 Homo sapiens cDNA |
| 3692 | 16580 | 29051 | 0.58 | 5.4E-02 | U85806.1 | NT | Hirudo medicinalis SNAP-25 homolog mRNA, complete cds |
| 5119 | 17691 | 30129 | 2.48 | 5.4E-02 | U53528.1 | NT | Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds |
| 8067 | 20609 | | 1.11 | 5.4E-02 | Z89116.1 | NT | Bacillus subtilis complete genome (section 13 of 21): from 2395281 to 2813730 |
| 9001 | 21538 | 34467 | 0.61 | 5.4E-02 | AF260225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 10578 | 23113 | 36126 | 1.89 | 5.4E-02 | U20790.1 | NT | Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds |
| 11058 | 23570 | 36606 | 1.56 | 5.4E-02 | BF371288.1 | EST_HUMAN | RC8-FN0112-180700-021-D06 FN0112 Homo sapiens cDNA |
| 11058 | 23570 | 36607 | 1.56 | 5.4E-02 | BF371289.1 | EST_HUMAN | RC8-FN0112-180700-021-D06 FN0112 Homo sapiens cDNA |
| 11968 | 24882 | | 2.9 | 5.4E-02 | U44894.1 | NT | Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds |
| 1091 | 13698 | 26205 | 1.58 | 5.3E-02 | AW391248.1 | EST_HUMAN | QV0-ST0213-021289-062-a09 ST0213 Homo sapiens cDNA |
| 1091 | 13698 | 26206 | 1.58 | 5.3E-02 | AW391248.1 | EST_HUMAN | QV0-ST0213-021289-062-a09 ST0213 Homo sapiens cDNA |
| | | | | | | | ye37112.1 Stragelene lung (#637210) Homo sapiens cDNA clone IMAGE:118951 5' similar to gb:K01508 |
| 1553 | 14145 | 28679 | 21.83 | 5.3E-02 | T94759.1 | EST_HUMAN | HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN); |
| 2541 | 15105 | 27677 | 2.71 | 5.3E-02 | AJ276408.1 | NT | Pseudomonas putida tlgS gene |
| 2869 | 15585 | 28066 | 0.88 | 5.3E-02 | M58417.1 | NT | Drosophila melanogaster laminin B2 gene, complete cds |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 2969 | 15595 | 28067 | 0.88 | 5.3E-02 | M58417.1 | NT | Drosophila melanogaster laminin B2 gene, complete cds |
| 3187 | 15799 | 28271 | 4.52 | 5.3E-02 | AJ276408.1 | NT | Pseudomonas putida tlgS gene |
| 5248 | 17811 | 30234 | 0.75 | 5.3E-02 | AB051897.1 | NT | Mus musculus Scya6, Scya6, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds |
| 5250 | 17813 | 30236 | 8.25 | 5.3E-02 | M80463.1 | NT | Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds |
| 5522 | 18154 | 30568 | 1.97 | 5.3E-02 | AE000527.1 | NT | Helicobacter pylori 26895 section 5 of 134 of the complete genome |
| 5522 | 18154 | 30569 | 1.97 | 5.3E-02 | AE000527.1 | NT | Helicobacter pylori 26895 section 5 of 134 of the complete genome |
| 6251 | 18880 | 31632 | 0.71 | 5.3E-02 | M85288.1 | NT | Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds |
| 6894 | 19541 | 32363 | 4.23 | 5.3E-02 | 9895413 | NT | Lymphocystis disease virus 1, complete genome |
| 7149 | 19882 | 32523 | 1.55 | 5.3E-02 | U32832.1 | NT | Haemophilus influenzae Rd section 147 of 163 of the complete genome |
| 7396 | 19821 | | 2.05 | 5.3E-02 | S78221.1 | NT | nuclear protein TIF1 isoform [mice, mRNA, 4053 nt] |
| 7818 | 20290 | 33189 | 0.52 | 5.3E-02 | P38742 | SWISSPROT | HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION |
| 8344 | 20885 | | 0.54 | 6.3E-02 | U10098.1 | NT | Mus musculus 128Sv cystatin C (cst3) gene, complete cds |
| 9053 | 21590 | 34521 | 1.83 | 5.3E-02 | X03127.1 | NT | Potocarpa anserina mitochondrial epsilon-sen DNA |
| 10038 | 22533 | 35529 | 0.54 | 5.3E-02 | AB022805.1 | NT | Homo sapiens hCMT1b mRNA for mRNA (guanine-7)-methyltransferase, complete cds |
| 10038 | 22533 | 35530 | 0.54 | 5.3E-02 | AB022805.1 | NT | Homo sapiens hCMT1b mRNA for mRNA (guanine-7)-methyltransferase, complete cds |
| 10156 | 22651 | | 0.82 | 5.3E-02 | Y07807.1 | NT | D. rerio mRNA for zp-23 POU gene, splice variant (neurons, 9-16 hpf and postmitogenesis, 20-28 hpf) |
| 10235 | 22730 | 36721 | 0.65 | 5.3E-02 | X68432.1 | NT | B. rerio pou3f1 mRNA for transcription factor |
| 2324 | 14895 | | 110.52 | 5.2E-02 | 5031908 | NT | Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA |
| 3148 | 15762 | 28228 | 2.4 | 5.2E-02 | AJ277661.1 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1 |
| 3148 | 15762 | 28229 | 2.4 | 5.2E-02 | AJ277661.1 | NT | Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1 |
| 4013 | 16611 | 29084 | 0.7 | 5.2E-02 | AF236101.1 | NT | Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds |
| 4365 | 16952 | 29392 | 3.61 | 5.2E-02 | U07132.1 | NT | Human steroid hormone receptor Nar-1 mRNA, complete cds |
| 4846 | 17424 | 29877 | 1.29 | 5.2E-02 | L33246.1 | NT | Drosophila melanogaster filament protein homolog (sepi) gene, complete cds |
| 6076 | 18893 | 31439 | 0.89 | 5.2E-02 | U14731.1 | NT | Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds |
| 6255 | 18884 | | 1.42 | 5.2E-02 | AJ830865.1 | EST_HUMAN | w80604.x1 NC1_CGAP_Lym12 Homo sapiens cDNA clone IMAGE-2408150 3' similar to contains MER15.b1 MER15 repetitive element |
| 7318 | 19845 | 32706 | 1.19 | 5.2E-02 | P36322 | SWISSPROT | DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN) |
| 8136 | 20677 | | 1.98 | 5.2E-02 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 9645 | 22145 | 35113 | 1.97 | 5.2E-02 | D10827.1 | NT | Turnip mosaic virus genomic RNA for Capsid protein, complete cds |
| 9645 | 22145 | 35114 | 1.97 | 5.2E-02 | D10827.1 | NT | Turnip mosaic virus genomic RNA for Capsid protein, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12224 | 24445 | | 1.84 | 5.2E-02 | Q03030 | SWISSPROT | OXALOACETATE DECARBOXYLASE ALPHA CHAIN |
| 12327 | 24513 | | 1.27 | 5.2E-02 | D63362.1 | NT | Mouse DNA for regilla gamma protein, complete cds |
| 2402 | 14970 | | 1.14 | 5.1E-02 | AL134071.1 | EST_HUMAN | DKFZp547D073_1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547D073 5' |
| 4282 | 16888 | 28315 | 0.73 | 5.1E-02 | AE001301.1 | NT | Chlamydia trachomatis section 28 of 87 of the complete genome |
| 4808 | 17483 | 28941 | 8.03 | 5.1E-02 | AF085167.1 | NT | Hordeum vulgare receptor-like kinase ARK1AS gene, partial cds |
| 5205 | 17770 | 30193 | 1.14 | 5.1E-02 | BE957423.2 | EST_HUMAN | 801653566R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3' |
| 6777 | 19369 | 32182 | 0.76 | 5.1E-02 | AF280389.1 | NT | HIV-1 patient 98 from Italy protease (pol) gene, complete cds |
| 6842 | 18050 | 30472 | 1.6 | 6.1E-02 | BF378625.1 | EST_HUMAN | QVD-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA |
| 8195 | 20736 | 33646 | 0.82 | 5.1E-02 | M26434.1 | NT | Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds |
| 8195 | 20736 | 33646 | 0.82 | 5.1E-02 | M26434.1 | NT | Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds |
| 8288 | 20828 | 33750 | 1.48 | 5.1E-02 | AJ131988.1 | NT | Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds |
| 8818 | 21357 | 34282 | 0.63 | 5.1E-02 | P02533 | SWISSPROT | Spodoptera littoralis mRNA for 3-dehydrocyclohexa-beta-reductase |
| 8818 | 21357 | 34283 | 0.63 | 5.1E-02 | P02533 | SWISSPROT | KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) |
| 9723 | 22221 | 35198 | 8.16 | 5.1E-02 | AF012898.1 | NT | KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) |
| 10084 | 22579 | 35572 | 1.83 | 5.1E-02 | P40603 | SWISSPROT | Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds |
| 10709 | 23237 | 36250 | 2.86 | 5.1E-02 | AF083930.1 | NT | ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) |
| 10709 | 23237 | 36251 | 2.86 | 5.1E-02 | AF083930.1 | NT | Homo sapiens ES18 mRNA, partial cds |
| 12332 | 24448 | | 1.51 | 5.1E-02 | AF062467.1 | NT | Homo sapiens ES18 mRNA, partial cds |
| 508 | 13141 | 25828 | 1.78 | 5.0E-02 | AF088004.1 | NT | Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds |
| 1246 | 13843 | 26360 | 6.63 | 5.0E-02 | Z99104.1 | NT | Mus musculus fatty acid amide hydrolase gene, exon 10 |
| | | | | | | | Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080 |
| 2034 | 14616 | 27182 | 3.63 | 5.0E-02 | P02810 | SWISSPROT | 4) (PIF-F/PIF-S) (PROTEIN APROTEIN C) (CONTAINS: PEPTIDE P-C) |
| 2846 | 13634 | 28150 | 1.78 | 5.0E-02 | U72742.1 | NT | SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-3) |
| 3391 | 15880 | | 1.42 | 5.0E-02 | 7305810 | NT | Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds |
| 3655 | 16258 | | 1.08 | 5.0E-02 | U32782.1 | NT | Mus musculus Ubc-51 like kinase 2 (C. elegans) (Ulk2), mRNA |
| 3747 | 16348 | 28816 | 5.6 | 5.0E-02 | U12769.2 | NT | Haemophilus influenzae Rd section 97 of 163 of the complete genome |
| 5102 | 17674 | 30114 | 1.11 | 5.0E-02 | AF188530.1 | NT | Antheraea pernyi period clock protein homolog mRNA, complete cds |
| 6279 | 18887 | 31856 | 0.74 | 5.0E-02 | AF086284.1 | NT | Homo sapiens ubiquitous tetrahydrocortisol containing protein RoXan mRNA, partial cds |
| 6450 | 19051 | | 1.23 | 5.0E-02 | AJ242823.1 | NT | Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds |
| 7544 | 20084 | 32938 | 10.74 | 5.0E-02 | P35616 | SWISSPROT | Mus musculus Dmp-1 gene, exons 1-6 |
| 10101 | 22586 | 35588 | 1.13 | 5.0E-02 | AF305238.1 | NT | NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L) |
| 11384 | 23816 | 36877 | 2.87 | 5.0E-02 | U67600.1 | NT | Mus musculus Fas-interacting serine/threonine kinase 3 (Fisd3) mRNA, complete cds |
| 11756 | 24924 | | 7.22 | 5.0E-02 | Q04047 | SWISSPROT | Methanococcus jannaschii section 142 of 150 of the complete genome |
| 242 | 12901 | | 23.23 | 4.9E-02 | M14230.1 | NT | NO-ON-TRANSIENT A PROTEIN |
| | | | | | | | Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 392 | 13038 | 25528 | 3.62 | 4.9E-02 | AF275948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 392 | 13038 | 25528 | 3.62 | 4.9E-02 | AF275948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 3328 | 15938 | 28414 | 1.58 | 4.9E-02 | P54258 | SWISSPROT | ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN) |
| 3628 | 16231 | | 0.83 | 4.9E-02 | AA189940.1 | EST_HUMAN | z48a12.s1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:832828 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element; |
| 3651 | 16254 | 28726 | 0.91 | 4.9E-02 | AA400814.1 | EST_HUMAN | z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3' |
| 3651 | 16254 | 28727 | 0.91 | 4.9E-02 | AA400814.1 | EST_HUMAN | z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3' |
| 4968 | 17540 | 28982 | 1.59 | 4.9E-02 | AW167821.1 | EST_HUMAN | xg56g10.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2832388 3' |
| 4968 | 17540 | 28983 | 1.59 | 4.9E-02 | AW167821.1 | EST_HUMAN | xg56g10.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2832388 3' |
| 5372 | 17831 | 30345 | 0.81 | 4.9E-02 | 7682816 | NT | Homo sapiens PRO1848 protein (PRO1848), mRNA |
| 5408 | 17884 | | 0.91 | 4.9E-02 | AF135416.1 | NT | Homo sapiens UDP-glucuronosyltransferase gene, complete cds |
| 5425 | 17882 | | 0.88 | 4.9E-02 | AE001774.1 | NT | Thermoplasma maritima section 88 of 136 of the complete genome |
| 5437 | 17882 | 30398 | 1.03 | 4.9E-02 | M84083.1 | NT | Brucella ovis heat shock protein hsp70 (dnaK) gene, complete cds; heat shock protein hsp40 (dnaJ) gene, complete cds |
| 5573 | 18204 | 30654 | 1.95 | 4.9E-02 | L00122.1 | NT | Rat elastase II gene, exon 6 |
| 5573 | 18204 | 30655 | 1.95 | 4.9E-02 | L00122.1 | NT | Rat elastase II gene, exon 6 |
| 7188 | 18727 | 32578 | 0.88 | 4.9E-02 | AE000980.1 | NT | Archaeoglobus fulgidus section 127 of 172 of the complete genome |
| 8551 | 21080 | | 0.7 | 4.9E-02 | AE002309.1 | NT | Chlamydia muridarum, section 40 of 85 of the complete genome |
| 8698 | 21228 | 34149 | 0.7 | 4.9E-02 | AL161559.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59 |
| 10183 | 22688 | 35681 | 0.54 | 4.9E-02 | P19532 | SWISSPROT | TRANSCRIPTION FACTOR E3 |
| 11280 | 23733 | 36788 | 3.87 | 4.9E-02 | AF008303.1 | NT | Homo sapiens prepro placental TGF-beta gene, complete cds |
| 12148 | 24391 | | 1.44 | 4.9E-02 | 8823980 | NT | Homo sapiens CS box-containing WD protein (LOC55884), mRNA |
| 12431 | 24573 | | 2.92 | 4.9E-02 | M18864.1 | NT | Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds |
| 352 | 13002 | 25487 | 1.15 | 4.8E-02 | D16471.1 | NT | Human mRNA, Xq terminal portion |
| 353 | 13002 | 26487 | 1.87 | 4.8E-02 | D16471.1 | NT | Human mRNA, Xq terminal portion |
| 514 | 13147 | 25631 | 9.43 | 4.8E-02 | AF003100.1 | NT | Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds |
| 2312 | 14884 | 27459 | 1.98 | 4.8E-02 | W51983.1 | EST_HUMAN | z48a02.s1 Soares_senescent_fibroblasts_NHISF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30838 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN); |
| 3244 | 15856 | 28338 | 2.34 | 4.8E-02 | X17144.1 | NT | Tetrahymena rostrata histone H3L1 and histone H4L1 intergenic DNA |
| 4778 | 17358 | | 1.32 | 4.8E-02 | Z54280.1 | NT | S. scrofa gene for skeletal muscle myosin receptor |
| 5309 | 17871 | 30293 | 0.67 | 4.8E-02 | U91814.1 | NT | Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds |
| 5380 | 17939 | 30352 | 4.1 | 4.8E-02 | AF198339.1 | NT | Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds |
| 5380 | 17939 | 30353 | 4.1 | 4.8E-02 | AF198339.1 | NT | Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds |

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8080 | 20622 | 33535 | 1.42 | 4.8E-02 | AW389497.1 | EST_HUMAN | MF2-ST0128-Z21088-012-b02 ST0128 Homo sapiens cDNA |
| 8057 | 21594 | 34524 | 1.3 | 4.8E-02 | AJ001398.1 | NT | Fugu rubripes rps24 gene |
| 8057 | 21594 | 34525 | 1.3 | 4.8E-02 | AJ001398.1 | NT | Fugu rubripes rps24 gene |
| 12018 | 24315 | | 1.93 | 4.8E-02 | Q632893 | NT | Streptococcus thermophilus bacteriophage Sf19, complete genome |
| 8918 | 19577 | 32408 | 2.88 | 4.7E-02 | W01153.1 | EST_HUMAN | yea7700.r1 Soares melanocyte ZNBM Homo sapiens cDNA clone IMAGE:281017 5' similar to contains Abu repetitive element; |
| 8985 | 19542 | 32384 | 0.78 | 4.7E-02 | BF688825.1 | EST_HUMAN | 602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5' |
| 8985 | 19542 | 32385 | 0.78 | 4.7E-02 | BF688825.1 | EST_HUMAN | 602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5' |
| 8908 | 19496 | 32317 | 1.57 | 4.7E-02 | M62752.1 | NT | Rat elastin-related protein (e1) gene, complete CDS |
| 8183 | 20734 | 33844 | 8.55 | 4.7E-02 | X15543.1 | NT | B. taurus mRNA for RF-38-DNA-binding protein |
| 8883 | 21421 | 34346 | 1.12 | 4.7E-02 | X89211.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 8808 | 21444 | | 2.29 | 4.7E-02 | AB026678.1 | NT | Gallus gallus Wpka1-8 gene, complete cds |
| 8154 | 21689 | 34633 | 8.81 | 4.7E-02 | X15543.1 | NT | B. taurus mRNA for RF-38-DNA-binding protein |
| 8965 | 22065 | 35024 | 0.55 | 4.7E-02 | BF305237.1 | EST_HUMAN | 601892682F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5' |
| 8950 | 22149 | | 0.55 | 4.7E-02 | A1873042.1 | EST_HUMAN | we79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3' |
| 10634 | 23186 | 36177 | 1.55 | 4.7E-02 | 6754565 | NT | Mus musculus ligand of numb-protein X (Lnx), mRNA |
| 11430 | 23881 | 36945 | 1.69 | 4.7E-02 | U73821.1 | NT | Bos taurus paired box protein (pax-6) gene, partial cds |
| 11430 | 23881 | 36946 | 1.69 | 4.7E-02 | U73821.1 | NT | Bos taurus paired box protein (pax-6) gene, partial cds |
| 11851 | 25087 | | 8.94 | 4.7E-02 | AV648521.1 | EST_HUMAN | AV648521 GLC Homo sapiens cDNA clone GLC8K02 3' |
| 12322 | 25089 | | 1.47 | 4.7E-02 | P52851 | SWISSPROT | HOMEOBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2) |
| 282 | 12848 | 25435 | 0.81 | 4.8E-02 | BE153583.1 | EST_HUMAN | PM0-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA |
| 769 | 13388 | 25887 | 2.44 | 4.8E-02 | AE000445.1 | NT | Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome |
| 1335 | 13928 | | 1.37 | 4.8E-02 | A014255.1 | EST_HUMAN | am50402.at Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TRP-P90533 |
| 1403 | 13908 | 26525 | 9 | 4.8E-02 | AV727056.1 | EST_HUMAN | P90533 LIMA : contains element LTR1 repetitive element ; |
| 2530 | 15094 | 27686 | 2.77 | 4.8E-02 | AW236023.1 | EST_HUMAN | AV727056 HTC Homo sapiens cDNA clone HTC8W/CD1 5' |
| 2834 | 12848 | 25435 | 1.83 | 4.8E-02 | BE153583.1 | EST_HUMAN | xn2403.x1 NCI_CGAP_Kdrl1 Homo sapiens cDNA clone IMAGE:2884653 3' similar to SW:GRF1_HUMAN |
| 3042 | 15658 | 28138 | 0.7 | 4.8E-02 | BE153583.1 | EST_HUMAN | Q12849 G-RICH SEQUENCE FACTOR-1 ; |
| 3543 | 15658 | 28138 | 0.85 | 4.8E-02 | BE153583.1 | EST_HUMAN | PM0-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA |
| 4201 | 16780 | | 0.97 | 4.8E-02 | AF220365.1 | NT | PM0-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA |
| 5809 | 18531 | 31256 | 1.44 | 4.8E-02 | AF078982.1 | NT | PM0-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA |
| 8377 | 19081 | 31760 | 3.77 | 4.8E-02 | X61824.1 | NT | PM0-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA |
| | | | | | | | PM0-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA |
| | | | | | | | Mus musculus nuclear RNA helicase II(Gu (dht21) gene, complete cds |
| | | | | | | | Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnrh2) gene, complete cds |
| | | | | | | | C.reinhardtii atp2 (atpB) mRNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6377 | 18881 | 31781 | 3.77 | 4.9E-02 | X61624.1 | NT | C. reinhardtii atp2 (atp8) mRNA |
| 6891 | 19825 | 32481 | 1.39 | 4.9E-02 | A1149574.1 | EST_HUMAN | qp00006.x1 Soares_placenta_860weeks_2Nbr-IP80b3W Homo sapiens cDNA clone IMAGE:1713971 3' |
| 8560 | 21129 | 34048 | 2.82 | 4.9E-02 | BE154008.1 | EST_HUMAN | similar to contains L1.13 L1 repetitive element; |
| 11281 | 23734 | 36789 | 4.26 | 4.9E-02 | AA913328.1 | EST_HUMAN | PMO-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA |
| 12541 | 24651 | | 2.54 | 4.9E-02 | X57608.1 | NT | cl27m08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3' |
| 472 | 13105 | 25598 | 2.71 | 4.5E-02 | P22448 | SWISSPROT | Human germline immunoglobulin lambda light chain gene |
| 1260 | 13857 | 28373 | 0.78 | 4.5E-02 | AF005730.1 | NT | RETINOIC ACID RECEPTOR BETA (RAR-BETA) |
| 1280 | 13857 | 26374 | 0.78 | 4.5E-02 | AF005730.1 | NT | Marburg virus strain MIS.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds |
| 1840 | 14428 | 26880 | 3.54 | 4.5E-02 | P32182 | SWISSPROT | Marburg virus strain MIS.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds |
| 2159 | 14733 | 27309 | 3.85 | 4.5E-02 | AE003984.1 | NT | HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B) |
| 3786 | 16386 | 28852 | 3.84 | 4.5E-02 | AL163278.2 | NT | Xyella fastidiosa, section 110 of 229 of the complete genome |
| 6378 | 18982 | 31782 | 1.88 | 4.5E-02 | AJ400877.1 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 6631 | 19227 | 32032 | 0.89 | 4.5E-02 | AL163280.2 | NT | Homo sapiens ASCL3 gene, OEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene |
| 8332 | 20873 | 33785 | 1.8 | 4.5E-02 | AF036984.1 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 9880 | 22357 | 35337 | 5.91 | 4.5E-02 | AA325216.1 | EST_HUMAN | Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds |
| 10117 | 22612 | 35602 | 0.77 | 4.5E-02 | AB000470.1 | NT | EST28167 Cerebellum II Homo sapiens cDNA 5' and similar to neuro-D4 protein |
| 11947 | 24276 | 31018 | 2.92 | 4.5E-02 | 11418013 | NT | Gallus gallus mRNA for alpha1 Integrin, complete cds |
| 12367 | 24973 | 30638 | 6.27 | 4.5E-02 | AA191087.1 | EST_HUMAN | Homo sapiens ret finger protein-like 3 (RFPL3), mRNA |
| 237 | 12897 | | 3.08 | 4.4E-02 | BE972733.1 | SWISSPROT | zq49f1.1 Strabegene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:332483 5' |
| 2144 | 14722 | | 6.8 | 4.4E-02 | P31568 | EST_HUMAN | 601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5' |
| 2532 | 15098 | 27688 | 2.82 | 4.4E-02 | AW875475.1 | EST_HUMAN | HYPOTHETICAL PROTEIN (ORF 2280) |
| 3702 | 16303 | 28771 | 1.5 | 4.4E-02 | AF159160.1 | NT | QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA |
| 4733 | 17314 | 29758 | 1.23 | 4.4E-02 | AF109907.1 | NT | Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds |
| 4733 | 17314 | 29757 | 1.23 | 4.4E-02 | AF109907.1 | NT | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 7172 | 19704 | 32551 | 1.56 | 4.4E-02 | AF085824.1 | NT | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 7172 | 19704 | 32552 | 1.56 | 4.4E-02 | AF085824.1 | NT | Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds |
| 8687 | 21226 | 34146 | 2.04 | 4.4E-02 | AA738968.1 | EST_HUMAN | Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds |
| 10951 | 23486 | 36489 | 4.58 | 4.4E-02 | AF080688.1 | NT | nm13h03.s1 NC1 CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3' |
| 11080 | 23592 | 36628 | 2.63 | 4.4E-02 | AA468739.1 | EST_HUMAN | Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds |
| | | | | | | | es3304.r1 Gossler Wllms tumor Homo sapiens cDNA clone IMAGE:887631 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11884 | 24088 | | 3.28 | 4.4E-02 | AB040928.1 | NT | Homo sapiens mRNA for KIAA1483 protein, partial cds |
| 813 | 13431 | 25836 | 8.91 | 4.3E-02 | AF003249.1 | NT | Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds |
| 2803 | 15185 | 27732 | 1.16 | 4.3E-02 | AV704878.1 | EST_HUMAN | AV704878 ADB Homo sapiens cDNA clone ADBA0408 5' |
| 3477 | 16083 | 28557 | 8.12 | 4.3E-02 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3720 | 16321 | | 1.12 | 4.3E-02 | AF060588.1 | NT | Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds |
| 6822 | 19219 | 32023 | 5.71 | 4.3E-02 | P30427 | SWISSPROT | PLECTIN |
| 6822 | 19219 | 32024 | 5.71 | 4.3E-02 | P30427 | SWISSPROT | PLECTIN |
| 6830 | 19420 | 32236 | 0.68 | 4.3E-02 | AA652268.1 | EST_HUMAN | ns68c12.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188886 |
| 8450 | 20880 | 33808 | 0.74 | 4.3E-02 | AF283359.1 | NT | Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced |
| 8738 | 21276 | 34198 | 0.98 | 4.3E-02 | X55322.1 | NT | H. sapiens NCAM mRNA for neural cell adhesion molecule |
| 8738 | 21275 | 34197 | 0.98 | 4.3E-02 | X55322.1 | NT | H. sapiens NCAM mRNA for neural cell adhesion molecule |
| 855 | 13471 | 25882 | 1.57 | 4.2E-02 | AU123327.1 | EST_HUMAN | AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5' |
| 889 | 13513 | | 2.24 | 4.2E-02 | AU123327.1 | EST_HUMAN | AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5' |
| 929 | 13542 | 28080 | 0.89 | 4.2E-02 | AW003645.1 | EST_HUMAN | w034g01.x1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291 |
| 1758 | 14348 | | 1.32 | 4.2E-02 | AL445066.1 | NT | L1 RETROPOS, ORF2 MRNA ; contains L1.13 L1 L1 repetitive element ; |
| | | | | | | | Thermoplasma acidophilum complete genome; segment 4/5 |
| | | | | | | | q05f10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:M35718 |
| 3180 | 15802 | 28274 | 0.98 | 4.2E-02 | AI469472.1 | EST_HUMAN | FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN); |
| 3726 | 16327 | 28794 | 1.36 | 4.2E-02 | P23081 | SWISSPROT | TRANSFORMING PROTEIN MAF |
| 4410 | 16885 | 28437 | 1.03 | 4.2E-02 | U26674.1 | NT | Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds |
| 4410 | 16885 | 28438 | 1.03 | 4.2E-02 | U26674.1 | NT | Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds |
| 4854 | 17432 | 28883 | 0.89 | 4.2E-02 | BF342895.1 | EST_HUMAN | 602017105F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152672 5' |
| | | | | | | | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 5902 | 18427 | 31145 | 1.49 | 4.2E-02 | AF280107.1 | NT | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 5802 | 18427 | 31146 | 1.49 | 4.2E-02 | AF280107.1 | NT | Legionella pneumophila catalase-peroxidase (katA) gene, complete cds |
| 7534 | 20054 | 32827 | 5.29 | 4.2E-02 | AF276752.1 | NT | ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN) |
| 8745 | 21284 | 34206 | 3.5 | 4.2E-02 | P05095 | SWISSPROT | T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56) |
| 10069 | 22564 | 35559 | 1.17 | 4.2E-02 | Q16850 | SWISSPROT | cn33b11.s1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65280 |
| 10919 | 23438 | 36459 | 3.12 | 4.2E-02 | AA976118.1 | EST_HUMAN | INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN); |
| 11187 | 23692 | 36739 | 2.3 | 4.2E-02 | BE815822.1 | EST_HUMAN | PM3-BN0174-250500-008-d10 BN0174 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11187 | 23892 | 36740 | 2.3 | 4.2E-02 | BE815822.1 | EST_HUMAN | PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA |
| 11378 | 23831 | 36894 | 2.06 | 4.2E-02 | AF178458.1 | NT | PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds |
| 12228 | 25023 | | 3.4 | 4.2E-02 | A1983494.1 | EST_HUMAN | w48g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3' |
| 538 | 13187 | 25848 | 0.7 | 4.1E-02 | AF200628.1 | NT | Homo sapiens HPS1 gene, intron 5 |
| 2701 | 15258 | 27828 | 2.87 | 4.1E-02 | AE002330.2 | NT | Chlamydia muridarum, section 60 of 85 of the complete genome |
| 4571 | 17154 | | 8.95 | 4.1E-02 | AW883484.1 | EST_HUMAN | QV1-NN0012-180400-164-R08 NN0012 Homo sapiens cDNA |
| 5285 | 17857 | | 0.89 | 4.1E-02 | X85880.1 | NT | Limonocycogenes type 3 partial lap gene (strain 443) |
| 5824 | 18448 | 31170 | 0.88 | 4.1E-02 | BE261894.1 | EST_HUMAN | 601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5' |
| 5824 | 18448 | 31171 | 0.88 | 4.1E-02 | BE261894.1 | EST_HUMAN | 601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5' |
| 6082 | 19530 | | 0.97 | 4.1E-02 | X75881.1 | NT | A.thaliana mRNA for plasma membrane intrinsic protein 1a |
| 7158 | 19688 | 32532 | 1.92 | 4.1E-02 | AE002132.1 | NT | Ureaplasma urealyticum section 33 of 59 of the complete genome |
| 7522 | 20042 | 32911 | 1.76 | 4.1E-02 | 7882347 | NT | Homo sapiens KIAA0887 protein (KIAA0887), mRNA |
| | | | | | | | Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit? |
| 7742 | 20250 | 33143 | 3.14 | 4.1E-02 | AF026188.1 | NT | CUTICLE COLLAGEN 34 |
| 8577 | 21118 | 34036 | 0.56 | 4.1E-02 | P34887 | SWISSPROT | EST84291 Coton adenocarcinoma IV Homo sapiens cDNA 5' and |
| 9081 | 21617 | 34552 | 0.85 | 4.1E-02 | AA373388.1 | EST_HUMAN | Brassica napus gin gene for plastid glutamine synthetase, exons 1-12 |
| 12572 | 25024 | 30618 | 24.9 | 4.1E-02 | AJ271809.1 | NT | Homo sapiens mRNA for KIAA1471 protein, partial cds |
| 3281 | 19882 | 28371 | 3.71 | 4.0E-02 | AB040904.1 | NT | Homo retinoblastoma susceptibility gene exons 1-27, complete cds |
| 3868 | 18468 | 28829 | 0.96 | 4.0E-02 | L11910.1 | NT | Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds |
| 5298 | 17858 | 30284 | 0.58 | 4.0E-02 | AB042287.1 | NT | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 5581 | 18212 | 30681 | 5.51 | 4.0E-02 | AF280107.1 | NT | 7h52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O75298 O75298 |
| 6382 | 18888 | 31744 | 1.86 | 4.0E-02 | BF110434.1 | EST_HUMAN | R28124_1.; |
| | | | | | | | Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds |
| 7678 | 20189 | 33078 | 6.8 | 4.0E-02 | L23838.1 | NT | Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds |
| 7743 | 20251 | 33144 | 0.87 | 4.0E-02 | AB000381.1 | NT | Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds |
| 7743 | 20251 | 33145 | 0.87 | 4.0E-02 | AB000381.1 | NT | GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) |
| 8651 | 21180 | 34108 | 2.64 | 4.0E-02 | P08840 | SWISSPROT | GLUCOHYDROLASE |
| 9562 | 22062 | | 0.84 | 4.0E-02 | BF078376.1 | EST_HUMAN | 602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5' |
| 9588 | 22088 | 35051 | 3.35 | 4.0E-02 | AJ000941.1 | NT | Methanobacterium thermoautotrophicum strain Marburg, Thiothymate reductase subunit A |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9885 | 22382 | | 1.28 | 4.0E-02 | D43949.1 | NT | Human mRNA for KIAA0082 gene, partial cds |
| 11608 | 24051 | | 1.62 | 4.0E-02 | AJ001018.1 | NT | Kluyveromyces fragilis gene for Cat+ ATPase |
| 11841 | 24834 | 30798 | 18.69 | 4.0E-02 | AJ001058.1 | NT | Ovis aries mRNA for acetyl-coA carboxylase |
| 1159 | 13782 | 28273 | 3.8 | 3.9E-02 | BF516149.1 | EST_HUMAN | UI-HBW1-ant-h-08-0-UI.s1 NCI CGAP. Sub7 Homo sapiens cDNA clone IMAGE:3084134 3' |
| 1390 | 13884 | 26510 | 1.88 | 3.9E-02 | P41047 | SWISSPROT | FAS ANTIGEN LIGAND |
| 2004 | 14588 | 27145 | 2.67 | 3.9E-02 | AJ403398.1 | NT | Mus musculus DNA for desmin-binding fragment DesD7 |
| 2728 | 15283 | | 1.85 | 3.9E-02 | 4508882 | NT | Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA |
| 5325 | 17887 | 30303 | 0.6 | 3.9E-02 | AW382417.1 | EST_HUMAN | RC8-ST0258-171198-021-C08 ST0258 Homo sapiens cDNA |
| 5344 | 17805 | 30320 | 1.14 | 3.9E-02 | 8824019 | NT | Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA |
| 5344 | 17805 | 30321 | 1.14 | 3.9E-02 | 8824019 | NT | Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA |
| 5687 | 18313 | 30810 | 0.73 | 3.9E-02 | D50608.1 | NT | Rat gene for cholesteryl ester transfer protein (CETP), complete cds |
| 5687 | 18313 | 30811 | 0.73 | 3.9E-02 | D50608.1 | NT | Rat gene for cholesteryl ester transfer protein (CETP), complete cds |
| 5806 | 18528 | 31254 | 1.24 | 3.9E-02 | BE98841.1 | EST_HUMAN | 601648874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3833842 5' |
| 6018 | 18637 | 31377 | 0.68 | 3.9E-02 | BF675203.1 | EST_HUMAN | 602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5' |
| 7118 | 19458 | 32273 | 1.01 | 3.9E-02 | BE271437.1 | EST_HUMAN | 601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3046830 5' |
| 7781 | 20324 | 33228 | 0.93 | 3.9E-02 | BF238613.1 | EST_HUMAN | 601908948F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5' |
| 8004 | 20546 | 33449 | 0.56 | 3.9E-02 | AJ228041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3 |
| 8004 | 20546 | 33450 | 0.56 | 3.9E-02 | AJ228041.1 | NT | Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3 |
| 11287 | 20289 | 33188 | 1.6 | 3.9E-02 | P48778 | SWISSPROT | ANTIGEN GOR |
| 11891 | 24881 | | 7.19 | 3.9E-02 | AB042553.1 | NT | Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds |
| 12373 | 24543 | | 1.73 | 3.9E-02 | U68061.1 | NT | Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY3, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, > |
| 12503 | 24902 | | 64.84 | 3.9E-02 | AL049886.2 | NT | Mus musculus chromosome X contig8; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmmq28orf |
| 1895 | 14577 | 27137 | 1.24 | 3.9E-02 | BE985137.1 | EST_HUMAN | 601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5' |
| 4897 | 17571 | 30015 | 0.99 | 3.9E-02 | BE983275.1 | EST_HUMAN | 601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628757 5' |
| 4897 | 17571 | 30016 | 0.99 | 3.9E-02 | BE983275.1 | EST_HUMAN | 601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628757 5' |
| 5062 | 17835 | 30078 | 0.93 | 3.9E-02 | AU124122.1 | EST_HUMAN | AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5' |
| 5632 | 18281 | 30733 | 1.19 | 3.9E-02 | M11228.1 | NT | Human protein C gene, complete cds |
| 6237 | 18846 | 31617 | 1.07 | 3.9E-02 | P10284 | SWISSPROT | HOMEOBOX PROTEIN HOXB4 (HOX-2.6) |
| 7359 | 18885 | 32748 | 1.43 | 3.9E-02 | 6005700 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8598 | 21137 | | 1.3 | 3.8E-02 | M60875.1 | NT | Human von Willebrand factor gene, exons 23 through 34 |
| 10506 | 23000 | | 0.47 | 3.8E-02 | AE001329.1 | NT | Chlamydia trachomatis section 56 of 87 of the complete genome |
| 10532 | 23059 | 36082 | 2.17 | 3.8E-02 | AF143852.2 | NT | Homo sapiens PELOTA (PELOTA) gene, complete cds |
| 1029 | 13639 | 28154 | 3.69 | 3.7E-02 | P19137 | SWISSPROT | LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) |
| 1432 | 14025 | 26553 | 1.15 | 3.7E-02 | L14581.1 | NT | Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds |
| 2278 | 14852 | 27430 | 4.48 | 3.7E-02 | AB94806.1 | EST_HUMAN | wrs508.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3' |
| 2613 | 15175 | 27743 | 0.93 | 3.7E-02 | AB018261.1 | NT | Homo sapiens mRNA for KIAA0718 protein, partial cds |
| 3086 | 15701 | 28174 | 0.97 | 3.7E-02 | P78944 | SWISSPROT | ECMESODERMIN |
| 3088 | 15703 | 28175 | 4.74 | 3.7E-02 | BF312863.1 | EST_HUMAN | 601868233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125594 5' |
| 7138 | 25118 | | 0.73 | 3.7E-02 | AP000083.1 | NT | Aeropyrum pernix genomic DNA, section 67 |
| 9828 | 22424 | | 0.89 | 3.7E-02 | AA782516.1 | EST_HUMAN | af55cd0.s1 Soares_parathyroid_tumor_Nbr-IPA Homo sapiens cDNA clone 1360812 3' |
| 11735 | 24139 | 37158 | 7.89 | 3.7E-02 | BF124974.1 | EST_HUMAN | 601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5' |
| 12435 | 24886 | 30707 | 3.02 | 3.7E-02 | 11418392 | NT | Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA |
| 3715 | 16316 | 28784 | 0.82 | 3.6E-02 | X73221.1 | NT | H. vulgare Ss1 gene for sucrose synthase |
| 3723 | 16324 | 28791 | 0.87 | 3.6E-02 | AL096806.1 | NT | Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q28.3] of Homo sapiens |
| 5620 | 18249 | 30701 | 0.77 | 3.6E-02 | X59403.1 | NT | C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase |
| 5620 | 18249 | 30717 | 0.77 | 3.6E-02 | X59403.1 | NT | C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase |
| 6808 | 18399 | 32213 | 5.32 | 3.6E-02 | AW945516.1 | EST_HUMAN | CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA |
| 6808 | 18399 | 32214 | 5.32 | 3.6E-02 | AW945516.1 | EST_HUMAN | CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA |
| 7143 | 19376 | 32516 | 1.68 | 3.6E-02 | AF025952.1 | NT | Chromatium vinosum sulfur globule protein Cyt precursor (sgp2) gene, complete cds |
| 7347 | 19873 | 32739 | 3.52 | 3.6E-02 | AA714521.1 | EST_HUMAN | rw20e05.s1 NCJ_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_mae2 |
| 7629 | 20141 | 33020 | 0.88 | 3.6E-02 | BE143078.1 | EST_HUMAN | TUBULIN BETA-1 CHAIN (HUMAN); |
| 9313 | 21827 | 34776 | 1.87 | 3.6E-02 | U20608.1 | NT | MRO-HT0158-030200-003-b08 HTD158 Homo sapiens cDNA |
| 9313 | 21827 | 34777 | 1.87 | 3.6E-02 | U20608.1 | NT | Dicystostellum discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds |
| 9530 | 22030 | 34889 | 0.72 | 3.6E-02 | BF347568.1 | EST_HUMAN | Dicystostellum discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds |
| 928 | 13541 | 26059 | 1.57 | 3.5E-02 | U06506.1 | NT | 602020453F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156116 5' |
| 1046 | 13654 | 26168 | 2.28 | 3.5E-02 | AF263417.1 | NT | Drosophila melanogaster tlggrin mRNA, complete cds |
| | | | | | | NT | Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1610 | 14203 | 28736 | 1.49 | 3.5E-02 | BF678085.1 | EST_HUMAN | 602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5' |
| 1610 | 14203 | 28737 | 1.49 | 3.5E-02 | BF678085.1 | EST_HUMAN | 602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5' |
| 4283 | 16879 | 28328 | 1.91 | 3.5E-02 | AE001773.1 | NT | Thermoplasma maritima section 85 of 136 of the complete genome |
| 4406 | 16681 | 28435 | 1.16 | 3.5E-02 | P53780 | SWISSPROT | CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE) |
| 6370 | 18974 | 31752 | 2.11 | 3.5E-02 | J01238.1 | NT | Maize eth1 gene (MAC1), complete cds |
| 7918 | 20480 | | 0.82 | 3.5E-02 | H28651.1 | EST_HUMAN | yp44a05.1 Scores refina N2551R Homo sapiens cDNA clone IMAGE:190258 5' similar to contains Abu repetitive element |
| 8558 | 21097 | 34018 | 3.5 | 3.5E-02 | BE958970.1 | EST_HUMAN | 601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3829737 3' |
| 8831 | 22427 | 35401 | 2.44 | 3.5E-02 | X76642.1 | NT | Lactis M31903 gpE and dnaK genes |
| 8877 | 22472 | 35455 | 0.49 | 3.5E-02 | BE661042.1 | EST_HUMAN | 601344681F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877654 5' |
| 11367 | 23819 | 36880 | 1.92 | 3.5E-02 | AW801641.1 | EST_HUMAN | PM1-CT0328-281288-002-h03 CT0328 Homo sapiens cDNA |
| 11367 | 23819 | 36881 | 1.92 | 3.5E-02 | AW801641.1 | EST_HUMAN | PM1-CT0328-281288-002-h03 CT0328 Homo sapiens cDNA |
| 12357 | 24534 | | 1.38 | 3.5E-02 | AF008683.1 | NT | Homo sapiens T cell receptor beta locus, TCRBV/BS5P to TCRBV21S2A2 region |
| 12428 | 24913 | | 4.38 | 3.5E-02 | BE278948.1 | EST_HUMAN | 601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5' |
| 604 | 13233 | 25708 | 1.18 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 604 | 13233 | 25707 | 1.18 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 605 | 13233 | 25706 | 3.27 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 605 | 13233 | 25707 | 3.27 | 3.4E-02 | AK024424.1 | NT | Homo sapiens mRNA for FLJ00013 protein, partial cds |
| 1089 | 13694 | 26203 | 3.22 | 3.4E-02 | AW274020.1 | EST_HUMAN | xy28407.x1 Scores NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2814283 3' similar to SW: C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR; |
| 1248 | 13845 | | 6.54 | 3.4E-02 | 11345459 | NT | Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA |
| 2435 | 15002 | 27574 | 1.92 | 3.4E-02 | T57180.1 | EST_HUMAN | yc20e08.r1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains |
| 3478 | 16084 | 28558 | 1.11 | 3.4E-02 | AL163208.2 | NT | MER29 repetitive element |
| 3843 | 16442 | 28903 | 0.88 | 3.4E-02 | BE836514.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C008 |
| 3893 | 16591 | 28063 | 4.28 | 3.4E-02 | AW784852.1 | EST_HUMAN | RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA |
| 4703 | 17285 | 28730 | 3.17 | 3.4E-02 | X59789.1 | NT | RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA |
| 5217 | 17782 | | 2.81 | 3.4E-02 | Q28457 | SWISSPROT | M.musculus S-antigen gene promoter region |
| 5237 | 17801 | 30220 | 1.47 | 3.4E-02 | AJ012488.1 | NT | LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG) |
| 6353 | 18958 | | 0.88 | 3.4E-02 | BF131628.1 | EST_HUMAN | Casorhabditis elegans mRNA for DYS-1 protein, partial |
| 6838 | 18046 | 30468 | 4.83 | 3.4E-02 | U24393.1 | NT | 601820445F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5' |
| 8204 | 20745 | | 3.76 | 3.4E-02 | AJ868829.1 | EST_HUMAN | Human lysyl oxidase-like protein gene, exon 3 |
| | | | | | | | wf89d04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:243031 3' |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8682 | 21221 | 34141 | 1.84 | 3.4E-02 | AA684886.1 | EST_HUMAN | nu70708.s1 NCI_CGAP_A11 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element; |
| 8948 | 21387 | | 5.71 | 3.4E-02 | AA194308.1 | EST_HUMAN | zfp04f11.s1 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425 |
| 9683 | 22182 | | 0.53 | 3.4E-02 | AB02719.1 | EST_HUMAN | IPISGKPLPKVTLSDGVPKATMRFRTEITAENLTNLKESVTADAGRYEITANSSGTTKAFINIVLDRPG |
| 365 | 13041 | | 11.74 | 3.3E-02 | AA308735.1 | EST_HUMAN | PPT GPVMSDITEESYTLKWEPPKYDGGSQVYLLKRETSYVWTEVSATVARTMMKVMKL ...; |
| 1209 | 13809 | 26322 | 18.12 | 3.3E-02 | AB035667.1 | EST_HUMAN | cc88108.x1 Soares parathyroid tumor NblHPA Homo sapiens cDNA clone IMAGE:1683519 3' |
| 1681 | 14273 | 26806 | 1.29 | 3.3E-02 | AF110783.1 | NT | z175e08.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728188 3' |
| 1775 | 14365 | | 1.28 | 3.3E-02 | AE000700.1 | NT | Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds |
| 2131 | 14709 | | 2.05 | 3.3E-02 | R08112.1 | EST_HUMAN | Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds |
| 3408 | 18015 | 28404 | 0.85 | 3.3E-02 | H02389.1 | EST_HUMAN | Aquifex aeolicus section 32 of 108 of the complete genome |
| 4256 | 14273 | 26808 | 2.91 | 3.3E-02 | AF110783.1 | NT | y25c09.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:127888 5' |
| 4566 | 17149 | 28586 | 2.15 | 3.3E-02 | 6755862 | NT | y25h02.r1 Soares placenta Nbl2HP Homo sapiens cDNA clone IMAGE:150771 5' |
| 6561 | 19159 | 31856 | 28.84 | 3.3E-02 | BF245895.1 | EST_HUMAN | Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds |
| 6561 | 19169 | 31857 | 28.84 | 3.3E-02 | BF245895.1 | EST_HUMAN | Mus musculus tumor rejection antigen gp98 (Tra1). mRNA |
| 9246 | 21772 | 34721 | 0.73 | 3.3E-02 | BF115621.1 | EST_HUMAN | 601853910F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4073787 5' |
| 9246 | 21772 | 34722 | 0.73 | 3.3E-02 | BF115621.1 | EST_HUMAN | 801853910F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4073787 5' |
| 9345 | 21858 | 34807 | 0.59 | 3.3E-02 | AA488202.1 | EST_HUMAN | 7m82d04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3' |
| 9345 | 21859 | 34808 | 0.59 | 3.3E-02 | AA488202.1 | EST_HUMAN | 7m82d04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3' |
| 10491 | 22865 | | 0.5 | 3.3E-02 | H38109.1 | EST_HUMAN | ad08709.s1 Soares NblHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:U70944_cds1 |
| 11000 | 23514 | 36548 | 3.5 | 3.3E-02 | BF081107.1 | EST_HUMAN | MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN); |
| 11832 | 24266 | | 2.14 | 3.3E-02 | T06545.1 | EST_HUMAN | MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN); |
| 12089 | 24358 | | 2.06 | 3.3E-02 | M81890.1 | NT | ad08709.s1 Soares NblHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:U70944_cds1 |
| 137 | 12802 | 25291 | 1.87 | 3.2E-02 | AJ002005.1 | NT | MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN); |
| 1165 | 13767 | 26277 | 19.04 | 3.2E-02 | AF086275.1 | NT | MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN); |
| 1165 | 13767 | 26278 | 19.04 | 3.2E-02 | AF086275.1 | NT | y65111.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190889 3' |
| 1808 | 14398 | 26843 | 1.36 | 3.2E-02 | AF128894.1 | NT | 602247171F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332497 5' |
| 2164 | 14741 | | 1.35 | 3.2E-02 | P28955 | SWISSPROT | y646911.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:121101 5' |
| 2865 | 12802 | 25291 | 0.59 | 3.2E-02 | AJ002005.1 | NT | Human Interleukin 11 (IL11) gene, complete mRNA |
| 3168 | 15782 | 28253 | 12.01 | 3.2E-02 | BE867353.1 | EST_HUMAN | Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter |
| | | | | | | | Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds |
| | | | | | | | Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds |
| | | | | | | | Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-10 and complete cds |
| | | | | | | | LARGE TEGUMENT PROTEIN |
| | | | | | | | Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter |
| | | | | | | | 601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5' |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3776 | 16376 | 28842 | 1.3 | 3.2E-02 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 4299 | 16885 | | 20.05 | 3.2E-02 | X94788.1 | NT | H. sapiens RP3 gene (XLRP gene 3) |
| 4882 | 17457 | 28909 | 3.35 | 3.2E-02 | AF114182.1 | NT | Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds |
| 5728 | 18352 | 31055 | 1.45 | 3.2E-02 | X68709.1 | NT | S. griseocarinum whiG-Stv gene |
| 5728 | 18352 | 31056 | 1.45 | 3.2E-02 | X68709.1 | NT | S. griseocarinum whiG-Stv gene |
| 6846 | 18242 | 32045 | 2.59 | 3.2E-02 | M32437.1 | NT | Rat polyomavirus left junction in cell line W98.14 |
| 6847 | 19243 | | 27.51 | 3.2E-02 | T89367.1 | EST_HUMAN | y433h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains |
| 6722 | 18316 | 32119 | 3.78 | 3.2E-02 | AF173845.1 | NT | Alu repetitive element/contains LTR1 repetitive element; |
| 7739 | 20247 | 33140 | 0.85 | 3.2E-02 | 11424049 | NT | Seguinus oedipus tissue kallikrein gene, complete cds |
| 8242 | 20783 | 33702 | 13.06 | 3.2E-02 | 6680565 | NT | Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA |
| 8871 | 21410 | | 0.89 | 3.2E-02 | AF109718.1 | NT | Mus musculus kinesin family member 3c (Kif3c), mRNA |
| 9152 | 21687 | 34630 | 1.06 | 3.2E-02 | A1278971.1 | EST_HUMAN | Homo sapiens chromosome 3 subtelomeric region |
| 9152 | 21687 | 34631 | 1.06 | 3.2E-02 | A1278971.1 | EST_HUMAN | qm17604.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3' |
| 9868 | 22464 | | 4.05 | 3.2E-02 | AA710795.1 | EST_HUMAN | qm17604.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3' |
| 10260 | 22755 | 35743 | 0.85 | 3.2E-02 | U96762.1 | NT | Macaca mulatta chemokine receptor CCR5 mRNA, complete cds |
| 1303 | 13897 | | 1.8 | 3.1E-02 | 4503416 | NT | Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA |
| 1348 | 13943 | 26486 | 1.28 | 3.1E-02 | P18945 | SWISSPROT | NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3) |
| 1836 | 14520 | 27076 | 1.52 | 3.1E-02 | 6671584 | NT | Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA |
| 2017 | 14569 | | 1.14 | 3.1E-02 | Z50097.1 | NT | Drosophila melanogaster mRNA for headcase protein |
| 5207 | 17772 | | 0.87 | 3.1E-02 | BE091869.1 | EST_HUMAN | IL2-BT0733-130400-067-A08 BT0733 Homo sapiens cDNA |
| 5331 | 17892 | | 3.09 | 3.1E-02 | AL161550.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50 |
| 5371 | 16916 | | 0.58 | 3.1E-02 | AU119006.1 | EST_HUMAN | AU119006 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5' |
| 5468 | 18102 | 30421 | 1.13 | 3.1E-02 | U78104.1 | NT | Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1 |
| 5563 | 18184 | | 2.32 | 3.1E-02 | AA278478.1 | EST_HUMAN | zs81a08.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5' |
| 5829 | 18453 | 31176 | 0.8 | 3.1E-02 | BF687742.1 | EST_HUMAN | 602068783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5' |
| 9844 | 22439 | 35417 | 3.63 | 3.1E-02 | AF034779.1 | NT | Enterococcus faecalis surface protein precursor, gene, complete cds |
| 12667 | 24737 | | 2.24 | 3.1E-02 | AW468414.1 | EST_HUMAN | he3707.x1 NCI CGAP_GML1 Homo sapiens cDNA clone IMAGE:2921221 3' |
| 1684 | 14257 | | 2.3 | 3.0E-02 | AF187125.1 | NT | Ptychocheilus minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product |
| 2621 | 15183 | 27749 | 0.9 | 3.0E-02 | AA402242.1 | EST_HUMAN | z05h03.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:727263 5' |
| 3823 | 18226 | 28704 | 1.24 | 3.0E-02 | IM94176.1 | NT | Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds |

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|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3714 | 16315 | 28763 | 3.07 | 3.0E-02 | AF247844.1 | NT | Pseudomonas fluorescens family II aminotransferase gene, complete cds |
| 3808 | 16407 | | 0.79 | 3.0E-02 | AW820223.1 | EST_HUMAN | QV2-ST0288-150200-040-e08 ST0286 Homo sapiens cDNA |
| 4021 | 16819 | | 0.74 | 3.0E-02 | AA364003.1 | EST_HUMAN | EST174530 Pineal gland II Homo sapiens cDNA 5' end |
| 5000 | 17573 | 30017 | 1.04 | 3.0E-02 | BE782830.1 | EST_HUMAN | 601472331F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3875503 5' |
| 5208 | 17773 | 30195 | 7.49 | 3.0E-02 | AF281074.1 | NT | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |
| 5208 | 17773 | 30196 | 7.49 | 3.0E-02 | AF281074.1 | NT | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |
| 5303 | 17865 | 30289 | 1.1 | 3.0E-02 | BE968917.1 | EST_HUMAN | 601649872R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3833928 3' |
| 5560 | 18221 | | 3.82 | 3.0E-02 | AB046783.1 | NT | Homo sapiens mRNA for KIAA1573 protein, partial cds |
| 6402 | 18005 | 31784 | 0.78 | 3.0E-02 | N88615.1 | EST_HUMAN | z389a10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element; |
| 6402 | 18005 | 31785 | 0.76 | 3.0E-02 | N88615.1 | EST_HUMAN | z389a10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element; |
| 6884 | 19819 | 32453 | 2.93 | 3.0E-02 | AJ242906.1 | NT | Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene |
| 6887 | 19485 | 32308 | 3.15 | 3.0E-02 | BE868948.1 | EST_HUMAN | 601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5' |
| 6887 | 19485 | 32307 | 3.15 | 3.0E-02 | BE868948.1 | EST_HUMAN | 601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5' |
| 7131 | 19471 | 32290 | 1.93 | 3.0E-02 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 7131 | 19471 | 32291 | 1.93 | 3.0E-02 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 7282 | 19810 | 32898 | 1.32 | 3.0E-02 | M86524.1 | NT | Human dystrophin gene |
| 7583 | 20088 | | 0.78 | 3.0E-02 | BF246381.1 | EST_HUMAN | 601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5' |
| 8575 | 21114 | 34033 | 0.79 | 3.0E-02 | BF353889.1 | EST_HUMAN | IL6-HT0704-280800-108-c04 HT0704 Homo sapiens cDNA |
| 8728 | 21287 | | 1.77 | 3.0E-02 | AF275654.1 | NT | Omithorhynchus anatinus coagulation factor X mRNA, complete cds |
| 10357 | 22851 | 35845 | 1.46 | 3.0E-02 | AE001787.1 | NT | Thermotoga maritima section 109 of 139 of the complete genome |
| 10441 | 22835 | 35944 | 0.46 | 3.0E-02 | Z21211.1 | EST_HUMAN | HSAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b) |
| 11111 | 23621 | 36962 | 4.11 | 3.0E-02 | M81357.1 | NT | Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1 |
| 11538 | 23866 | 37057 | 8.47 | 3.0E-02 | AA483216.1 | EST_HUMAN | ne8704.s1 NCJ_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911283 |
| 12043 | 25078 | 30515 | 2.58 | 3.0E-02 | R32019.1 | EST_HUMAN | Y63404.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3' |
| 12417 | 24670 | | 18.42 | 3.0E-02 | AW885565.1 | EST_HUMAN | QV4-NN0038-270400-167-H05 NN0038 Homo sapiens cDNA |
| 12480 | 25068 | | 3.53 | 3.0E-02 | AF048887.1 | NT | Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds |
| 2478 | 15487 | 27614 | 1.05 | 2.9E-02 | AF228703.1 | NT | Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced |
| 3021 | 15637 | 28114 | 1.11 | 2.8E-02 | BE565844.1 | EST_HUMAN | 601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680685 5' |

Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3021 | 15637 | 28115 | 1.11 | 2.9E-02 | BE565844.1 | EST_HUMAN | 601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5' |
| 3616 | 16219 | 28698 | 0.64 | 2.9E-02 | X55294.1 | NT | Sheep gene for ultra high-sulphur keratin protein |
| 4003 | 16601 | 28075 | 0.68 | 2.9E-02 | H72803.1 | EST_HUMAN | y407e10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5' |
| 5272 | 18016 | | 62.36 | 2.9E-02 | R09112.1 | EST_HUMAN | v25c09.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5' |
| 6213 | 18823 | 31594 | 1.31 | 2.9E-02 | AF060221.1 | NT | Sus scrofa deoxyribonuclease II mRNA, complete cds |
| 6434 | 19037 | 31824 | 6.5 | 2.9E-02 | BF032233.1 | EST_HUMAN | 601452861F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856598 5' |
| 7288 | 19824 | 32883 | 10.37 | 2.9E-02 | BE271437.1 | EST_HUMAN | 601140728F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3046830 5' |
| 7455 | 19879 | 32845 | 0.87 | 2.9E-02 | D29214.1 | EST_HUMAN | HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262 |
| 7940 | 20482 | 33393 | 0.91 | 2.9E-02 | AF128278.1 | NT | Buchnera aphidicola natural-host Schlechtendalia chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds |
| 7940 | 20482 | 33394 | 0.91 | 2.9E-02 | AF128278.1 | NT | Buchnera aphidicola natural-host Schlechtendalia chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds |
| 8577 | 22077 | 35040 | 2.16 | 2.9E-02 | AW875879.1 | EST_HUMAN | GM3-PT0014-071298-051 c04 PT0014 Homo sapiens cDNA |
| 9577 | 22077 | 35041 | 2.16 | 2.9E-02 | AW875879.1 | EST_HUMAN | GM3-PT0014-071298-051 c04 PT0014 Homo sapiens cDNA |
| 9788 | 22286 | | 0.59 | 2.9E-02 | AW976597.1 | EST_HUMAN | EST388708 MAGE resequences, MAGN Homo sapiens cDNA |
| 10247 | 22742 | 35732 | 0.94 | 2.9E-02 | AP000064.1 | NT | Aeropyrum pernix genome DNA, section 7/7 |
| 10925 | 16219 | 28698 | 1.73 | 2.9E-02 | X55294.1 | NT | Sheep gene for ultra high-sulphur keratin protein |
| 12045 | 24979 | | 1.89 | 2.9E-02 | AU135817.1 | EST_HUMAN | AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002962 5' |
| 591 | 13221 | | 0.89 | 2.9E-02 | AW970153.1 | EST_HUMAN | EST382234 MAGE resequences, MAGK Homo sapiens cDNA |
| 3414 | 18022 | 28502 | 1.82 | 2.9E-02 | AF068063.1 | NT | Homo sapiens retinal fascic (FSCN2) gene, exon 2 |
| 3414 | 18022 | 28503 | 1.82 | 2.9E-02 | AF068063.1 | NT | Homo sapiens retinal fascic (FSCN2) gene, exon 2 |
| 4401 | 18886 | | 0.71 | 2.9E-02 | 8393751 | NT | Rattus norvegicus microtubule-associated protein tau (Map2), mRNA |
| 5337 | 17698 | 30313 | 0.82 | 2.9E-02 | N87073.1 | EST_HUMAN | L2083F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone L2083 5' similar to TRNA-GUANINE TRANSGLYCOSYLASE |
| 5679 | 18308 | 30802 | 11.28 | 2.9E-02 | BE741083.1 | EST_HUMAN | 601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948087 5' |
| 6900 | 19634 | 32472 | 1.14 | 2.9E-02 | T78960.1 | EST_HUMAN | y21b08.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5' |
| 8270 | 20811 | 33732 | 1.6 | 2.9E-02 | AJ005820.1 | NT | Cratichneumon plantigradum mRNA for homeodomain leucine zipper protein (hb-1) |
| 8947 | 21485 | 34407 | 0.74 | 2.9E-02 | AA280782.1 | EST_HUMAN | zs06c08.1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5' |
| 9135 | 21670 | 34612 | 0.91 | 2.9E-02 | AF187872.1 | NT | Canis porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds |
| 9237 | 21763 | 34709 | 0.84 | 2.9E-02 | AE001092.1 | NT | Archaeoglobus fulgidus section 15 of 172 of the complete genome |
| 10498 | 22892 | 36002 | 1.81 | 2.9E-02 | BF527244.1 | EST_HUMAN | 602039477F2 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:417267 5' |
| 3479 | 18085 | 28559 | 4.18 | 2.7E-02 | AL161404.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6 |
| 4280 | 18888 | 29312 | 1.81 | 2.7E-02 | NA17258.1 | EST_HUMAN | y96h12.1 Soares multiple sclerosis_2N1bHMSF Homo sapiens cDNA clone IMAGE:280487 5' |
| 4280 | 18888 | 29313 | 1.91 | 2.7E-02 | NA17258.1 | EST_HUMAN | y96h12.1 Soares multiple sclerosis_2N1bHMSF Homo sapiens cDNA clone IMAGE:280487 5' |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5833 | 18282 | 30734 | 1.11 | 2.7E-02 | R12245.1 | EST_HUMAN | y33409.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP:JC2284 JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS; |
| 6061 | 18678 | 31420 | 0.7 | 2.7E-02 | X61670.1 | NT | T. aestivum pTTH20 mRNA for wheat type V thionin |
| 6713 | 19307 | | 0.9 | 2.7E-02 | X97580.1 | NT | A.bisporus poka gene |
| 7127 | 19487 | 32285 | 2.08 | 2.7E-02 | AA93571.1 | EST_HUMAN | 0898h03.s1 Soares total_fetus_Nb2-HF8 9w Homo sapiens cDNA clone IMAGE:1624861 3' |
| 8295 | 20836 | | 1.21 | 2.7E-02 | A1377038.1 | EST_HUMAN | tc28g08.x1 Soares total_fetus_Nb2-HF8 9w Homo sapiens cDNA clone IMAGE:2085982 3' similar to contains Alu repetitive element |
| 597 | 13228 | 25700 | 1.52 | 2.6E-02 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 2404 | 14872 | 27544 | 2.79 | 2.6E-02 | AA490021.1 | EST_HUMAN | ab02b02.s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3' |
| 2408 | 14874 | 27546 | 7.33 | 2.6E-02 | 6754241 | NT | Mus musculus histidine rich calcium binding protein (Hirc), mRNA |
| 2408 | 14874 | 27547 | 7.33 | 2.6E-02 | 6754241 | NT | Mus musculus histidine rich calcium binding protein (Hirc), mRNA |
| 2940 | 15558 | | 1.17 | 2.6E-02 | AF109008.1 | NT | Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9a, NG22, G9, HSP70, HSP70, HSC70L, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes |
| 5031 | 17605 | 30049 | 4.74 | 2.6E-02 | L12032.1 | NT | Chicken dorsalis-1 mRNA, complete cds |
| 6224 | 17789 | 30208 | 1.58 | 2.6E-02 | AE002014.1 | NT | Deinococcus radiodurans R1 section 151 of 228 of the complete chromosome 1 |
| 5254 | 17817 | 30241 | 2.34 | 2.6E-02 | AW241154.1 | EST_HUMAN | xs52b04.x1 NCJ CGAP Ser4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN |
| 6388 | 18972 | | 6.32 | 2.6E-02 | A1206030.1 | EST_HUMAN | Q15041 HYPOTHETICAL PROTEIN KIAA0089; |
| 6556 | 19154 | 31850 | 2.29 | 2.6E-02 | BE621748.1 | EST_HUMAN | qg27f11.x1 NCJ CGAP_K43 Homo sapiens cDNA clone IMAGE:1762317 3' |
| 6815 | 19574 | 32402 | 0.75 | 2.6E-02 | Z98094.1 | NT | 801493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3' |
| 6815 | 19574 | 32403 | 0.75 | 2.6E-02 | Z98094.1 | NT | Vaccinia virus ORF1L, strain W yeth |
| 6880 | 19488 | 32310 | 6.45 | 2.6E-02 | 6981271 | NT | Vaccinia virus ORF1L, strain W yeth |
| 8442 | 20982 | 33687 | 0.77 | 2.6E-02 | AA860948.1 | EST_HUMAN | Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA |
| 9282 | 21882 | 34827 | 1.41 | 2.6E-02 | 11432020 | NT | ek22f04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1408719 3' |
| 9630 | 22130 | 35094 | 0.8 | 2.6E-02 | AF114852.1 | NT | Homo sapiens KIAA1070 protein (KIAA1070), mRNA |
| 9630 | 22130 | 35095 | 0.8 | 2.6E-02 | AF114852.1 | NT | Saccharomyces dairenensis NRRL Y-12538(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds |
| 10302 | 22798 | 35787 | 4.1 | 2.6E-02 | AL163303.2 | NT | Saccharomyces dairenensis NRRL Y-12538(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds |
| 11265 | 23783 | | 2.44 | 2.6E-02 | AA278351.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C103 |
| 11437 | 23887 | 36955 | 1.83 | 2.6E-02 | AW500547.1 | EST_HUMAN | zs84c02.r1 NCJ CGAP GC81 Homo sapiens cDNA clone IMAGE:704162 5' |
| 11865 | 25060 | 30512 | 1.26 | 2.6E-02 | BF343827.1 | EST_HUMAN | UHF-BNO-ek-10-Q.UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077488 5' |
| 12083 | 24354 | | 1.29 | 2.6E-02 | 11422898 | NT | 602015501F1 NCJ CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150944 5' |
| 557 | 13188 | 25668 | 1.76 | 2.5E-02 | AJ783130.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|---|
| 557 | 13188 | 25867 | 1.78 | 2.5E-02 | A1783130.1 | EST_HUMAN | 0128008.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5' |
| 842 | 13458 | 25867 | 19.88 | 2.5E-02 | BE974314.1 | EST_HUMAN | 601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850885 3' |
| 902 | 13516 | 28034 | 4.46 | 2.5E-02 | BE974314.1 | EST_HUMAN | 601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850885 3' |
| 2781 | 15344 | | 2.84 | 2.5E-02 | U12571.1 | NT | Rattus norvegicus retpilin-3A mRNA, complete cds |
| 2863 | 15589 | 28078 | 3.52 | 2.5E-02 | X88897.1 | NT | H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1 |
| 2883 | 15589 | 28078 | 3.52 | 2.5E-02 | X88897.1 | NT | H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1 |
| 4119 | 18005 | 28167 | 0.77 | 2.5E-02 | BE701166.1 | EST_HUMAN | PM2-NN0128-080700-001-at12 NN0128 Homo sapiens cDNA |
| 4119 | 18005 | 28168 | 0.77 | 2.5E-02 | BE701166.1 | EST_HUMAN | PM2-NN0128-080700-001-at12 NN0128 Homo sapiens cDNA |
| 4284 | 18870 | 28316 | 5.25 | 2.5E-02 | AW582114.1 | EST_HUMAN | h36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3' |
| 5889 | 18512 | 31238 | 0.7 | 2.5E-02 | A1732778.1 | EST_HUMAN | z63c10.x5 Soares_ova tumor N6HOT Homo sapiens cDNA clone IMAGE:810354 3' |
| 6340 | 18948 | | 4.9 | 2.5E-02 | BE670128.1 | EST_HUMAN | 7a30a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1 |
| 6357 | 18981 | | 4.3 | 2.5E-02 | BE746888.1 | EST_HUMAN | repetitive element ; |
| 6478 | 19079 | 31802 | 0.72 | 2.5E-02 | L28029.1 | NT | 601578393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5' |
| 7680 | 20172 | 33058 | 1.52 | 2.5E-02 | BF526722.1 | EST_HUMAN | Chlamydomonas reinhardtii VSP-3 mRNA, complete cds |
| 7680 | 20172 | 33059 | 1.52 | 2.5E-02 | BF526722.1 | EST_HUMAN | 602070562F1 NCI_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4213408 5' |
| 7820 | 20482 | 33368 | 0.48 | 2.5E-02 | BE252488.1 | EST_HUMAN | 602070562F1 NCI_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4213408 5' |
| 8759 | 21268 | 34219 | 0.83 | 2.5E-02 | O81713 | SWISSPROT | 601108281F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344278 5' |
| 8894 | 21432 | 34355 | 0.45 | 2.5E-02 | AW025821.1 | EST_HUMAN | CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR) |
| 8878 | 22473 | | 0.6 | 2.5E-02 | X71303.1 | NT | wu08c10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2516370 3' |
| 10475 | 22869 | 35978 | 0.73 | 2.5E-02 | A1147815.1 | EST_HUMAN | D. radiatum 28S ribosomal RNA, D2 domain |
| 10689 | 23219 | 36231 | 2.04 | 2.5E-02 | Q10335 | SWISSPROT | qb22a08.x1 Soares_pregnant uterus Nbr-IPU Homo sapiens cDNA clone IMAGE:1686882 3' |
| 10689 | 23219 | 36232 | 2.04 | 2.5E-02 | Q10335 | SWISSPROT | HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1 |
| | | | | | | | HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1 |
| | | | | | | | Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; |
| 10761 | 23285 | | 4.04 | 2.5E-02 | AF050157.1 | NT | butyrophilin-like (NG9), butyrophilin-4 |
| 11802 | 24045 | | 1.73 | 2.5E-02 | AB007548.1 | NT | Homo sapiens gene for LECT2, complete cds |
| 11922 | 24963 | | 3.33 | 2.5E-02 | 11433220 | NT | Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC83634), mRNA |
| 12115 | 24855 | | 1.53 | 2.5E-02 | U60169.1 | NT | Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA |
| 12215 | 24438 | | 2.17 | 2.5E-02 | U60169.1 | NT | Dicotyledonous discoidium putative protein kinase Mica (MicaA) gene, complete cds |
| 12242 | 24454 | 30857 | 1.31 | 2.5E-02 | BE973327.1 | EST_HUMAN | 601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3835513 3' |
| 185 | 12848 | 28332 | 0.75 | 2.4E-02 | A578582.1 | EST_HUMAN | bc72c07.x1 Soares_NIH-IMPu_S1 Homo sapiens cDNA clone IMAGE:2070158 3' |
| 1642 | 14234 | 28768 | 2.08 | 2.4E-02 | H65884.1 | EST_HUMAN | y75f11.1 Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:21149 5' |
| 2088 | 15457 | 27239 | 2.02 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |

Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2088 | 15457 | 27240 | 2.02 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 4458 | 17044 | 29487 | 1.89 | 2.4E-02 | J05110.1 | NT | T. thermophilus calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds |
| 4619 | 17202 | 29850 | 1.83 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 4619 | 17202 | 29851 | 1.83 | 2.4E-02 | P01901 | SWISSPROT | H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B)) |
| 6383 | 18967 | 31745 | 0.94 | 2.4E-02 | W86980.1 | EST_HUMAN | zh83h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3' |
| 7273 | 19801 | 32658 | 1.08 | 2.4E-02 | Z20573.1 | EST_HUMAN | HSAAACKVX.T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA |
| 7287 | 19815 | 32672 | 0.95 | 2.4E-02 | X12925.1 | NT | Rat gene for uncoupling protein (UCP) |
| 7287 | 19815 | 32673 | 0.95 | 2.4E-02 | X12925.1 | NT | Rat gene for uncoupling protein (UCP) |
| 7831 | 20373 | | 0.89 | 2.4E-02 | AW813007.1 | EST_HUMAN | RC3-ST0188-230300-019-108 ST0188 Homo sapiens cDNA |
| 7884 | 20426 | | 0.8 | 2.4E-02 | M16780.1 | NT | Human retrotransposon 3' long terminal repeat |
| 8379 | 20919 | | 0.88 | 2.4E-02 | H78376.1 | EST_HUMAN | yu12c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element ; |
| 8488 | 21008 | 33925 | 10.74 | 2.4E-02 | N68442.1 | EST_HUMAN | z835g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294598 3' similar to gbJ02809jRATSR7K Rat (rRNA); contains A3R.b1 A3R repetitive element ; |
| 8917 | 21455 | 34375 | 0.54 | 2.4E-02 | AE001125.1 | NT | Borrelia burgdorferi (section 11 of 70) of the complete genome |
| | | | | | | | z181c06.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gbJ04422 ISLET |
| 8939 | 21477 | 34398 | 0.75 | 2.4E-02 | AA625680.1 | EST_HUMAN | AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR |
| 9720 | 22218 | 35193 | 2.76 | 2.4E-02 | AV682954.1 | EST_HUMAN | XTR repetitive element ; |
| 9891 | 22388 | 36398 | 2.9 | 2.4E-02 | AA483894.1 | EST_HUMAN | AV682954 GK Homo sapiens cDNA clone GKCDSC03 5' |
| | | | | | | | nt07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943883 similar to contains Alu repetitive element; contains element PTR5 repetitive element ; |
| 11447 | 23887 | 36862 | 1.9 | 2.4E-02 | AF109805.1 | NT | Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds, and unknown genes |
| 11447 | 23887 | 36863 | 1.9 | 2.4E-02 | AF109805.1 | NT | Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes |
| 11716 | 24127 | | 3.56 | 2.4E-02 | 9627809 | NT | Bacteriophage bIL67, complete genome |
| 11868 | 24222 | 31044 | 2.48 | 2.4E-02 | 6753635 | NT | Mus musculus Dmb homolog 1 (E. coli) (Dmb1), mRNA |
| 11924 | 24259 | 31013 | 1.36 | 2.4E-02 | BE928869.1 | EST_HUMAN | MRO-FT0175-310800-202-008 FT0175 Homo sapiens cDNA |
| 11984 | 24284 | 30981 | 1.38 | 2.4E-02 | U78167.1 | NT | Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds |
| 11984 | 24284 | 31025 | 1.38 | 2.4E-02 | U78167.1 | NT | Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12164 | 24404 | | 8.87 | 2.4E-02 | AB008558.1 | NT | Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds |
| 12191 | 24422 | | 2.11 | 2.4E-02 | N42880.1 | EST_HUMAN | y08a08.r1 Soares melanocyte 2N18HM Homo sapiens cDNA clone IMAGE:270610 5' |
| 12197 | 24425 | | 1.55 | 2.4E-02 | BF078477.1 | EST_HUMAN | 602153281F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294173 5' |
| 12362 | 24827 | 30795 | 1.48 | 2.4E-02 | AA178983.1 | EST_HUMAN | zp13h01.r1 Stratiagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361 5' |
| 1913 | 14498 | | 5.46 | 2.3E-02 | W05340.1 | EST_HUMAN | z894g08.r1 Soares fetal_lung_Nb-L19W Homo sapiens cDNA clone IMAGE:289294 5' |
| 1931 | 14515 | | 21.98 | 2.3E-02 | U94165.1 | NT | 4 Homo sapiens mammary tumor-associated protein INT8 (INT8) gene, exon 4 |
| 2053 | 14634 | 27205 | 0.96 | 2.3E-02 | AW79355.1 | EST_HUMAN | GM2-UM0038-280400-172-b11 UM0038 Homo sapiens cDNA |
| 2389 | 14657 | 27529 | 2.31 | 2.3E-02 | Z74293.1 | NT | S.cerevisiae chromosome IV reading frame ORF YDL245c |
| 3745 | 16348 | 28814 | 6.21 | 2.3E-02 | Z20377.1 | EST_HUMAN | HSAACADH P, Human fetal Brain Whole tissue Homo sapiens cDNA |
| 3777 | 16377 | | 0.82 | 2.3E-02 | L29428.1 | NT | Canis beta-galactosidase-binding lectin (LGALS3) mRNA, 3'end |
| 4230 | 16818 | 28268 | 0.75 | 2.3E-02 | L24798.1 | NT | Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds |
| 4230 | 16818 | 28267 | 0.75 | 2.3E-02 | L24799.1 | NT | Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds |
| 4511 | 17095 | 28542 | 1.21 | 2.3E-02 | AW699107.1 | EST_HUMAN | GM4-NN0080-280400-160-b04 NN0080 Homo sapiens cDNA |
| 4546 | 17130 | 28574 | 0.91 | 2.3E-02 | BE935225.1 | EST_HUMAN | GM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA |
| 4546 | 17130 | 28576 | 0.91 | 2.3E-02 | BE935225.1 | EST_HUMAN | GM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA |
| 4547 | 18006 | 28578 | 1.05 | 2.3E-02 | AW693693.1 | EST_HUMAN | xa25d08.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3' |
| 4547 | 18006 | 28577 | 1.05 | 2.3E-02 | AW693693.1 | EST_HUMAN | xa25d08.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3' |
| 4638 | 17280 | 28726 | 2.96 | 2.3E-02 | BF028487.1 | EST_HUMAN | 601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5' |
| 4638 | 17280 | 28727 | 2.96 | 2.3E-02 | BF028487.1 | EST_HUMAN | 601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5' |
| 5182 | 17748 | 30177 | 0.93 | 2.3E-02 | AW844307.1 | EST_HUMAN | RC2-CN0051-280100-011-a07 CN0051 Homo sapiens cDNA |
| 5368 | 17828 | 30342 | 2.72 | 2.3E-02 | AI038078.1 | EST_HUMAN | ca21c10.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656978 3' similar to gb:X69908.maf1 ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (HUMAN); |
| 5578 | 18209 | 30659 | 3.34 | 2.3E-02 | U95903.1 | NT | Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds |
| 6733 | 19327 | 32132 | 4.43 | 2.3E-02 | AL161505.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17 |
| 7056 | 18075 | 30428 | 0.88 | 2.3E-02 | BE141475.1 | EST_HUMAN | MR0-HT0080-011099-002-c09 HT0080 Homo sapiens cDNA |
| 7817 | 20360 | 33266 | 6 | 2.3E-02 | U63610.1 | NT | Human plectin (PLEC1) gene, exons 3-32, and complete cds |
| 8407 | 20947 | 33867 | 0.74 | 2.3E-02 | AJ298105.1 | NT | Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11 |
| 8407 | 20947 | 33868 | 0.74 | 2.3E-02 | AJ298105.1 | NT | Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11 |
| 8630 | 21169 | 34085 | 0.83 | 2.3E-02 | AI665380.1 | EST_HUMAN | wa78h10.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2302147 3' |
| 8630 | 21169 | 34086 | 0.83 | 2.3E-02 | AI665380.1 | EST_HUMAN | wa78h10.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2302147 3' |
| 9065 | 21602 | 34532 | 0.81 | 2.3E-02 | P41998 | SWISSPROT | HYPOTHEICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR |
| 9773 | 22271 | 35256 | 0.72 | 2.3E-02 | PF0532 | SWISSPROT | CHROMOSOME ASSEMBLY PROTEIN XCAP-C |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|---|
| 9843 | 22438 | 35415 | 1.4 | 2.3E-02 | AE000198.1 | NT | Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome |
| 9843 | 22438 | 35416 | 1.4 | 2.3E-02 | AE000198.1 | NT | Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome |
| 10661 | 23193 | 36208 | 2.37 | 2.3E-02 | P08840 | SWISSPROT | GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) |
| 11828 | 24070 | | 1.87 | 2.3E-02 | AF158132.1 | NT | Metapneus ensis fushi tarazu-factor 1 mRNA, complete cds |
| 11846 | 24843 | | 5.2 | 2.3E-02 | BE278331.1 | EST_HUMAN | 601178658F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5' |
| 12282 | 24485 | 30940 | 1.69 | 2.3E-02 | BF528482.1 | EST_HUMAN | 602043829F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5' |
| 12282 | 24485 | 30941 | 1.59 | 2.3E-02 | BF528482.1 | EST_HUMAN | 602043829F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5' |
| 12302 | 24562 | 30807 | 2.2 | 2.3E-02 | U38394.1 | NT | Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds |
| 12447 | 25100 | | 3.04 | 2.3E-02 | U11077.1 | NT | Dicystatium discoidium extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds |
| 12660 | 24940 | | 1.73 | 2.3E-02 | 11428388 | NT | Homo sapiens dead ringer (Drosophila) like 1 (DRIL1), mRNA |
| 787 | 13388 | 25885 | 3 | 2.2E-02 | AF018287.1 | NT | Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds |
| 1783 | 14373 | | 1.03 | 2.2E-02 | 4557448 | NT | Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA |
| 2059 | 14639 | 27212 | 1.33 | 2.2E-02 | Z82001.1 | NT | S. pneumoniae pcgA gene and open reading frames |
| 3482 | 16088 | | 2.1 | 2.2E-02 | AA577785.1 | EST_HUMAN | nt24604.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3' |
| 3708 | 16309 | | 3.58 | 2.2E-02 | AF063094.1 | NT | Infectious burial disease virus segment B strain IL4 VP1 gene, complete cds |
| 3920 | 16518 | 28984 | 1.11 | 2.2E-02 | AW601317.1 | EST_HUMAN | PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA |
| 3932 | 16580 | 28062 | 0.85 | 2.2E-02 | Z74283.1 | NT | S. cerevisiae chromosome IV reading frame ORF YDL245c |
| 5225 | 17780 | 30209 | 0.92 | 2.2E-02 | Z73587.1 | NT | S. cerevisiae chromosome XVI reading frame ORF YPL241c |
| 7294 | 19822 | 32881 | 3.52 | 2.2E-02 | AV689721.1 | EST_HUMAN | AV689721 GKB Homo sapiens cDNA clone GKBAND003 3' |
| 8312 | 20853 | 33778 | 2.56 | 2.2E-02 | AL181515.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 8312 | 20853 | 33779 | 2.56 | 2.2E-02 | AL181515.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27 |
| 8744 | 21283 | 34205 | 0.75 | 2.2E-02 | AT9488.1 | NT | P. vulgaris alpha tub 2 mRNA |
| 9574 | 22074 | 35036 | 0.57 | 2.2E-02 | AJ243025.1 | NT | Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5 |
| 9574 | 22074 | 35037 | 0.57 | 2.2E-02 | AJ243025.1 | NT | Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5 |
| 9604 | 22104 | 35068 | 1.88 | 2.2E-02 | AB028898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 9604 | 22104 | 35067 | 1.88 | 2.2E-02 | AB028898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 10106 | 22801 | | 0.86 | 2.2E-02 | 6678140 | NT | Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA |
| 12120 | 24378 | | 3.95 | 2.2E-02 | AA503553.1 | EST_HUMAN | ne47907.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:800541 3' similar to contains Alu repetitive element |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 444 | 13077 | | 4.45 | 2.1E-02 | AV761502.1 | EST_HUMAN | AV761502 MDS Homo sapiens cDNA clone MDSADG01 5' |
| 474 | 13107 | | 5.21 | 2.1E-02 | AF029728.1 | NT | Dicystallum discoidium histidine kinase C (dhkc) mRNA, complete cds |
| 1308 | 13800 | 26420 | 8.16 | 2.1E-02 | U72073.1 | NT | Bacillus subtilis cotLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds |
| 1430 | 14022 | 26550 | 1.46 | 2.1E-02 | AF204395.1 | NT | Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds |
| 1430 | 14022 | 26551 | 1.46 | 2.1E-02 | AF204395.1 | NT | Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds |
| 2642 | 13426 | 25934 | 3.37 | 2.1E-02 | N29268.1 | EST_HUMAN | y43h07.1 Soares melanocyte 2NbtHM Homo sapiens cDNA clone IMAGE:264541 5' |
| 3184 | 14660 | 27231 | 0.93 | 2.1E-02 | BE072546.1 | EST_HUMAN | PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA |
| 3184 | 14660 | 27231 | 0.93 | 2.1E-02 | BE072546.1 | EST_HUMAN | PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA |
| 3843 | 16248 | 27232 | 1.47 | 2.1E-02 | AA481271.1 | EST_HUMAN | z63509.1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:708121 5' |
| 4211 | 16800 | 28248 | 0.77 | 2.1E-02 | Z74283.1 | NT | S. cerevisiae chromosome IV reading frame ORF YDL245c |
| 4398 | 16883 | 28428 | 0.93 | 2.1E-02 | BF343655.1 | EST_HUMAN | 802015306F1 NCL_CGAP_Brr64 Homo sapiens cDNA clone IMAGE:4131161 5' |
| 4540 | 17124 | 28568 | 1.64 | 2.1E-02 | U44914.1 | NT | Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes |
| 4552 | 17135 | 28583 | 1.3 | 2.1E-02 | A768127.1 | EST_HUMAN | wg81d1.1 x1 Soares NSF F8 9W OT PA_P S1 Homo sapiens cDNA clone IMAGE:2371509 3' |
| 4820 | 17398 | 28852 | 5.95 | 2.1E-02 | Y08501.1 | NT | A. thaliana mitochondrial genome, part A |
| 4836 | 17414 | 28897 | 0.57 | 2.1E-02 | AA695737.1 | EST_HUMAN | ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1128918 3' |
| 4944 | 17519 | 28961 | 0.93 | 2.1E-02 | A1823432.1 | EST_HUMAN | wh54e05.x1 NCL_CGAP_Ku411 Homo sapiens cDNA clone IMAGE:2394528 3' |
| 5321 | 17883 | | 1.52 | 2.1E-02 | S82470.1 | NT | BB1-malignant cell expression-enhanced gene/tumor progression-enhanced gene (human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt) |
| 5821 | 18445 | 31167 | 0.9 | 2.1E-02 | AW379529.1 | EST_HUMAN | GM4-HT0244-111189-040-h05 HT0244 Homo sapiens cDNA |
| 7126 | 18466 | 32284 | 0.74 | 2.1E-02 | BF098198.1 | EST_HUMAN | QV3-GN0058-120900-328-a12 GN0058 Homo sapiens cDNA |
| 8456 | 20998 | 33914 | 0.66 | 2.1E-02 | 9780238 | NT | Mus musculus sorting nexin 1 (Snx1), mRNA |
| 9422 | 21831 | 34879 | 0.56 | 2.1E-02 | AA984288.1 | EST_HUMAN | em83e07.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains |
| 9549 | 22049 | 35010 | 2.41 | 2.1E-02 | AJ243213.1 | NT | Alu repetitive element: contains element MER11 repetitive element; |
| 9549 | 22049 | 35011 | 2.41 | 2.1E-02 | AJ243213.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 9894 | 22391 | 35369 | 1.22 | 2.1E-02 | L26824.1 | NT | Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 |
| 9894 | 22391 | 35369 | 1.22 | 2.1E-02 | L26824.1 | NT | Streptococcus pneumoniae integrase, excisionase, repressor protein, release, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes |
| 9894 | 22391 | 35369 | 1.22 | 2.1E-02 | L26824.1 | NT | UmuD MucA homolog genes, complete cds; and unknown genes |
| 9894 | 22391 | 35369 | 1.22 | 2.1E-02 | L26824.1 | NT | em83e07.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains |
| 9894 | 22391 | 35369 | 1.22 | 2.1E-02 | L26824.1 | NT | Alu repetitive element: contains element MER11 repetitive element; |
| 9894 | 22391 | 35369 | 1.22 | 2.1E-02 | L26824.1 | NT | Alu repetitive element: contains element MER11 repetitive element; |
| 12089 | 18030 | | 11.53 | 2.1E-02 | Y19213.1 | NT | Homo sapiens putative psfH-Iba pseudogene for hair keratin, exons 2 to 7 |
| 12141 | 24839 | 30798 | 1.31 | 2.1E-02 | L34170.1 | NT | Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22 |
| 12552 | 24655 | 30871 | 16.83 | 2.1E-02 | AF183913.1 | NT | Azospirillum brasilense major outer membrane protein OmeA precursor (omeA) gene, complete cds |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 20 | 12689 | 25155 | 1.34 | 2.0E-02 | BF002832.1 | EST_HUMAN | 7q51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3306888 3' similar to contains MER1.13 |
| 21 | 12700 | 25156 | 9.6 | 2.0E-02 | AW855565.1 | EST_HUMAN | MER1 repetitive element: |
| 280 | 12837 | 25422 | 2.31 | 2.0E-02 | 6753635 | NT | QV4-NN0038-270-400-187-H05 NN0038 Homo sapiens cDNA |
| 317 | 12871 | 25480 | 2.42 | 2.0E-02 | AA456538.1 | EST_HUMAN | Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA |
| 831 | 13448 | 25855 | 1.2 | 2.0E-02 | 6753635 | NT | sa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5' |
| 1126 | 13729 | 26240 | 1.32 | 2.0E-02 | AL068805.1 | NT | Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA |
| 1241 | 13839 | 26356 | 0.79 | 2.0E-02 | 8822391 | NT | Homo sapiens genomic region containing hypervariable minisatellites chromosome 1(p36.33) of Homo sapiens |
| 1241 | 13839 | 26357 | 0.79 | 2.0E-02 | 8822391 | NT | Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA |
| 1814 | 14488 | 27053 | 2.3 | 2.0E-02 | 8822453 | NT | Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA |
| 1814 | 14489 | 27054 | 2.3 | 2.0E-02 | 8822453 | NT | Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA |
| 2824 | 15378 | | 3.19 | 2.0E-02 | AL161532.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32 |
| 3115 | 12689 | 25155 | 1.84 | 2.0E-02 | BF002832.1 | EST_HUMAN | 7q51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3306888 3' similar to contains MER1.13 |
| 3178 | 15791 | | 1.38 | 2.0E-02 | 7305474 | NT | MER1 repetitive element: |
| 3284 | 15876 | | 1.57 | 2.0E-02 | AF085588.1 | NT | Mus musculus scema domain, transmembrane domain (TM), and cytoplasmic domain, (sennaphorin) 68 |
| 4078 | 16874 | 28135 | 1.54 | 2.0E-02 | M18095.1 | NT | (Sema6b), mRNA |
| 5268 | 17830 | 30255 | 1.12 | 2.0E-02 | AF188368.1 | NT | Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds |
| 6056 | 18873 | 31414 | 0.87 | 2.0E-02 | L36321.2 | NT | P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end |
| 7553 | 20072 | 32847 | 1.28 | 2.0E-02 | AP000004.1 | NT | Agaromyces capsulatus catalase isozyme A (CATA) mRNA, complete cds |
| 7553 | 20072 | 32848 | 1.28 | 2.0E-02 | AP000004.1 | NT | Dichostelium discoideum class VII unconventional myosin (myosin) gene, complete cds |
| 9781 | 22289 | | 2.5 | 2.0E-02 | U70408.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (4/7) |
| 10284 | 22759 | 35746 | 1.63 | 2.0E-02 | A1840342.1 | EST_HUMAN | Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (4/7) |
| 10522 | 23060 | 36070 | 2.05 | 2.0E-02 | Z73986.1 | NT | Japanese encephalitis virus envelope protein mRNA, partial cds |
| 11250 | 23780 | 36836 | 2.85 | 2.0E-02 | D88184.1 | NT | wt17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288315 3' |
| 11530 | 23978 | 37047 | 1.58 | 2.0E-02 | 10947055 | NT | Mycobacterium tuberculosis H37Rv complete genome; segment 83/162 |
| 11530 | 23978 | 37048 | 1.58 | 2.0E-02 | 10947055 | NT | Equus caballus DNA for 17alpha-hydroxysteroid/17,20-lyase, complete cds |
| 11654 | 18034 | 30494 | 1.81 | 2.0E-02 | AA456538.1 | EST_HUMAN | Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA |
| 12138 | 15378 | | 1.94 | 2.0E-02 | AL161532.2 | NT | sa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5' |
| 12635 | 24711 | | 8.4 | 2.0E-02 | T80037.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32 |
| 722 | 13342 | 25832 | 1.93 | 1.8E-02 | AA572784.1 | EST_HUMAN | sa15b10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24675 5' |
| | | | | | | | repetitive element: |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1658 | 14251 | 26785 | 0.96 | 1.9E-02 | P18488 | SWISSPROT | EMPTY SPIRACLES HOMEOTIC PROTEIN |
| 2083 | 14684 | 27234 | 1.96 | 1.9E-02 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2083 | 14684 | 27235 | 1.96 | 1.9E-02 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2549 | 15113 | 27683 | 0.9 | 1.9E-02 | AL161550.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50 |
| 2630 | 15546 | 28021 | 8.7 | 1.9E-02 | AA713856.1 | EST_HUMAN | nm04805.s1 NCL_CGAP SS1 Homo sapiens cDNA clone IMAGE:1298337 3' |
| 2680 | 15596 | 28076 | 1.56 | 1.9E-02 | AV848696.1 | EST_HUMAN | AV848696 GLC Homo sapiens cDNA clone G1CBLH07 3' |
| 3288 | 15909 | | 0.75 | 1.9E-02 | AB033611.1 | NT | Urethrichus talpoides mitochondrial gene for cytochrome b, complete cds |
| 3671 | 16272 | | 1.09 | 1.9E-02 | N52250.1 | EST_HUMAN | Y228502.s1 Soares_multiple sclerosis_2NtHMSF Homo sapiens cDNA clone IMAGE:284331 3' |
| 3766 | 16367 | | 6.81 | 1.9E-02 | BE738098.1 | EST_HUMAN | 601572882F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5' |
| 4121 | 16714 | 28170 | 1.48 | 1.9E-02 | AF141940.1 | NT | Mycoplasma litans VHA1 precursor (vha1) and VHA2 precursor (vha2) genes, partial cds |
| 4271 | 16857 | 28305 | 1.57 | 1.9E-02 | P09081 | SWISSPROT | HOMEOTIC BICOID PROTEIN (PRD-4) |
| 4271 | 16857 | 28306 | 1.57 | 1.9E-02 | P09081 | SWISSPROT | HOMEOTIC BICOID PROTEIN (PRD-4) |
| 4639 | 17221 | 28675 | 3.21 | 1.9E-02 | AI452869.1 | EST_HUMAN | U46404.x1 Soares_NSF F8 9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Abi repetitive element |
| 5157 | 15113 | 27683 | 2.73 | 1.9E-02 | AL161550.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50 |
| 5519 | 18151 | 30565 | 0.83 | 1.9E-02 | AF037352.1 | NT | Mus musculus T cell receptor gamma locus, TOR gamma 1 and gamma 3 gene clusters |
| 5660 | 18287 | 30765 | 1.38 | 1.9E-02 | L47572.1 | NT | Meleagris gallopavo paracetamol-2 (PON2) mRNA, complete cds |
| 5958 | 18581 | | 0.81 | 1.9E-02 | AB019607.1 | NT | Drosophila kankai gene for glycerol-3-phosphate dehydrogenase, complete cds |
| 7158 | 18680 | 32534 | 1.41 | 1.9E-02 | U19241.1 | NT | Homo sapiens interferon-gamma receptor alpha chain gene, exon 1 |
| 7168 | 18680 | 32535 | 1.41 | 1.9E-02 | U19241.1 | NT | Homo sapiens interferon-gamma receptor alpha chain gene, exon 1 |
| 8506 | 21045 | | 1.06 | 1.9E-02 | AL162764.2 | NT | Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 3/7 |
| 9254 | 21780 | 34732 | 0.94 | 1.9E-02 | BF316128.1 | EST_HUMAN | 601889130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5' |
| 9628 | 22129 | 35093 | 0.86 | 1.9E-02 | L10114.1 | NT | Nicotiana tabacum type II phytochrome (phyB) gene, complete cds |
| 9958 | 22453 | 35435 | 1.04 | 1.9E-02 | BF096832.1 | EST_HUMAN | 601852385F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:4078253 5' |
| 10054 | 22549 | 35543 | 0.49 | 1.9E-02 | N39160.1 | EST_HUMAN | yy46h08.s1 Soares_multiple sclerosis_2NtHMSF Homo sapiens cDNA clone IMAGE:2766339 3' |
| 10151 | 22648 | 35639 | 0.56 | 1.9E-02 | D64001.1 | NT | Synechocystis sp. PCC6803 complete genome, 2027, 2530000-2644704 |
| 11878 | 24847 | 30801 | 4.29 | 1.9E-02 | AF101065.1 | NT | Hirudo medicinalis intermediate filament gelsolin mRNA, complete cds |
| 12477 | 24818 | | 1.27 | 1.9E-02 | L11068.1 | NT | Candida albicans lambda Ca3B fragment |
| 12587 | 24680 | 30879 | 1.7 | 1.9E-02 | X68271.1 | NT | H. sapiens MUC18 gene exon 16 |
| 368 | 13017 | 25500 | 1.84 | 1.9E-02 | AW771104.1 | EST_HUMAN | hm5206.x1 NCL_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element |
| 714 | 13335 | 25821 | 2.26 | 1.9E-02 | BF308122.1 | EST_HUMAN | MER29 repetitive element |
| 1202 | 13802 | 26315 | 1.51 | 1.9E-02 | X17684.1 | NT | 601884329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5' |
| 1484 | 14077 | 26615 | 2.3 | 1.9E-02 | AF243382.1 | NT | H. fructidici mRNA for myelin basic protein (MBP) |
| | | | | | | | Drosophila melanogaster cytoplasmic protein encase (enc) mRNA, complete cds |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2704 | 15261 | 27828 | 1.22 | 1.8E-02 | AE004544.1 | NT | Pseudomonas aeruginosa PAO1, section 105 of 528 of the complete genome |
| 3247 | 15859 | | 0.72 | 1.8E-02 | A1805829.1 | EST_HUMAN | hs2a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3' |
| 3958 | 16554 | 29023 | 1.07 | 1.8E-02 | AW878122.1 | EST_HUMAN | MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA |
| 3956 | 16554 | 29024 | 1.07 | 1.8E-02 | AW878122.1 | EST_HUMAN | MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA |
| 4160 | 16752 | | 1.41 | 1.8E-02 | AA861446.1 | EST_HUMAN | af24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408835 3' |
| 4621 | 17105 | 28551 | 1.67 | 1.8E-02 | AW836363.1 | EST_HUMAN | QV4-OT0021-301289-071-b11 DT0021 Homo sapiens cDNA |
| 5090 | 17663 | 30103 | 1.06 | 1.8E-02 | O60810 | SWISSPROT | HYPOTHETICAL PROTEIN DJ845024.2 |
| 6901 | 19835 | 32473 | 4.27 | 1.8E-02 | P14310 | SWISSPROT | HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5REGION |
| 8071 | 20613 | 33527 | 0.81 | 1.8E-02 | U37091.1 | NT | Mus musculus carbonic anhydrase IV gene, complete cds |
| 8404 | 20944 | 33866 | 0.91 | 1.8E-02 | AW80537.1 | EST_HUMAN | QV2-NN1073-220400-158-P09 NN1073 Homo sapiens cDNA |
| 8449 | 20989 | 33907 | 0.75 | 1.8E-02 | 6878943 | NT | Mus musculus microtubule-associated protein 2 (Map2), mRNA |
| 9413 | 21922 | 34870 | 0.45 | 1.8E-02 | BF241824.1 | EST_HUMAN | 601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5' |
| 9413 | 21822 | 34871 | 0.45 | 1.8E-02 | BF241824.1 | EST_HUMAN | 601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5' |
| 9560 | 22080 | | 2.41 | 1.8E-02 | AA897543.1 | EST_HUMAN | af24h08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394821 3' similar to gbl:11672 ZINC FINGER PROTEIN 91 (HUMAN); |
| 9975 | 22470 | 35453 | 1.72 | 1.8E-02 | BE778274.1 | EST_HUMAN | 601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869863 5' |
| 10126 | 22621 | 35611 | 1.12 | 1.8E-02 | X98933.1 | NT | L. stagnalis mRNA for myomodulin neuro-peptide precursor |
| 11313 | 23011 | 36019 | 1.79 | 1.8E-02 | AB002337.2 | NT | Homo sapiens mRNA for KIAA0339 protein, partial cds |
| 11313 | 23011 | 36020 | 1.79 | 1.8E-02 | AB002337.2 | NT | Homo sapiens mRNA for KIAA0339 protein, partial cds |
| 11480 | 23630 | 37001 | 1.73 | 1.8E-02 | AP000006.1 | NT | Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (817) |
| 11489 | 23638 | 37008 | 3.88 | 1.8E-02 | U62749.1 | NT | Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds |
| 839 | 13552 | 28068 | 0.77 | 1.7E-02 | BE394889.1 | EST_HUMAN | 601310628F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5' |
| 1827 | 14416 | 26963 | 1.89 | 1.7E-02 | AW573183.1 | EST_HUMAN | hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element; |
| 1827 | 14416 | 26964 | 1.89 | 1.7E-02 | AW573183.1 | EST_HUMAN | hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.1 L1 repetitive element; |
| 1912 | 14497 | | 3.27 | 1.7E-02 | AL163204.2 | NT | Homo sapiens chromosome 21 segment HS21C004 |
| 2159 | 14736 | | 12.81 | 1.7E-02 | AB004816.1 | NT | Oryctolagus cuniculus mRNA for mitsugumin28, complete cds |
| 2332 | 14903 | 27474 | 4.64 | 1.7E-02 | S74186.1 | NT | (microsatellite INRA41) [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2] |
| 3028 | 15944 | 28123 | 0.84 | 1.7E-02 | A1147815.1 | EST_HUMAN | qf22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1686982 3' |
| 3582 | 16166 | | 4.33 | 1.7E-02 | AW827368.1 | EST_HUMAN | hm45a04.x1 NC1_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element; |
| 3687 | 16268 | | 0.65 | 1.7E-02 | P04929 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4248 | 16836 | | 1.08 | 1.7E-02 | AA069818.1 | EST_HUMAN | ac19f04.s1 Stragene ovary (#937217) Homo sapiens cDNA clone IMAGE:856827 3' similar to contains Alu repetitive element; contains element MER24 repetitive element; |
| 4278 | 16884 | | 2.52 | 1.7E-02 | R02506.1 | EST_HUMAN | y86f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5' |
| 4551 | 17134 | 28582 | 0.61 | 1.7E-02 | A1305279.1 | EST_HUMAN | qm08g07.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN); |
| 4826 | 17209 | 29859 | 1.44 | 1.7E-02 | AW573183.1 | EST_HUMAN | h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.1 L1 repetitive element; |
| 4824 | 17402 | 29855 | 1.78 | 1.7E-02 | V00641.1 | NT | Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II |
| 4838 | 17511 | | 5.59 | 1.7E-02 | A1015076.1 | EST_HUMAN | ov51a02.g1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1840858 3' |
| 6274 | 18882 | 31660 | 1.8 | 1.7E-02 | A1769247.1 | EST_HUMAN | wg35f09.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387113 3' similar to contains Alu repetitive element; |
| 6693 | 18289 | 32091 | 1.98 | 1.7E-02 | A1038280.1 | EST_HUMAN | cy65p03.x1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672681 3' |
| 7112 | 19452 | 32268 | 1.05 | 1.7E-02 | AF180930.1 | NT | Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds |
| 7255 | 19783 | 32639 | 1.96 | 1.7E-02 | | NT | Homo sapiens nebulin (NEB), mRNA |
| 7394 | 19919 | 32763 | 1.07 | 1.7E-02 | L07899.1 | NT | Human apolipoprotein (a) gene, exon 1 |
| 7394 | 19919 | 32764 | 1.07 | 1.7E-02 | L07899.1 | NT | Human apolipoprotein (a) gene, exon 1 |
| 7724 | 20232 | 32764 | 1.7 | 1.7E-02 | AJ010770.1 | NT | Homo sapiens hyperion gene, exons 1-50 |
| 8357 | 20296 | 33186 | 0.97 | 1.7E-02 | U21854.1 | NT | Caenorhabditis elegans CCAF1 protein gene, complete cds |
| 8615 | 22115 | 35079 | 1.31 | 1.7E-02 | AL040554.1 | EST_HUMAN | DKFZp434I0314_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434I0314 5' |
| 12482 | 25025 | 30619 | 3.35 | 1.7E-02 | AW903482.1 | EST_HUMAN | GM4-NN1030-040400-130-406 NN1030 Homo sapiens cDNA |
| 537 | 13168 | | 3.38 | 1.6E-02 | AL021928.1 | NT | Mycobacterium tuberculosis H37Rv complete genome; segment 13/162 |
| 1696 | 14289 | 26825 | 1.05 | 1.6E-02 | Y18889.1 | NT | Treponema maltophilum flaB2, flaB3 and flhD genes for flagellin subunit proteins and CAP protein homologue |
| 2280 | 14864 | 27438 | 2.13 | 1.6E-02 | Q64176 | SWISSPROT | LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22) |
| 2280 | 14864 | 27439 | 2.13 | 1.6E-02 | Q64176 | SWISSPROT | LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22) |
| 2600 | 15182 | 27730 | 0.98 | 1.6E-02 | AJ008345.1 | NT | Homo sapiens KVLQ11 gene |
| 2668 | 15227 | 27796 | 1.82 | 1.6E-02 | AA494872.1 | EST_HUMAN | ne81d06.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667 |
| 2718 | 15275 | | 1.14 | 1.6E-02 | AB014534.1 | NT | Homo sapiens mRNA for KIAA0634 protein, partial cds |
| 3052 | 15668 | 28146 | 0.73 | 1.6E-02 | AF112282.1 | NT | Lassaea sp. isolate lBd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product |
| 3578 | 18182 | 28684 | 5.61 | 1.6E-02 | AW850652.1 | EST_HUMAN | IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA |
| 3914 | 16512 | 28974 | 0.82 | 1.6E-02 | AL163301.2 | NT | Homo sapiens chromosome 21 segment HS21C101 |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4254 | 16842 | | 1.77 | 1.0E-02 | AF110520.1 | NT | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial> |
| 4388 | 16974 | 29424 | 1.26 | 1.0E-02 | AW875407.1 | EST_HUMAN | QV2-PT0012-140100-030-07 PT0012 Homo sapiens cDNA |
| 4801 | 17476 | 29832 | 3.89 | 1.0E-02 | AJ769132.1 | EST_HUMAN | wg34009.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2369889 3' |
| 5308 | 17868 | | 0.61 | 1.0E-02 | N80156.1 | EST_HUMAN | zaf6607.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:297444 3' |
| 5807 | 18432 | 31153 | 1.26 | 1.0E-02 | 6871715 | NT | Mus musculus CD5 antigen (Cd5), mRNA |
| 6752 | 18345 | 32152 | 2 | 1.0E-02 | AB015281.1 | NT | Candida albicans CaGCR3 gene, complete cds |
| 7011 | 19509 | 32329 | 1.22 | 1.0E-02 | AB027571.1 | NT | Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds |
| 7011 | 19509 | 32330 | 1.22 | 1.0E-02 | AB027571.1 | NT | Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds |
| 7896 | 20205 | 33092 | 0.9 | 1.0E-02 | AL161508.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20 |
| 8084 | 20808 | 33518 | 0.78 | 1.0E-02 | AJ277682.1 | NT | Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein |
| 8119 | 20860 | | 1.55 | 1.0E-02 | X05151.1 | NT | Human apoC-II gene for preproapolipoprotein C-II |
| 9653 | 22448 | | 2.32 | 1.0E-02 | AF079784.1 | NT | Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds |
| 10317 | 22811 | 36805 | 1.17 | 1.0E-02 | AA572818.1 | EST_HUMAN | nf16g03.s1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:914280 similar to SW:TELO_RABIT |
| 10317 | 22811 | 36806 | 1.17 | 1.0E-02 | AA572818.1 | EST_HUMAN | P28294 TELOKIN. [1]: |
| 10786 | 24800 | 36319 | 2.38 | 1.0E-02 | Z94828.1 | NT | G.gallus microsatellite DNA (LE10260 (=T16III(1))) |
| 11080 | 23602 | 36640 | 2.5 | 1.0E-02 | AL161508.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20 |
| 11090 | 23602 | 36641 | 2.5 | 1.0E-02 | AL161508.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20 |
| 11365 | 23837 | 36899 | 2.38 | 1.0E-02 | AJ373558.1 | EST_HUMAN | qz86a10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3' |
| 11855 | 14864 | 27438 | 3.63 | 1.0E-02 | Q84176 | SWISSPROT | LIVER CARBOXYLTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22) |
| 11855 | 14864 | 27439 | 3.63 | 1.0E-02 | Q84176 | SWISSPROT | LIVER CARBOXYLTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22) |
| 781 | 13400 | | 51.07 | 1.5E-02 | 8923734 | NT | Homo sapiens transcription factor (HSA130894), mRNA |
| 2187 | 14763 | 27332 | 4.36 | 1.5E-02 | N39521.1 | EST_HUMAN | y27807.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3' |
| 2219 | 14764 | 27367 | 1.76 | 1.5E-02 | AL161504.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80 |
| 3097 | 15712 | 28183 | 0.99 | 1.5E-02 | AJ006216.1 | NT | Homo sapiens CACNA1F gene, exons 1 to 48 |
| 3097 | 15712 | 28184 | 0.99 | 1.5E-02 | AJ006216.1 | NT | Homo sapiens CACNA1F gene, exons 1 to 48 |
| 3787 | 16387 | 28653 | 0.96 | 1.5E-02 | BF082942.1 | EST_HUMAN | MIR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA |
| 4222 | 16810 | 29257 | 0.86 | 1.5E-02 | AA160987.1 | EST_HUMAN | zq40g10.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:832228 5' |
| 5160 | 17729 | | 0.78 | 1.5E-02 | M13879.1 | NT | Human Interleukin 2 gene, exons 1 and 2 |
| 5403 | 17963 | 30374 | 1.14 | 1.5E-02 | AW770341.1 | EST_HUMAN | h76h11.x1 NCI CGAP_Kd13 Homo sapiens cDNA clone IMAGE:3007173 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6436 | 18039 | 31828 | 1.31 | 1.5E-02 | Q09711 | SWISSPROT | HYPOTHETICAL CALCIUM-BINDING PROTEIN G18B11.04 IN CHROMOSOME 1 |
| 7360 | 19888 | | 1.62 | 1.5E-02 | 11467282 | NT | Cyanophora paradoxa cyanelle, complete genome |
| 7432 | 19856 | 32821 | 1.36 | 1.5E-02 | 11418713 | NT | Homo sapiens KIAA1009 protein (KIAA1009), mRNA |
| 7816 | 20358 | 33265 | 1.44 | 1.5E-02 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 7822 | 20364 | 33273 | 4.16 | 1.5E-02 | 11417739 | NT | Homo sapiens vally-HRNA synthetase 2 (VARS2), mRNA |
| 8764 | 21303 | 34224 | 1.62 | 1.5E-02 | BF345554.1 | EST_HUMAN | 802019135F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154504 5' |
| 8389 | 21812 | | 0.51 | 1.5E-02 | AF068774.1 | NT | Homo sapiens kinase-related protein isoform 1 mRNA, complete cds |
| 9490 | 21949 | 34885 | 1.64 | 1.5E-02 | D44608.1 | NT | Saccharomyces cerevisiae chromosome VI plasmid GapC |
| 9725 | 22223 | 35199 | 1.08 | 1.5E-02 | R32867.1 | EST_HUMAN | YH54B10.1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:133531 5' |
| 9725 | 22223 | 35200 | 1.08 | 1.5E-02 | R32867.1 | EST_HUMAN | YH54B10.1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:133531 5' |
| 10687 | 23227 | | 1.71 | 1.5E-02 | D28547.1 | NT | Rice gene for thiodiosin h, complete cds |
| 11047 | 23580 | 36587 | 2.32 | 1.5E-02 | L40609.1 | NT | Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's |
| 12078 | 24892 | | 2.26 | 1.5E-02 | AW750834.1 | EST_HUMAN | RC4-GN0049-140100-011-CT1 CN0049 Homo sapiens cDNA |
| 12636 | 24712 | | 1.55 | 1.5E-02 | A1763127.1 | EST_HUMAN | w08h03.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2389463 3' similar to contains Alu repetitive element; contains element MER26 MSR1 repetitive element; |
| 442 | 13075 | | 1.41 | 1.4E-02 | AE002230.2 | NT | Chlamydia pneumoniae AF39, section 58 of 94 of the complete genome |
| 1157 | 13780 | 26270 | 4.22 | 1.4E-02 | 7705880 | NT | Homo sapiens NESH protein (LOC51225), mRNA |
| 1289 | 13893 | | 1.28 | 1.4E-02 | U32800.1 | NT | Haemophilus influenzae Rd section 115 of 163 of the complete genome |
| 1341 | 13836 | | 3.36 | 1.4E-02 | U87779.1 | NT | Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds |
| 1564 | 14156 | | 1.09 | 1.4E-02 | AV723785.1 | EST_HUMAN | AV723785 HTB Homo sapiens cDNA clone HTBAF-H11 5' |
| 3249 | 15861 | 28342 | 1.91 | 1.4E-02 | AF160688.2 | NT | Bifidobacterium longum Nac/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (eglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xyR) gene, partial cds |
| 3445 | 16053 | 28530 | 0.96 | 1.4E-02 | AW074212.1 | EST_HUMAN | xb08d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3' |
| 3531 | 16136 | 28616 | 5.67 | 1.4E-02 | AL161586.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82 |
| 3531 | 16136 | 28617 | 5.67 | 1.4E-02 | AL161586.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82 |
| 3571 | 16175 | 28657 | 0.88 | 1.4E-02 | 4503628 | NT | Homo sapiens coagulation factor XII (Hageman factor) (F-12), mRNA |
| 3717 | 16318 | 28788 | 6.27 | 1.4E-02 | 6996918 | NT | Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA |
| 4567 | 17170 | 28614 | 8.86 | 1.4E-02 | AW962688.1 | EST_HUMAN | EST374761 MAGG cDNAs, MAGG Homo sapiens cDNA |
| 4567 | 17170 | 28615 | 8.86 | 1.4E-02 | AW962688.1 | EST_HUMAN | EST374761 MAGG cDNAs, MAGG Homo sapiens cDNA |
| 4767 | 17348 | 28797 | 1.2 | 1.4E-02 | 8922391 | NT | Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA |
| 4767 | 17348 | 28798 | 1.2 | 1.4E-02 | 8922391 | NT | Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA |
| 5003 | 17576 | 30020 | 6.84 | 1.4E-02 | BE733142.1 | EST_HUMAN | 601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5003 | 17576 | 30021 | 6.64 | 1.4E-02 | BE733142.1 | EST_HUMAN | 601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3942280 5' |
| 6547 | 19145 | 31841 | 4.61 | 1.4E-02 | AA559030.1 | EST_HUMAN | nt11c04.s1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1028960 3' similar to contains Alu repetitive element; |
| 6547 | 19145 | 31842 | 4.61 | 1.4E-02 | AA559030.1 | EST_HUMAN | nt11c04.s1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1028960 3' similar to contains Alu repetitive element; |
| 8081 | 20623 | | 1.97 | 1.4E-02 | AL022073.1 | NT | Mycobacterium tuberculosis H37Rv complete genome; segment 887162 |
| 8829 | 21368 | 34292 | 1.24 | 1.4E-02 | AB1702.1 | NT | Candida boidinii methanol oxidase (AOD1) gene, complete cds |
| 9082 | 21618 | 34553 | 0.99 | 1.4E-02 | AB72285.1 | NT | Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8 |
| 9321 | 21835 | 34786 | 2.48 | 1.4E-02 | BE544661.1 | EST_HUMAN | 601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5' |
| 10451 | 22945 | | 0.81 | 1.4E-02 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 11765 | 24156 | 36772 | 12.79 | 1.4E-02 | X60456.1 | NT | Human IFNAR gene for interferon alpha/beta receptor |
| 12134 | 24387 | | 3.62 | 1.4E-02 | AF324985.1 | NT | Arabidopsis thaliana F21J9.2 mRNA, complete cds |
| 12433 | 24574 | | 2.32 | 1.4E-02 | 11426968 | NT | Homo sapiens sperm associated antigen 7 (SPAG7), mRNA |
| 1905 | 14490 | | 1.18 | 1.3E-02 | BE739263.1 | EST_HUMAN | 601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5' |
| 1998 | 14590 | 27138 | 2.55 | 1.3E-02 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 3250 | 15662 | 26343 | 1.91 | 1.3E-02 | BF687081.1 | EST_HUMAN | 602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5' |
| 3250 | 15662 | 26344 | 1.91 | 1.3E-02 | BF687081.1 | EST_HUMAN | 602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5' |
| 4041 | 16639 | | 1.66 | 1.3E-02 | AF169288.1 | NT | Mus musculus beta-sarcoglycan gene, complete cds |
| | | | | | | | Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmmq28orf |
| 5455 | 18090 | 30447 | 1.46 | 1.3E-02 | AL049866.2 | NT | Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmmq28orf |
| 5455 | 18090 | 30448 | 1.46 | 1.3E-02 | AL049866.2 | NT | Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmmq28orf |
| 6312 | 18919 | 31694 | 1.4 | 1.3E-02 | U80017.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds |
| 6345 | 18951 | 31729 | 0.86 | 1.3E-02 | M82862.1 | NT | C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds |
| 7041 | 18061 | 30449 | 1.25 | 1.3E-02 | AL161546.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48 |
| 7041 | 18061 | 30450 | 1.25 | 1.3E-02 | AL161546.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48 |
| | | | | | | | aw06g05.x1 Soares_parathyroid_tumor_Nb1-IPA Homo sapiens cDNA clone IMAGE:1846072 3' similar to contains Alu repetitive element; |
| 7578 | 20094 | 32971 | 4.79 | 1.3E-02 | A031593.1 | EST_HUMAN | Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds |
| 8418 | 20958 | 33876 | 1.03 | 1.3E-02 | AF156961.1 | NT | Mouse kidney androgen-regulated protein (KAP) gene, complete cds |
| 10108 | 22603 | 35563 | 1.71 | 1.3E-02 | M63707.1 | NT | Chlamydia trachomatis section 31 of 87 of the complete genome |
| 10178 | 22673 | 35665 | 0.77 | 1.3E-02 | AE001304.1 | NT | xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3' |
| 10871 | 23392 | 36408 | 4.07 | 1.3E-02 | AW268563.1 | EST_HUMAN | xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3' |
| 10871 | 23392 | 36407 | 4.07 | 1.3E-02 | AW268563.1 | EST_HUMAN | xx34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 11742 | 25051 | | 2.12 | 1.3E-02 | X51780.1 | NT | Yeast ABP1 gene for actin binding protein |
| 12139 | 25039 | | 2 | 1.3E-02 | Z98117.1 | NT | Bacillus subtilis complete genome (section 14 of 21): from 2589451 to 2612870 |
| 12246 | 24457 | | 2.77 | 1.3E-02 | 9633068 | NT | Human herpesvirus 6B, complete genome |
| 12438 | 24813 | | 47.13 | 1.3E-02 | AF152238.1 | NT | Human sapient V1b vasopressin receptor (VPR3) gene, complete cds |
| 228 | 12888 | | 20.25 | 1.2E-02 | X87344.1 | NT | H. sapiens DMA, DMB, HLA-Z1, PIP2, LIMP2, TAP1, LIMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 377 | 13025 | 25511 | 3.79 | 1.2E-02 | AA06289.1 | EST_HUMAN | z85501.1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element: |
| 478 | 13111 | 25601 | 1.71 | 1.2E-02 | P38896 | SWISSPROT | HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3REGION |
| 768 | 13387 | 25888 | 8.37 | 1.2E-02 | A118352.1 | EST_HUMAN | q488a12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1794870 3' similar to contains L1.H L1 repetitive element: |
| 2221 | 14788 | 27369 | 1.85 | 1.2E-02 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 2223 | 14798 | 27371 | 1.15 | 1.2E-02 | AV731704.1 | EST_HUMAN | AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5' |
| 2487 | 15052 | 27824 | 1 | 1.2E-02 | AW172350.1 | EST_HUMAN | X37609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3' |
| 2542 | 15106 | 27878 | 1.05 | 1.2E-02 | BE588310.1 | EST_HUMAN | 601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5' |
| 2542 | 15108 | 27879 | 1.05 | 1.2E-02 | BE588310.1 | EST_HUMAN | 601088406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5' |
| 3135 | 15749 | | 7.56 | 1.2E-02 | AA075418.1 | EST_HUMAN | z88603.1 Stratagene ovarian cancer (8837219) Homo sapiens cDNA clone IMAGE:545020 5' |
| 3327 | 15837 | 28413 | 2.02 | 1.2E-02 | R62805.1 | EST_HUMAN | y11b08.s1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:138903 3' |
| 4838 | 17513 | 28659 | 0.61 | 1.2E-02 | AL161593.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89 |
| 5040 | 17613 | 30057 | 2.85 | 1.2E-02 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 5194 | 17759 | | 1.61 | 1.2E-02 | AB019786.1 | NT | Oryzops pythogaster Cplbq1 mRNA, partial cds |
| 5244 | 17808 | 30230 | 2.01 | 1.2E-02 | AV731704.1 | EST_HUMAN | AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5' |
| 5827 | 18548 | 31275 | 1.76 | 1.2E-02 | D78589.1 | NT | Rana rugosa mRNA for calreticulin, complete cds |
| 7078 | 19650 | 32489 | 5.21 | 1.2E-02 | AF175412.1 | NT | Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5 |
| 7334 | 19861 | 32725 | 1.06 | 1.2E-02 | H02197.1 | EST_HUMAN | y94h12.s1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:150885 3' |
| 7353 | 19879 | 32744 | 19.46 | 1.2E-02 | AV732093.1 | EST_HUMAN | AV732093 HTF Homo sapiens cDNA clone HTFBHC09 5' |
| 7839 | 20481 | 33382 | 2.3 | 1.2E-02 | Q11205 | SWISSPROT | CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B) |
| 8133 | 20674 | 33585 | 1.2 | 1.2E-02 | AF183612.1 | NT | Homo sapiens fringe protein mRNA, partial cds |
| 8133 | 20674 | 33586 | 1.2 | 1.2E-02 | AF183612.1 | NT | Homo sapiens fringe protein mRNA, partial cds |
| 8822 | 21361 | | 1.06 | 1.2E-02 | T76987.1 | EST_HUMAN | yd72c08.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:113774 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top Hit) BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9557 | 22057 | 35018 | 2.7 | 1.2E-02 | AB031013.1 | NT | Norwalk-like virus genogroup 2 gene for capsid protein, complete cds |
| 9588 | 22089 | 35053 | 1.74 | 1.2E-02 | AJ248003.1 | NT | Homo sapiens Spast gene for spastin protein |
| 12446 | 24582 | | 4.73 | 1.2E-02 | C18119.1 | EST_HUMAN | C18119 Human placenta cDNA (Tfujlwara) Homo sapiens cDNA clone GEN-557/G08 5' |
| 1312 | 13906 | 28428 | 1.49 | 1.1E-02 | AA070364.1 | EST_HUMAN | zmf68e11.s1 Stratiogene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:530824 3' |
| 1744 | 14334 | 28880 | 1.91 | 1.1E-02 | X75491.1 | NT | H. sapiens LIPA gene, exon 4 |
| 1744 | 14334 | 28881 | 1.91 | 1.1E-02 | X75491.1 | NT | H. sapiens LIPA gene, exon 4 |
| 2082 | 14883 | 27253 | 5.42 | 1.1E-02 | BF345263.1 | EST_HUMAN | 602018037.F1 NCJ_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153808 5' |
| 2802 | 15519 | | 4.2 | 1.1E-02 | N88523.1 | EST_HUMAN | za40e05.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285040 5' |
| 3575 | 16179 | 28682 | 2.88 | 1.1E-02 | A1653508.1 | EST_HUMAN | 1q55b10.x1 NCJ_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN |
| 4084 | 16889 | | 2.1 | 1.1E-02 | BE144637.1 | EST_HUMAN | Q22889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ; |
| 4183 | 16773 | | 0.81 | 1.1E-02 | AW813786.1 | EST_HUMAN | PK3-HT0175-300889-001-J06 HT0175 Homo sapiens cDNA |
| 4856 | 17531 | 28973 | 2.09 | 1.1E-02 | AL048383.2 | EST_HUMAN | RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA |
| | | | | | | | DKFZp586E0924_s1 588 (synonym: hube1) Homo sapiens cDNA clone DKFZp586E0924 |
| 6298 | 18906 | 31677 | 1.03 | 1.1E-02 | U68480.1 | NT | Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GhrR (ghrR), glutamine synthetase (ghsA), YnaA (ynaA), YnaB (ynbB), YnaC (ynbC), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH), YnaI (ynbI), YnaJ (ynbJ), xylan beta-1,4-xylosyl> |
| 7584 | 20108 | 32383 | 2.55 | 1.1E-02 | BE149811.1 | EST_HUMAN | RC1-HT0256-100300-016-H07 HT0256 Homo sapiens cDNA |
| 8188 | 20740 | 33852 | 0.49 | 1.1E-02 | P80394 | SWISSPROT | METALLOTHIONEIN (MT-1/MT-2) |
| 8188 | 20740 | 33853 | 0.49 | 1.1E-02 | P80394 | SWISSPROT | METALLOTHIONEIN (MT-1/MT-2) |
| 8574 | 21113 | 34032 | 0.64 | 1.1E-02 | AW588180.1 | EST_HUMAN | QV3-BN0045-220300-128-H02 BN0045 Homo sapiens cDNA |
| 8756 | 21285 | 34215 | 0.69 | 1.1E-02 | C04803.1 | EST_HUMAN | C04803 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NH4040 |
| 8833 | 21372 | 34297 | 7.39 | 1.1E-02 | Q61882 | SWISSPROT | NEUROGENIC LOCUS NOTCH 3 PROTEIN |
| 9842 | 22340 | 35322 | 2.07 | 1.1E-02 | AA082578.1 | EST_HUMAN | zn24e01.r1 Stratiogene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5' |
| 10006 | 22501 | 35492 | 3.79 | 1.1E-02 | AA314885.1 | EST_HUMAN | EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end |
| 10858 | 23379 | 36398 | 3.88 | 1.1E-02 | 11435505 | NT | Homo sapiens T-box 5 (TBX5), mRNA |
| 11702 | 24115 | | 2.67 | 1.1E-02 | AA688239.1 | EST_HUMAN | ab7711.s1 Stratiogene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains |
| 12512 | 16773 | | 1.87 | 1.1E-02 | AW813796.1 | EST_HUMAN | Alu repetitive element. |
| 7 | 12688 | 25144 | 6.97 | 1.0E-02 | AW846120.1 | EST_HUMAN | RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA |
| 1570 | 14163 | 26894 | 2.93 | 1.0E-02 | AA368128.1 | EST_HUMAN | MR3-ST0197-111089-003-e10 CT0178 Homo sapiens cDNA |
| 2806 | 15168 | | 1.9 | 1.0E-02 | AA368389.1 | EST_HUMAN | CM2-HT0177-041089-017-h12 HT0177 Homo sapiens cDNA |
| 3126 | 15740 | 28209 | 3.7 | 1.0E-02 | BE835556.1 | EST_HUMAN | cc22f08.s1 NCJ_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1350495 3' |
| 3302 | 15913 | 28391 | 1.41 | 1.0E-02 | BE868688.1 | EST_HUMAN | RCO-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA |
| | | | | | | | 601849867R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3558 | 16162 | | 0.83 | 1.0E-02 | AW846821.1 | EST_HUMAN | MRO-CT0060-081089-003-H10 CT0060 Homo sapiens cDNA |
| 3950 | 18548 | 29016 | 0.68 | 1.0E-02 | AI095098.1 | EST_HUMAN | HA0921 Human fetal liver cDNA library Homo sapiens cDNA |
| 4881 | 17488 | 29921 | 5.12 | 1.0E-02 | 6753521 | NT | Mus musculus corticotroph releasing hormone receptor 2 (Chr2), mRNA |
| 4970 | 17544 | 29888 | 5.03 | 1.0E-02 | R08587.1 | EST_HUMAN | Y554H01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:188633 5' |
| 5221 | 17788 | 30204 | 1.01 | 1.0E-02 | AF218910.1 | NT | Homo sapiens attractin precursor (ATRIN) gene, exon 25 and complete cds, alternatively spliced |
| 5317 | 17879 | 30288 | 0.98 | 1.0E-02 | P06599 | SWISSPROT | EXTENSIN PRECURSOR |
| 5394 | 17952 | | 16.85 | 1.0E-02 | AV723678.1 | EST_HUMAN | AV723678 HTB Homo sapiens cDNA clone HTBAPF08 5' |
| 5445 | 18000 | | 3.87 | 1.0E-02 | D34632.1 | NT | Arabidopsis thaliana acc2 gene for acetyl-CoA carboxylase, partial cds |
| 5610 | 18239 | 30888 | 0.8 | 1.0E-02 | H52881.1 | EST_HUMAN | YU36H11.1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:235941 5' |
| 5921 | 18543 | 31269 | 0.7 | 1.0E-02 | AF309388.1 | NT | Mus musculus transcription complex subunit NF-A-Tc4 (Nfat4) gene, exons 1 and 2 |
| 6284 | 18872 | 31842 | 0.89 | 1.0E-02 | AF267303.1 | NT | Mus musculus synaptotagmin II (Sy2) gene, complete cds |
| 6328 | 18934 | 31709 | 2.67 | 1.0E-02 | AW577113.1 | EST_HUMAN | MR4-BT0358-070100-201-H01 BT0358 Homo sapiens cDNA |
| 8328 | 18934 | 31710 | 2.67 | 1.0E-02 | AW577113.1 | EST_HUMAN | MR4-BT0358-070100-201-H01 BT0358 Homo sapiens cDNA |
| 8859 | 19583 | 32425 | 2.22 | 1.0E-02 | Z28842.1 | NT | Z.mays U3snRNA pseudogene |
| 8240 | 20781 | | 0.46 | 1.0E-02 | Z28107.1 | NT | S.cerevisiae chromosome XI reading frame ORF_YKL107W |
| 9314 | 21828 | 34778 | 4.29 | 1.0E-02 | BF036331.1 | EST_HUMAN | 601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5' |
| 9314 | 21828 | 34779 | 4.28 | 1.0E-02 | BF036331.1 | EST_HUMAN | 601459570F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863177 5' |
| 11143 | 23651 | | 2.17 | 1.0E-02 | AF157559.1 | NT | Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product |
| 11248 | 23778 | 36833 | 2.02 | 1.0E-02 | AV760016.1 | EST_HUMAN | AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5' |
| 11785 | 25110 | | 2.16 | 1.0E-02 | Q62203 | SWISSPROT | SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A68) |
| 11847 | 24862 | 30705 | 4.64 | 1.0E-02 | AW835521.1 | EST_HUMAN | RC2-DT0007-120200-018-H02 DT0007 Homo sapiens cDNA |
| 11861 | 24822 | | 6.07 | 1.0E-02 | S70330.1 | NT | Homo sapiens renal dipeptidase (RDP) gene, complete cds |
| 12254 | 24898 | | 1.53 | 1.0E-02 | AJ276505.1 | NT | Mus musculus genomic fragment, 279 Kb, chromosome 7 |
| 12422 | 24882 | | 4.42 | 1.0E-02 | X62854.1 | NT | H.sapiens gene for Me491/CD63 antigen |
| 928 | 13538 | 26057 | 3.16 | 9.0E-03 | A1798128.1 | EST_HUMAN | WH4209.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element |
| 1307 | 13901 | | 1.28 | 9.0E-03 | BE781889.1 | EST_HUMAN | MER22 MER22 repetitive element |
| 2439 | 15006 | 27578 | 3.82 | 9.0E-03 | AL161559.2 | NT | 601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5' |
| 2449 | 15016 | 27598 | 0.87 | 9.0E-03 | AF068634.1 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59 |
| 2831 | 15547 | 28022 | 0.61 | 9.0E-03 | AI251744.1 | EST_HUMAN | Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds |
| 2831 | 15547 | 28023 | 0.61 | 9.0E-03 | AI251744.1 | EST_HUMAN | qf60R09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3' |
| 3731 | 16332 | 28798 | 0.8 | 9.0E-03 | J05184.1 | NT | qf60R09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3' |
| 5978 | 18598 | | 1.17 | 9.0E-03 | AI809782.1 | EST_HUMAN | S.acidocalcaris thermopsis gene, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6741 | 19335 | | 4.24 | 9.0E-03 | BE745988.1 | EST_HUMAN | 601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834762 5' |
| 7487 | 20010 | 32876 | 0.79 | 9.0E-03 | 8822570 | NT | Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA |
| 7816 | 20359 | | 0.83 | 9.0E-03 | AL039891.1 | EST_HUMAN | DKFZp434L0412_1 434 (synonym: hbes3) Homo sapiens cDNA clone DKFZp434L0412 5' |
| 8191 | 20732 | | 0.56 | 9.0E-03 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 9759 | 22257 | 35240 | 0.5 | 9.0E-03 | P2601.1 | SWISSPROT | INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN) |
| 9778 | 22274 | 35258 | 1.26 | 9.0E-03 | P20908 | SWISSPROT | COLLAGEN ALPHA 1(V) CHAIN PRECURSOR |
| 10885 | 23386 | | 1.8 | 9.0E-03 | Y18000.1 | NT | Homo sapiens NF2 gene |
| 10891 | 23412 | 36431 | 1.71 | 9.0E-03 | BE395380.1 | EST_HUMAN | 601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632161 5' |
| 11505 | 23954 | 37022 | 1.58 | 9.0E-03 | L11144.1 | NT | Homo sapiens progesterone (GAL1) gene, exons 1, 2, and 3 |
| 11505 | 23954 | 37023 | 1.58 | 9.0E-03 | L11144.1 | NT | Homo sapiens progesterone (GAL1) gene, exons 1, 2, and 3 |
| 12001 | 25111 | | 1.79 | 9.0E-03 | BF351141.1 | EST_HUMAN | PM1-HT0452-291289-001-e09 HT0452 Homo sapiens cDNA |
| 12221 | 25105 | | 36.8 | 9.0E-03 | BE346385.1 | EST_HUMAN | hw17b09.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3' |
| 12319 | 24509 | 30943 | 1.38 | 9.0E-03 | AL163287.2 | NT | Homo sapiens chromosome 21 segment HS21C087 |
| 12539 | 24649 | | 31.87 | 9.0E-03 | BF351141.1 | EST_HUMAN | PM1-HT0452-291289-001-e09 HT0452 Homo sapiens cDNA |
| 527 | 13159 | | 2.87 | 8.0E-03 | AA723007.1 | EST_HUMAN | zh30e03.a1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:413598 3' similar to contains |
| 1028 | 13637 | 28152 | 35.57 | 8.0E-03 | AF108856.1 | NT | Alu repetitive element |
| 2203 | 14779 | 27351 | 1.26 | 8.0E-03 | AL163283.2 | NT | Homo sapiens adenylsuccinate lyase gene, complete cds |
| 3351 | 15959 | 28436 | 0.99 | 8.0E-03 | BE171225.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C083 |
| 3404 | 16013 | 28492 | 0.89 | 8.0E-03 | AJ131016.1 | NT | RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA |
| 3738 | 16339 | 28805 | 1.77 | 8.0E-03 | P32844 | SWISSPROT | Homo sapiens SCL gene locus |
| 3738 | 16339 | 28808 | 1.77 | 8.0E-03 | P32844 | SWISSPROT | HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION |
| 4343 | 16930 | 29371 | 1.19 | 8.0E-03 | BE840049.1 | EST_HUMAN | HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION |
| 4472 | 17058 | 29505 | 6.36 | 8.0E-03 | BF363327.1 | EST_HUMAN | QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA |
| 5378 | 17837 | 30350 | 1.02 | 8.0E-03 | U02970.1 | NT | CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA |
| 5410 | 17967 | 30376 | 0.88 | 8.0E-03 | P01871 | SWISSPROT | Prototheca wickerhamii 283-11 complete mitochondrial DNA |
| 5714 | 18340 | 30848 | 2.89 | 8.0E-03 | AF110520.1 | NT | IG MU CHAIN C REGION |
| 6346 | 24762 | 31730 | 1.34 | 8.0E-03 | AF000002.1 | NT | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, taspasin, RafGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial> |
| 6846 | 19436 | 32251 | 4.45 | 8.0E-03 | P55577 | SWISSPROT | Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (27) |
| 6999 | 19497 | | 1.72 | 8.0E-03 | V01108.1 | NT | PROBABLE PEPTIDASE Y4NA |
| 7259 | 19787 | 32843 | 1.8 | 8.0E-03 | M17197.1 | NT | Human BK virus (strain MM) genome. (Closely related to SV40.) |
| | | | | | | NT | A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7547 | 20067 | | 1.84 | 8.0E-03 | AB038267.1 | NT | Tursiops truncatus mRNA for p40-phox, complete cds |
| 8816 | 21355 | 34279 | 0.62 | 8.0E-03 | P08160 | SWISSPROT | BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN |
| 8841 | 21380 | 34304 | 3.73 | 8.0E-03 | AW808692.1 | EST_HUMAN | PRECURSOR (HSPG) (PERLECAN) (PLC) |
| 8910 | 21448 | 34370 | 0.68 | 8.0E-03 | 9789956 | NT | MR1-ST0111-111189-011-008 ST0111 Homo sapiens cDNA |
| 9859 | 22359 | | 4.78 | 8.0E-03 | BE086509.1 | EST_HUMAN | Mus musculus fusion 2 (human) (Fus2), mRNA |
| 10864 | 23385 | | 3.01 | 8.0E-03 | Z49652.1 | NT | QV1-BT0677-040-000-131-g03 BT0677 Homo sapiens cDNA |
| 11259 | 23789 | 36845 | 1.97 | 8.0E-03 | AA828817.1 | EST_HUMAN | S. cerevisiae chromosome X reading frame ORF YJR152w |
| 11259 | 23789 | 36846 | 1.97 | 8.0E-03 | AA828817.1 | EST_HUMAN | cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232 |
| 11562 | 24009 | 37079 | 4.96 | 8.0E-03 | AF084589.1 | NT | cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232 |
| 11713 | 24123 | | 2.81 | 8.0E-03 | M69035.1 | NT | Homo sapiens melanoma-associated antigen (IMAGE-C1) gene, complete cds |
| | | | | | | | Oryzias latipes curvulus eIF-2a kinase mRNA, complete cds |
| | | | | | | | Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds |
| 11761 | 24154 | | 5.99 | 8.0E-03 | AB039161.1 | NT | |
| 723 | 13343 | 25833 | 14.03 | 7.0E-03 | AF097183.1 | NT | Cryptosporidium parvum HC-10 gene, complete cds |
| 723 | 13343 | 25834 | 14.03 | 7.0E-03 | AF097183.1 | NT | Cryptosporidium parvum HC-10 gene, complete cds |
| 1012 | 13622 | 26137 | 5.78 | 7.0E-03 | AF243376.1 | NT | Glycine max glutathione S-transferase GST 21 mRNA, partial cds |
| 1155 | 13758 | 26268 | 3.21 | 7.0E-03 | AV731712.1 | EST_HUMAN | AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5' |
| | | | | | | | FORKHEAD BOX PROTEIN D3 (HNF3/TF TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE |
| 1408 | 14001 | | 1.28 | 7.0E-03 | Q61090 | SWISSPROT | NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HIF-2) |
| 1439 | 14032 | 26560 | 4.09 | 7.0E-03 | AA668286.1 | EST_HUMAN | ab78509.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3' |
| 1550 | 14142 | 26875 | 3.14 | 7.0E-03 | AW303596.1 | EST_HUMAN | ix21b02.x1 Soares_NFL_T_G8C.S1 Homo sapiens cDNA clone IMAGE:2813739 3' |
| 2287 | 15462 | 27447 | 2.12 | 7.0E-03 | P04929 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 3614 | 16217 | 28698 | 0.58 | 7.0E-03 | A1150273.1 | EST_HUMAN | q34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3' |
| 3830 | 16430 | 28892 | 0.91 | 7.0E-03 | AW444463.1 | EST_HUMAN | UHH-B13-akb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3' |
| | | | | | | | Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds |
| 3885 | 16483 | 28945 | 1.01 | 7.0E-03 | AF196344.1 | NT | UHH-B13-akb-c-10-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3' |
| 4091 | 16430 | 28992 | 0.63 | 7.0E-03 | AW444463.1 | EST_HUMAN | hn88a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869896 5' |
| 4704 | 17296 | | 1.1 | 7.0E-03 | AW630888.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C078 |
| 5125 | 17697 | | 2.08 | 7.0E-03 | AL163278.2 | NT | y82g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to |
| 5885 | 18605 | | 0.79 | 7.0E-03 | H71108.1 | EST_HUMAN | gb:X14723 CLUSTERIN PRECURSOR (HUMAN); |
| 6280 | 24760 | | 5.32 | 7.0E-03 | AW861059.1 | EST_HUMAN | RC1-CT0288-050400-018-c08 CT0288 Homo sapiens cDNA |
| 8458 | 19057 | 31842 | 1.45 | 7.0E-03 | W68251.1 | EST_HUMAN | z833f10.r1 Soares_fetal_heart_NH-H16W Homo sapiens cDNA clone IMAGE:342475 5' |
| 6658 | 19254 | 32056 | 2.98 | 7.0E-03 | AA327126.1 | EST_HUMAN | EST30874 Cdon1 Homo sapiens cDNA 5' end |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 6881 | 18277 | 32080 | 0.92 | 7.0E-03 | BE857385.1 | EST_HUMAN | 7q34b10.x1 NC1_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR-Q13387 |
| 7139 | 19519 | 32341 | 2.12 | 7.0E-03 | BE928133.1 | EST_HUMAN | Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.12 TAR1 repetitive element; |
| 7528 | 20049 | 32921 | 6.78 | 7.0E-03 | Z35838.1 | NT | CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA |
| 7528 | 20049 | 32922 | 5.78 | 7.0E-03 | Z35838.1 | NT | S.cerevisiae chromosome II reading frame ORF YBL077w |
| 7789 | 20332 | 33238 | 0.54 | 7.0E-03 | AJ28043.1 | NT | S.cerevisiae chromosome II reading frame ORF YBL077w |
| 7789 | 20332 | 33239 | 0.54 | 7.0E-03 | AJ28043.1 | NT | Homo sapiens 659 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3 |
| 8055 | 20597 | 33504 | 2.36 | 7.0E-03 | BE175687.1 | EST_HUMAN | Homo sapiens 659 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3 |
| 8318 | 21832 | | 0.6 | 7.0E-03 | AF111188.2 | NT | RCS-HT0582-160300-011-002 HT0582 Homo sapiens cDNA |
| 8513 | 22013 | 34972 | 0.87 | 7.0E-03 | NS2378.1 | EST_HUMAN | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| 8636 | 22136 | 35101 | 2.48 | 7.0E-03 | P48982 | SWISSPROT | Y149c10.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246068 3' similar to contains |
| 8636 | 22136 | 35102 | 2.48 | 7.0E-03 | P48982 | SWISSPROT | Alu repetitive element; |
| 10207 | 22702 | | 0.99 | 7.0E-03 | AV687379.1 | EST_HUMAN | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 10381 | 22875 | | 0.93 | 7.0E-03 | AI799794.1 | EST_HUMAN | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 10708 | 23235 | 36248 | 3.48 | 7.0E-03 | AB008852.1 | NT | AV687379 GKC Homo sapiens cDNA clone GKCAF007 5' |
| 10780 | 23304 | 36311 | 1.61 | 7.0E-03 | AJ004862.1 | NT | wc37c08.x1 NC1_CGAP_P728 Homo sapiens cDNA clone IMAGE:2320840 3' |
| 10780 | 23304 | 36312 | 1.61 | 7.0E-03 | AJ004862.1 | NT | Bos taurus mRNA for NDP52, complete cds |
| 10830 | 23448 | | 1.68 | 7.0E-03 | AJ242804.1 | NT | Homo sapiens partial MUC5B gene, exon 1-29 |
| 12273 | 25095 | | 1.83 | 7.0E-03 | H84085.1 | EST_HUMAN | Homo sapiens partial MUC5B gene, exon 1-29 |
| 12281 | 24484 | | 1.58 | 7.0E-03 | BE263253.1 | EST_HUMAN | Sporobolus stipticus mRNA for putative glycine and proline-rich protein |
| 12382 | 24549 | | 1.88 | 7.0E-03 | Y17455.1 | NT | Y115h01.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains |
| 12527 | 25082 | | 1.38 | 7.0E-03 | AL183300.2 | NT | Alu repetitive element |
| 12664 | 24734 | | 3.16 | 7.0E-03 | AW888110.1 | EST_HUMAN | 601145154F2 NIH_MGC, 19 Homo sapiens cDNA clone IMAGE:3160476 5' |
| 1283 | 13879 | 28400 | 10.8 | 6.0E-03 | AW511148.1 | EST_HUMAN | Homo sapiens LSFR2 gene, penultimate exon |
| 1283 | 13879 | 28401 | 10.8 | 6.0E-03 | AW511148.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21G100 |
| 2800 | 16352 | 27821 | 1.82 | 6.0E-03 | AF112374.1 | NT | RCD-SN0032-110400-021-e04 SN0032 Homo sapiens cDNA |
| 2916 | 15533 | 28004 | 3.54 | 6.0E-03 | AA759135.1 | EST_HUMAN | hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to |
| 2916 | 15533 | 28005 | 3.54 | 6.0E-03 | AA759135.1 | EST_HUMAN | SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR; |
| 3283 | 15894 | | 2.17 | 6.0E-03 | H76890.1 | EST_HUMAN | hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to |
| | | | | | | | SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR; |
| | | | | | | | Danio rerio odorant receptor gene cluster |
| | | | | | | | ah78a11.a1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3' |
| | | | | | | | ah78a11.a1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3' |
| | | | | | | | y77h04.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3344 | 15854 | | 0.79 | 6.0E-03 | AF180338.1 | NT | Notocarus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product |
| 3429 | 16037 | 28518 | 1.14 | 6.0E-03 | U90880.1 | NT | Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vesotocin genes, complete cds |
| 3429 | 16037 | 28519 | 1.14 | 6.0E-03 | U90880.1 | NT | Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vesotocin genes, complete cds |
| 3600 | 16204 | | 1.13 | 6.0E-03 | W37985.1 | EST_HUMAN | zc13a11.1 Soares parathyroid tumor NIH-HPA Homo sapiens cDNA clone IMAGE:322172 5' |
| 3721 | 16322 | 28789 | 2.6 | 6.0E-03 | BF510888.1 | EST_HUMAN | UHH-B14-epm-c06-D-U1.51 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3087754 3' |
| 3757 | 16358 | 28828 | 1.53 | 6.0E-03 | BE077356.1 | EST_HUMAN | RC1-B10606-200-400-014-a07 BT0606 Homo sapiens cDNA |
| 3945 | 16444 | 28905 | 1.14 | 6.0E-03 | 6754028 | NT | Mus musculus glucosamine-6-phosphate deaminase (Gnpi), mRNA |
| 3985 | 16583 | 29068 | 0.83 | 6.0E-03 | AW847284.1 | EST_HUMAN | RC0-CT0204-240889-021-b10 CT0204 Homo sapiens cDNA |
| 4030 | 16628 | | 0.92 | 6.0E-03 | BE250108.1 | EST_HUMAN | 600942804F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859513 5' |
| 4419 | 17004 | | 1.1 | 6.0E-03 | N58948.1 | EST_HUMAN | Y62H110.31 Soares multiple sclerosis 2Nbr-IMSP Homo sapiens cDNA clone IMAGE:278178 3' |
| 4454 | 17040 | | 1.58 | 6.0E-03 | A1016833.1 | EST_HUMAN | o3c11.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1639124 3' |
| 4805 | 17383 | 28633 | 8.21 | 6.0E-03 | AA324242.1 | EST_HUMAN | EST27116 Ceratium II Homo sapiens cDNA 5' end similar to EST containing Alu repeat |
| 5280 | 17832 | | 0.92 | 6.0E-03 | L34170.1 | NT | Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22 |
| 6301 | 24761 | 31680 | 0.72 | 6.0E-03 | 9827521 | NT | Varicella virus, complete genome |
| 6808 | 18840 | 32478 | 0.73 | 6.0E-03 | O14984 | SWISSPROT | SYNAPSIN III |
| 6839 | 18047 | 30469 | 0.72 | 6.0E-03 | BE253748.1 | EST_HUMAN | 601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5' |
| 7642 | 20154 | 33040 | 0.78 | 6.0E-03 | AF128894.1 | NT | Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds |
| 7774 | 20283 | 33180 | 24.22 | 6.0E-03 | AJ243211.1 | NT | Homo sapiens DMBT1 candidate tumor suppressor gene, exons 1 to 55 |
| 7799 | 20342 | 33251 | 6.91 | 6.0E-03 | A1033990.1 | EST_HUMAN | aw13604.x1 Soares parathyroid tumor NIH-HPA Homo sapiens cDNA clone IMAGE:1648670 3' similar to contains MER10.b1 MER10 repetitive element |
| 7915 | 20457 | 33363 | 2.45 | 6.0E-03 | AW798337.1 | EST_HUMAN | RC0-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA |
| 7980 | 20532 | | 1.59 | 6.0E-03 | BF038198.1 | EST_HUMAN | 601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5' |
| 9473 | 21872 | 34821 | 8.46 | 6.0E-03 | D10548.1 | NT | Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein |
| 9958 | 22451 | | 2.15 | 6.0E-03 | AJ432661.1 | EST_HUMAN | h22c02.x1 NCI CGAP K1f11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN |
| 10067 | 22582 | 35557 | 0.73 | 6.0E-03 | AJ011848.1 | NT | P40428 60S RIBOSOMAL PROTEIN L13A ; |
| | | | | | | NT | Bacillus subtilis ferD gene |
| 10197 | 22692 | | 0.91 | 6.0E-03 | AF084555.1 | NT | Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds |
| 10303 | 22797 | 35788 | 0.63 | 6.0E-03 | X68368.1 | NT | M.thermoformicum complete plasmid pFV1 DNA |
| 10623 | 23155 | 36168 | 2.04 | 6.0E-03 | AW982184.1 | EST_HUMAN | EST374237 MAGE reassortment, MAGG Homo sapiens cDNA |
| 10690 | 23220 | | 2.23 | 6.0E-03 | 11545814 | NT | Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10728 | 23252 | 36268 | 2.16 | 6.0E-03 | AI420786.1 | EST_HUMAN | ts01c12.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ; |
| 10728 | 23252 | 36270 | 2.16 | 6.0E-03 | AI420786.1 | EST_HUMAN | ts01c12.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ; |
| 10881 | 23382 | | 2.08 | 6.0E-03 | U14556.1 | NT | Mus musculus zinc-finger protein mRNA, complete cds |
| 10882 | 23383 | 36401 | 2.4 | 6.0E-03 | BE737865.1 | EST_HUMAN | 601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5' |
| 11630 | 24072 | 37134 | 1.57 | 6.0E-03 | H70298.1 | EST_HUMAN | yr05f01.11 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:213049 5' similar to SP:SPGD_PIG P14332 8-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING ; |
| 11828 | 24195 | | 3.52 | 6.0E-03 | AF010486.1 | NT | Rhodobacter capsulatus strain SB1003, partial genome |
| 11856 | 24848 | | 5.1 | 6.0E-03 | AE000833.1 | NT | Methanobacterium thermoautotrophicum from bases 428192 to 450296 (section 39 of 148) of the complete genome |
| 12038 | 24814 | | 3.02 | 6.0E-03 | U30780.1 | NT | Pneumocystis carinii f. sp. reitii guanine nucleotide binding protein alpha subunit (pgt1) gene, complete cds |
| 12088 | 24357 | | 1.81 | 6.0E-03 | Q62209 | SWISSPROT | SYNAPTOMEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN) |
| 12402 | 24581 | | 1.49 | 6.0E-03 | BE788019.1 | EST_HUMAN | 601482821F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5' |
| 12418 | 24571 | | 1.52 | 6.0E-03 | AJ245480.1 | NT | Brassica napus sgl gene for S-locus glycoprotein, cultivar T2 |
| 12556 | 24942 | | 1.6 | 6.0E-03 | X74807.1 | NT | R. norvegicus VEGP2 gene |
| 229 | 12889 | 25375 | 5.16 | 5.0E-03 | X87344.1 | NT | H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 687 | 13320 | 25806 | 1.73 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORF8; aminocycl-IRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds |
| 687 | 13320 | 25807 | 1.73 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORF8; aminocycl-IRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds |
| 688 | 13320 | 25806 | 2.74 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORF8; aminocycl-IRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds |
| 688 | 13320 | 25807 | 2.74 | 5.0E-03 | L25105.1 | NT | Chlamydia trachomatis partial ORF8; aminocycl-IRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds |
| 1151 | 13754 | 28264 | 0.91 | 5.0E-03 | AJ010457.1 | NT | Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3 |
| 2706 | 15263 | 27830 | 2.77 | 5.0E-03 | AB033008.1 | NT | Homo sapiens mRNA for KIAA1190 protein, partial cds |
| 2982 | 15578 | 28057 | 0.88 | 5.0E-03 | BE268057.1 | EST_HUMAN | 601194798F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538769 5' |
| 3170 | 15784 | 28256 | 4.54 | 5.0E-03 | T87823.1 | EST_HUMAN | yc81f09.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:22385 3' |
| 3188 | 15801 | | 2.22 | 5.0E-03 | AL161491.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3 |
| 3202 | 15814 | 28289 | 1.15 | 5.0E-03 | IR171794.1 | EST_HUMAN | y98g02.s1 Soares breast 2NH8st Homo sapiens cDNA clone IMAGE:155668 3' |
| 3316 | 15828 | | 0.88 | 5.0E-03 | AJ297357.1 | NT | Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3728 | 16328 | 28785 | 5.04 | 5.0E-03 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 3762 | 16303 | 28831 | 4.88 | 5.0E-03 | AF147449.2 | NT | Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 18 (penB) gene, complete cds |
| 3822 | 16422 | 28884 | 0.68 | 5.0E-03 | U36914.1 | NT | Citrus sinensis seed storage protein cDNA, complete cds |
| 4043 | 16841 | | 1.78 | 5.0E-03 | AA200875.1 | EST_HUMAN | EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end |
| 4204 | 16793 | 29239 | 0.57 | 5.0E-03 | AJ002125.1 | NT | Natrix domestica Zfx type gene |
| 4392 | 16978 | 29425 | 0.88 | 5.0E-03 | H78355.1 | EST_HUMAN | y478g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240068 5' |
| 4394 | 16422 | 28884 | 0.71 | 5.0E-03 | U36914.1 | NT | Citrus sinensis seed storage protein cDNA, complete cds |
| 4670 | 17252 | 29704 | 0.68 | 5.0E-03 | U46691.1 | NT | Human putative chromatin structure regulator (SUPT6H) mRNA, complete cds |
| 4714 | 17295 | 29739 | 0.8 | 5.0E-03 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 4828 | 17406 | 29860 | 1.72 | 5.0E-03 | A1752367.1 | EST_HUMAN | cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random |
| 5067 | 17840 | 30083 | 1.02 | 5.0E-03 | P15265 | SWISSPROT | SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS) |
| 5391 | 17949 | 30362 | 0.95 | 5.0E-03 | AF171688.1 | NT | Bos taurus acidic alpha-glucosidase gene, exons 2 through 20 and complete cds |
| 5664 | 18598 | 31320 | 7.68 | 5.0E-03 | P35500 | SWISSPROT | SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN) |
| | | | | | | | PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y-CHROMOSOME) |
| 6195 | 18805 | 31574 | 2.33 | 5.0E-03 | Q00507 | SWISSPROT | Chlamydia pneumoniae AR39, section 62 of 94 of the complete genome |
| 6230 | 18838 | | 0.91 | 5.0E-03 | AE002234.2 | NT | 600944504T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2880871 3' |
| 6708 | 18302 | | 10.88 | 5.0E-03 | BE300091.1 | EST_HUMAN | Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds |
| 6832 | 18040 | 30483 | 6.39 | 5.0E-03 | AB025024.1 | NT | Tursiops truncatus mRNA for p40-phox, complete cds |
| 7106 | 18446 | | 0.85 | 5.0E-03 | AB038267.1 | NT | RC3-CT0255-031099-011-407 CT0255 Homo sapiens cDNA |
| 7595 | 20109 | | 1.16 | 5.0E-03 | AW854327.1 | EST_HUMAN | Homo sapiens MASL1 mRNA, complete cds |
| 7744 | 20252 | 33146 | 7.43 | 5.0E-03 | AB016816.1 | NT | RC8-CT0281-081198-011-A05 CT0281 Homo sapiens cDNA |
| 8162 | 20703 | 33618 | 1 | 5.0E-03 | AW855907.1 | EST_HUMAN | RC8-CT0281-081198-011-A05 CT0281 Homo sapiens cDNA |
| 8162 | 20703 | 33619 | 1 | 5.0E-03 | AW855907.1 | EST_HUMAN | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 8181 | 20722 | 33636 | 2.28 | 5.0E-03 | P46882 | SWISSPROT | Mouse complement receptor (CR2) mRNA, 3' end |
| 8548 | 21087 | | 6.36 | 5.0E-03 | M61132.1 | NT | Escherichia coli genomic DNA. (19.1 - 19.4 min) |
| 8742 | 21281 | 34204 | 1.47 | 5.0E-03 | D90723.1 | NT | Rabbit uteroglobin (UGL) gene, exon 1 |
| 8870 | 21408 | 34333 | 0.69 | 5.0E-03 | M25090.1 | NT | SOF1 PROTEIN |
| 9503 | 22003 | 34960 | 0.45 | 5.0E-03 | P33750 | SWISSPROT | Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds |
| 9753 | 22251 | 35254 | 0.82 | 5.0E-03 | L21710.1 | NT | RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA |
| 9861 | 22378 | 35354 | 0.77 | 5.0E-03 | AW821888.1 | EST_HUMAN | RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA |
| 10062 | 22557 | 35552 | 0.49 | 5.0E-03 | AA533143.1 | EST_HUMAN | h46h10.s1 NCI_CGAP_P9 Homo sapiens cDNA clone IMAGE:985587 |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10238 | 22731 | 35722 | 0.92 | 5.0E-03 | 7882557 | NT | Homo sapiens PRO0471 protein (PRO0471), mRNA |
| 10599 | 23133 | | 10.33 | 5.0E-03 | T10598.1 | EST_HUMAN | 684F Heart Homo sapiens cDNA clone 894 |
| 10831 | 23183 | 36175 | 2.28 | 5.0E-03 | D28273.1 | NT | Unknown nitrogen-fixing bacteria nifD gene encoding alpha subunit of dinitrogenase (MoFe protein) |
| 10819 | 23340 | 36355 | 2.94 | 5.0E-03 | AW170334.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 10820 | 23439 | 36460 | 2.02 | 5.0E-03 | T49183.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 11212 | 23715 | | 3.91 | 5.0E-03 | BE048055.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 11972 | 25054 | | 8.12 | 5.0E-03 | AF047874.1 | NT | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 12111 | 24372 | | 21.73 | 5.0E-03 | AF067263.1 | NT | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 12217 | 24440 | | 1.81 | 5.0E-03 | L10347.1 | NT | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 12250 | 24461 | | 1.78 | 5.0E-03 | AA456597.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 12283 | 24558 | | 5.46 | 5.0E-03 | BF572332.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 12473 | 24598 | 30883 | 2.21 | 5.0E-03 | AW449109.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 12498 | 24832 | | 1.42 | 5.0E-03 | Q02388 | SWISSPROT | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 253 | 12913 | 25387 | 2.58 | 4.0E-03 | AW500198.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 343 | 12965 | 25480 | 1.77 | 4.0E-03 | R49482.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 468 | 13101 | 25594 | 0.89 | 4.0E-03 | P54675 | SWISSPROT | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 629 | 13258 | 25730 | 3.12 | 4.0E-03 | AA938339.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 910 | 13323 | 26043 | 1.75 | 4.0E-03 | R49482.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 944 | 13557 | | 3.19 | 4.0E-03 | AW749101.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 1180 | 13781 | 26302 | 25.91 | 4.0E-03 | AA088777.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 1211 | 13811 | 26325 | 1.71 | 4.0E-03 | AW784740.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 1346 | 13941 | 28463 | 1.4 | 4.0E-03 | AA284374.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 1630 | 14222 | | 1.06 | 4.0E-03 | AV708305.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 1770 | 14369 | 26913 | 2.74 | 4.0E-03 | U33472.1 | NT | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 2062 | 14842 | 27217 | 14.12 | 4.0E-03 | AA088777.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 2289 | 14863 | | 1.92 | 4.0E-03 | BE410556.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |
| 2317 | 14889 | 27484 | 2.83 | 4.0E-03 | AW784740.1 | EST_HUMAN | XR50G05.X1 Soares_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12 L1 repetitive element: |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2608 | 15170 | 27737 | 1.6 | 4.0E-03 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 2608 | 15170 | 27738 | 1.6 | 4.0E-03 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 2715 | 15272 | 27838 | 3.14 | 4.0E-03 | AJ277365.1 | NT | Homo sapiens polyglutamine-containing G14ORF4 gene |
| 2715 | 15272 | 27839 | 3.14 | 4.0E-03 | AJ277365.1 | NT | Homo sapiens polyglutamine-containing G14ORF4 gene |
| 2721 | 15277 | 27842 | 1.25 | 4.0E-03 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 3262 | 15874 | 28355 | 1.07 | 4.0E-03 | BE154134.1 | EST_HUMAN | PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA |
| 3262 | 15874 | 28356 | 1.07 | 4.0E-03 | BE154134.1 | EST_HUMAN | PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA |
| 3583 | 16187 | 28689 | 0.85 | 4.0E-03 | AW188426.1 | EST_HUMAN | x88804.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2685279 3' |
| 3583 | 16187 | 28670 | 0.85 | 4.0E-03 | AW188426.1 | EST_HUMAN | x88804.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2685279 3' |
| 3685 | 16286 | 28755 | 0.63 | 4.0E-03 | Q13606 | SWISSPROT | OLFACTORY RECEPTOR 51 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1) |
| 3698 | 16287 | 28767 | 0.63 | 4.0E-03 | AV646253.1 | EST_HUMAN | AV646253 GLC Homo sapiens cDNA clone GLC202 3' |
| 4067 | 16863 | | 1.93 | 4.0E-03 | AJ011712.1 | NT | Homo sapiens TNNT1 gene, exon 1-11 (and joined CDS) |
| 4323 | 16909 | 28350 | 1.88 | 4.0E-03 | AI786727.1 | EST_HUMAN | w87408.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2400274 3' |
| 5307 | 17899 | 30291 | 2.1 | 4.0E-03 | AW103719.1 | EST_HUMAN | x863403.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2814469 3' similar to contains L1.11 L1 |
| 5354 | 17814 | 30329 | 1.17 | 4.0E-03 | AA686995.1 | EST_HUMAN | L1 repetitive element |
| 6433 | 17899 | 30395 | 1.19 | 4.0E-03 | AL163284.2 | NT | z88601.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:438009 3' |
| 5480 | 18114 | 30523 | 1.36 | 4.0E-03 | AF005858.1 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 5598 | 18226 | 30873 | 21.16 | 4.0E-03 | AF169825.1 | NT | Drosophila melanogaster anon207 (anon207) mRNA, complete cds |
| 5983 | 18585 | 31319 | 3.31 | 4.0E-03 | P04186 | SWISSPROT | Rattus norvegicus beta-catenin binding protein mRNA, complete cds |
| 5985 | 18587 | 31321 | 1.56 | 4.0E-03 | P21849 | SWISSPROT | (HPRG) |
| 6042 | 18661 | 31400 | 0.97 | 4.0E-03 | AL133871.1 | EST_HUMAN | MAJOR SURFACE-LABELLED TROPHOZONTE ANTIGEN PRECURSOR |
| 6235 | 18844 | | 3.41 | 4.0E-03 | U22180.1 | NT | DKF7p7811014.1 781 (synonym: hamy2) Homo sapiens cDNA clone DKF7p7811014 5' |
| 6381 | 18985 | 31765 | 0.98 | 4.0E-03 | AW590572.1 | EST_HUMAN | Rattus norvegicus opsin gene, complete cds |
| 6451 | 19052 | 31837 | 1.95 | 4.0E-03 | BE548453.1 | EST_HUMAN | hg46c07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2948652 3' |
| 6775 | 19367 | 32179 | 1.04 | 4.0E-03 | AA813222.1 | EST_HUMAN | 601076019F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5' |
| 6872 | 19608 | 32440 | 1.51 | 4.0E-03 | U78408.1 | NT | ap32f11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1992045 3' |
| 7130 | 19470 | 32268 | 1.13 | 4.0E-03 | AL163278.2 | NT | Lycopodium obscurum knotted 3 protein (TKN3) mRNA, complete cds |
| 7130 | 19470 | 32269 | 1.13 | 4.0E-03 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 7249 | 19778 | 32633 | 6.45 | 4.0E-03 | Q02817 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C078 |
| | | | | | | | MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2) |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7459 | 19882 | 32847 | 1.14 | 4.0E-03 | AI681483.1 | EST_HUMAN | 537g12.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3' |
| 7461 | 19884 | 32849 | 0.95 | 4.0E-03 | BE670170.1 | EST_HUMAN | 7e31b02.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3' |
| 7883 | 20425 | 33334 | 0.83 | 4.0E-03 | Q9TT92 | SWISSPROT | ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) |
| 7882 | 20534 | 33438 | 4.22 | 4.0E-03 | AF111944.1 | NT | ADAMTS-5 (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11) |
| 8145 | 20688 | 33568 | 1.94 | 4.0E-03 | 7682087 | NT | Dicystallum discoidium AX4 development protein DG1122 (DG1122) gene, partial cds |
| 8848 | 21187 | 34105 | 8.89 | 4.0E-03 | AI553983.1 | EST_HUMAN | Homo sapiens KIAA0345 gene product (KIAA0345), mRNA |
| 8821 | 21360 | | 4.46 | 4.0E-03 | AL163209.2 | NT | te49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080013 3' similar to contains Alu repetitive element |
| 8830 | 21369 | 34293 | 3.12 | 4.0E-03 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C008 |
| 9840 | 22338 | 35319 | 0.78 | 4.0E-03 | H30684.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C078 |
| 10278 | 22773 | 35782 | 0.7 | 4.0E-03 | AL161555.2 | NT | yp42g12.11 Soares retina N2b5fR Homo sapiens cDNA clone IMAGE:190150 5' |
| 11008 | 23523 | 36557 | 6.06 | 4.0E-03 | AL163209.2 | NT | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55 |
| 11393 | 23845 | 36809 | 1.69 | 4.0E-03 | AL208703.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C006 |
| 11393 | 23846 | 36910 | 1.69 | 4.0E-03 | AL208703.1 | EST_HUMAN | qp56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839178 3' |
| 11807 | 24050 | 37116 | 1.62 | 4.0E-03 | AE002102.1 | NT | qp56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839178 3' |
| 11838 | 25071 | | 10.45 | 4.0E-03 | BE915173.1 | EST_HUMAN | Ureaplasma urealyticum section 3 of 59 of the complete genome |
| 11862 | 24284 | | 1.62 | 4.0E-03 | BE298290.1 | EST_HUMAN | PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA |
| 12047 | 24331 | | 2.71 | 4.0E-03 | AW504273.1 | EST_HUMAN | 801118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5' |
| 12294 | 24493 | | 3.86 | 4.0E-03 | BF224125.1 | EST_HUMAN | U1-HF-BND-9-04-0-U1.H1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5' |
| 12341 | 24975 | | 2.24 | 4.0E-03 | AW614598.1 | EST_HUMAN | 7q74c08.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element; contains element MER31 repetitive element; |
| 12352 | 24532 | | 3.01 | 4.0E-03 | AW819141.1 | EST_HUMAN | HN02c07.x1 NC1_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element; |
| 394 | 13040 | 25531 | 1.73 | 3.0E-03 | AF011920.1 | NT | RC3-ST0281-240400-015-f03 S10281 Homo sapiens cDNA |
| 912 | 13525 | 26044 | 5.57 | 3.0E-03 | AF011920.1 | NT | Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1 |
| 1701 | 14294 | 26829 | 2.85 | 3.0E-03 | AA468110.1 | EST_HUMAN | Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1 |
| 2288 | 14871 | | 1.78 | 3.0E-03 | AF055088.1 | NT | nc73c05.s1 NC1_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element; |
| 2333 | 14904 | | 4.14 | 3.0E-03 | Z32521.1 | NT | Homo sapiens MHC class 1 region |
| 2334 | 14905 | 27476 | 1.03 | 3.0E-03 | U46858.1 | NT | S.cereale (cv. Halo) mRNA for triosephosphate isomerase |
| 2334 | 14905 | 27476 | 1.03 | 3.0E-03 | U46858.1 | NT | Mus musculus intestinal trefoil factor gene, partial cds |
| 2448 | 15015 | 27587 | 1.13 | 3.0E-03 | AF240786.1 | NT | Mus musculus intestinal trefoil factor gene, partial cds |
| | | | | | | | Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds |

Table 4

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| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3022 | 15638 | | 0.66 | 3.0E-03 | Y08006.1 | NT | Arabidopsis thaliana rpoMt gene |
| 3119 | 15733 | 28203 | 3.26 | 3.0E-03 | BE379286.1 | EST_HUMAN | 601237882F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3008933 5' |
| 3186 | 15798 | 28270 | 3.21 | 3.0E-03 | AW802887.1 | EST_HUMAN | IL2-UM0078-240300-056-D03 UM0078 Homo sapiens cDNA |
| 3464 | 16071 | 28544 | 2.13 | 3.0E-03 | U34608.1 | NT | Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2 |
| 3473 | 16079 | | 7.31 | 3.0E-03 | Y12500.1 | NT | C.elegans samdc gene |
| 4049 | 16846 | 28114 | 7.57 | 3.0E-03 | AV762382.1 | EST_HUMAN | AV762382 MDS Homo sapiens cDNA clone MDSBSG01 5' |
| 4049 | 16846 | 28115 | 7.57 | 3.0E-03 | AV762382.1 | EST_HUMAN | AV762382 MDS Homo sapiens cDNA clone MDSBSG01 5' |
| 4109 | 16703 | 28158 | 1.75 | 3.0E-03 | AI792278.1 | EST_HUMAN | af04f09.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155889 5' |
| 4485 | 17070 | 28520 | 6.2 | 3.0E-03 | AJ011432.1 | NT | Rattus norvegicus gdnf gene |
| 4580 | 17143 | | 0.71 | 3.0E-03 | BE348738.1 | EST_HUMAN | h88g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151834 3' |
| 4616 | 17169 | 28647 | 5.79 | 3.0E-03 | AI538141.1 | EST_HUMAN | ab18a08.x5 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element |
| 4680 | 17535 | 28977 | 2.45 | 3.0E-03 | AI732754.1 | EST_HUMAN | 601482719F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5' |
| 4978 | 17553 | 28996 | 6.1 | 3.0E-03 | BE787845.1 | EST_HUMAN | Oryctolagus cuniculus sod gene |
| 5069 | 17642 | 30084 | 1.01 | 3.0E-03 | AJ007044.1 | NT | Oryctolagus cuniculus sod gene |
| 5069 | 17642 | 30085 | 1.01 | 3.0E-03 | AJ007044.1 | NT | Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA |
| 5470 | 18104 | 30423 | 3.56 | 3.0E-03 | 8822498 | NT | Mus musculus mRNA for hypothetical protein (ORF2 ortholog) |
| 5744 | 18370 | 31078 | 1.18 | 3.0E-03 | AJ248081.1 | NT | Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds |
| 5809 | 18434 | 31155 | 13.97 | 3.0E-03 | U35323.1 | NT | aat13f10.r1 Soares_NIH-IMPu_S1 Homo sapiens cDNA clone IMAGE:813183 5' |
| 6670 | 19268 | 32070 | 10.41 | 3.0E-03 | AA456701.1 | EST_HUMAN | Kluyveromyces marianus pop3 gene for purine-cytosine permease |
| 7256 | 19784 | 32640 | 1.45 | 3.0E-03 | AJ011418.1 | NT | Oryza sativa gene for bZIP protein, complete cds |
| 7531 | 20051 | 32824 | 3.37 | 3.0E-03 | AB021736.1 | NT | RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA |
| 7879 | 20421 | 33329 | 0.91 | 3.0E-03 | BF333058.1 | EST_HUMAN | RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA |
| 7879 | 20421 | 33330 | 0.91 | 3.0E-03 | BF333058.1 | EST_HUMAN | z627b04.s1 Soares_papillary tumor_NHPPA Homo sapiens cDNA clone IMAGE:304783 3' |
| 8097 | 20638 | 33549 | 4.71 | 3.0E-03 | N82580.1 | EST_HUMAN | S.cerevisiae UGA35 gene, complete cds |
| 8257 | 20788 | | 0.55 | 3.0E-03 | M63488.1 | NT | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A)) |
| 8397 | 20837 | 33860 | 1.11 | 3.0E-03 | P51989 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C088 |
| 8419 | 20859 | 33877 | 1.31 | 3.0E-03 | AL163268.2 | NT | NONSTRUCTURAL PROTEIN V |
| 8522 | 21061 | | 1.37 | 3.0E-03 | O8QM81 | SWISSPROT | h88f010.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2889131 3' similar to contains L1.11 L1 repetitive element |
| 8922 | 21460 | | 12.62 | 3.0E-03 | AW813774.1 | EST_HUMAN | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85 |
| 8976 | 21513 | 34436 | 4.44 | 3.0E-03 | AL161589.2 | NT | |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8969 | 21536 | 34486 | 8.98 | 3.0E-03 | A018731.1 | EST_HUMAN | 0403d12x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:57138_mna1 |
| 9008 | 21545 | 34474 | 0.82 | 3.0E-03 | BF338078.1 | EST_HUMAN | HISTONE H2B.2 (HUMAN); |
| 9030 | 21844 | | 1 | 3.0E-03 | D00001.1 | NT | 8020359880F1 NCI_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4183638 5' |
| 9068 | 20307 | 33210 | 0.86 | 3.0E-03 | BE154670.1 | EST_HUMAN | Synchocystis sp. PCC8803 complete genome, 3/27, 271600-402289 |
| 9554 | 22054 | | 0.87 | 3.0E-03 | P03355 | SWISSPROT | PM3-HT0344-071289-003-407 HT0344 Homo sapiens cDNA |
| 9823 | 22123 | | 5.92 | 3.0E-03 | P08672 | SWISSPROT | POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H] |
| | | | | | | | CIRCUMSPOROITE PROTEIN PRECURSOR (CS) |
| | | | | | | | RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; |
| | | | | | | | ENDONUCLEASE] |
| 9809 | 22307 | 35281 | 1.98 | 3.0E-03 | P11369 | SWISSPROT | |
| 9907 | 22404 | 35379 | 1.3 | 3.0E-03 | P51889 | SWISSPROT | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A)) |
| 10048 | 22541 | 35538 | 3.96 | 3.0E-03 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 10728 | 23254 | | 4.26 | 3.0E-03 | 5903028 | NT | Homo sapiens ATP/GTP-binding protein (HEAB), mRNA |
| 11257 | 23787 | 36843 | 2.21 | 3.0E-03 | AF008222.1 | NT | Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds |
| 11321 | 23019 | 36028 | 1.99 | 3.0E-03 | AF266285.1 | NT | Homo sapiens goggin-like protein (GLP) gene, complete cds |
| 11354 | 23808 | 36887 | 3.96 | 3.0E-03 | AF094481.1 | NT | Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds |
| 11354 | 23808 | 36888 | 3.96 | 3.0E-03 | AF094481.1 | NT | Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds |
| 11707 | 24869 | | 2.32 | 3.0E-03 | AI525058.1 | EST_HUMAN | prmrna-5.E07.1 brtumor Homo sapiens cDNA 5' |
| | | | | | | | cd77b10.s1 Soares_tetel_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to |
| | | | | | | | contains L1.13 MER26 repetitive element; |
| 11743 | 24142 | 36763 | 1.31 | 3.0E-03 | AA983154.1 | EST_HUMAN | Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds |
| 11804 | 25007 | | 1.81 | 3.0E-03 | AB009688.1 | NT | Rattus norvegicus mRNA for connexin36 (cx36 gene) |
| 11898 | 24298 | 30884 | 2.87 | 3.0E-03 | AJ286282.1 | NT | |
| 541 | 13172 | 25651 | 0.8 | 2.0E-03 | Q04652 | SWISSPROT | RING CANAL PROTEIN (KELCH PROTEIN) |
| 541 | 13172 | 25652 | 0.8 | 2.0E-03 | Q04652 | SWISSPROT | RING CANAL PROTEIN (KELCH PROTEIN) |
| 818 | 15426 | | 11.05 | 2.0E-03 | T70874.1 | EST_HUMAN | Yd15H03.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5' |
| 1407 | 14000 | 26529 | 2.25 | 2.0E-03 | M20783.1 | NT | Human alpha-2-plasmin inhibitor gene, exons 6 and 7 |
| 1410 | 14003 | 26531 | 1.35 | 2.0E-03 | AA661805.1 | EST_HUMAN | nu8801.s1 NCI_CGAP_Av1 Homo sapiens cDNA clone IMAGE:1217563 |
| 1418 | 14011 | 26540 | 20.98 | 2.0E-03 | AF284448.1 | NT | Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds |
| | | | | | | | PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN |
| | | | | | | | SFA-1) (CD151 ANTIGEN) |
| 1528 | 14128 | 26884 | 1.04 | 2.0E-03 | P48509 | SWISSPROT | Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome |
| | | | | | | | type VI) (PLOD) mRNA |
| 1563 | 14155 | 26886 | 2.05 | 2.0E-03 | 4557836 | NT | Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome |
| 1563 | 14155 | 26887 | 2.05 | 2.0E-03 | 4557836 | NT | type VI) (PLOD) mRNA |
| 1635 | 14277 | | 5.58 | 2.0E-03 | P28400 | SWISSPROT | COLLAGEN ALPHA 5(V) CHAIN PRECURSOR |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1807 | 14397 | 28942 | 1.01 | 2.0E-03 | AA450138.1 | EST_HUMAN | z42a10.1 Soares total_fetus Nb2-IF8_9w Homo sapiens cDNA clone IMAGE:789114 5' |
| 1922 | 14507 | | 0.89 | 2.0E-03 | BE144908.1 | EST_HUMAN | CM2-HT0183-061089-018-d03 HT0183 Homo sapiens cDNA |
| 2038 | 14620 | 27188 | 1.25 | 2.0E-03 | AF302891.1 | NT | Mus musculus myelin expression factor-3-like protein gene, partial cds |
| 2291 | 14885 | 27440 | 0.97 | 2.0E-03 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 2815 | 15177 | | 4.13 | 2.0E-03 | AW137782.1 | EST_HUMAN | UI-H-B11-adi-g-10-0-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3' |
| 3463 | 16070 | 28543 | 4.95 | 2.0E-03 | AA450138.1 | EST_HUMAN | z42a10.1 Soares total_fetus Nb2-IF8_9w Homo sapiens cDNA clone IMAGE:789114 5' |
| 3470 | 16076 | 28549 | 0.76 | 2.0E-03 | BF568955.1 | EST_HUMAN | 602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3' |
| 3729 | 16330 | 28798 | 6.87 | 2.0E-03 | X87344.1 | NT | H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 4024 | 16622 | 28084 | 0.89 | 2.0E-03 | AB040802.1 | NT | Rattus norvegicus mRNA for SREB1, complete cds |
| 4191 | 16780 | 29228 | 2.48 | 2.0E-03 | P03374 | SWISSPROT | ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52, COAT PROTEIN GP36] |
| 4302 | 16888 | | 12.85 | 2.0E-03 | U68491.1 | NT | Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds |
| 4502 | 17088 | | 1.09 | 2.0E-03 | L35078.1 | NT | Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds |
| 4518 | 17102 | | 1.34 | 2.0E-03 | AW297380.1 | EST_HUMAN | UI-H-BW0-ar-g-03-0-UI.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3' |
| 4523 | 17107 | 29553 | 0.96 | 2.0E-03 | A1084746.1 | EST_HUMAN | HA0507 Human fetal liver cDNA library Homo sapiens cDNA |
| 4844 | 17228 | 29680 | 1.82 | 2.0E-03 | L42512.1 | NT | Drosophila melanogaster shorttailed class 2 (shc) mRNA, complete cds |
| 4844 | 17228 | 29681 | 1.82 | 2.0E-03 | L42512.1 | NT | Drosophila melanogaster shorttailed class 2 (shc) mRNA, complete cds |
| 4821 | 17399 | | 1.92 | 2.0E-03 | R87773.1 | EST_HUMAN | yo45e02 s1 Soares adult brain N2b4HBS5Y Homo sapiens cDNA clone IMAGE:1803890 3' |
| 4848 | 17426 | 29878 | 5.2 | 2.0E-03 | AA908488.1 | EST_HUMAN | d14f05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1523457 3' |
| 5167 | 17738 | 30163 | 0.81 | 2.0E-03 | AF003528.1 | NT | Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 5428 | 17885 | | 0.9 | 2.0E-03 | AF205067.1 | NT | Desulfovibrio desulfuricans cytochrome c3 precursor (cycA) gene, complete cds |
| 5678 | 18305 | 30787 | 1.16 | 2.0E-03 | BF241410.1 | EST_HUMAN | 601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104892 5' |
| 5810 | 24749 | 31158 | 2.28 | 2.0E-03 | AB014583.1 | NT | Homo sapiens mRNA for KIAA0683 protein, partial cds |
| 5887 | 18510 | 31238 | 2.11 | 2.0E-03 | U63711.1 | NT | Xenopus laevis xellitin mRNA, complete cds |
| 6258 | 18967 | 31636 | 4.06 | 2.0E-03 | P23477 | SWISSPROT | ATP-DEPENDENT NUCLEASE SUBUNIT B |
| 6258 | 18967 | 31637 | 4.06 | 2.0E-03 | P23477 | SWISSPROT | ATP-DEPENDENT NUCLEASE SUBUNIT B |
| 6488 | 19087 | 31689 | 2.98 | 2.0E-03 | Q96203 | SWISSPROT | CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XI) |
| 6488 | 19087 | 31870 | 2.98 | 2.0E-03 | Q96203 | SWISSPROT | CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XI) |
| 6488 | 19089 | 31972 | 7 | 2.0E-03 | BF308187.1 | EST_HUMAN | 601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5' |
| 6521 | 19121 | 31912 | 2.17 | 2.0E-03 | Q8UKP4 | SWISSPROT | ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAM-TS7) |
| 6546 | 19144 | 31940 | 1.46 | 2.0E-03 | X94451.1 | NT | L. esculentum mRNA for lysyl-tRNA synthetase (LysRS) |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6715 | 19309 | | 2.03 | 2.0E-03 | AB991089.1 | EST_HUMAN | wu36109.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW RL28_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 : contains element MSR1 repetitive element : |
| 7038 | 18058 | 30480 | 0.99 | 2.0E-03 | AB038502.1 | NT | Caenorhabditis elegans mRNA for galectin LEC-11, complete cds |
| 7104 | 19874 | 32513 | 1.54 | 2.0E-03 | 5031884 | NT | Homo sapiens lipoma HMIGIC fusion partner (LHFP) mRNA |
| 7104 | 19874 | 32514 | 1.54 | 2.0E-03 | 5031884 | NT | Homo sapiens lipoma HMIGIC fusion partner (LHFP) mRNA |
| 7141 | 19521 | 32343 | 3.59 | 2.0E-03 | BE067986.1 | EST_HUMAN | CMA-BT0368-061290-054-d01 BT0368 Homo sapiens cDNA |
| 7198 | 19729 | 32590 | 0.7 | 2.0E-03 | AI298883.1 | EST_HUMAN | qim9d11.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896885 3' |
| 7335 | 19882 | 32726 | 0.87 | 2.0E-03 | T86569.1 | EST_HUMAN | yd77g10.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:114306 5' |
| 7613 | 20128 | 33003 | 1.49 | 2.0E-03 | P07354 | SWISSPROT | PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN)(LP) |
| 7895 | 20537 | 33440 | 2.47 | 2.0E-03 | AW592004.1 | EST_HUMAN | h97b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR:Q60978 |
| 8159 | 20700 | 33814 | 5.98 | 2.0E-03 | N20287.1 | EST_HUMAN | Q60978.JERKY. ; yk42g08.s1 Soares melanocyte 2NfLHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element ; |
| 8159 | 20700 | 33815 | 5.98 | 2.0E-03 | N20287.1 | EST_HUMAN | yk42g08.s1 Soares melanocyte 2NfLHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2 L1 repetitive element ; |
| 8208 | 20749 | 33682 | 0.52 | 2.0E-03 | Q92350 | SWISSPROT | HYPOTHETICAL 32.8 KD PROTEIN O6G9.05 IN CHROMOSOME 1 |
| 8228 | 20789 | 33688 | 0.94 | 2.0E-03 | P19137 | SWISSPROT | LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) |
| 8262 | 20823 | 33743 | 0.82 | 2.0E-03 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 8282 | 20823 | 33744 | 0.82 | 2.0E-03 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 8307 | 20848 | 33771 | 0.8 | 2.0E-03 | AU136678.1 | EST_HUMAN | AU136678 PLACE1 Homo sapiens cDNA clone IMAGE:1004638 5' |
| 8358 | 20898 | | 2.04 | 2.0E-03 | AJ400877.1 | NT | Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene |
| 9123 | 18508 | 31253 | 0.89 | 2.0E-03 | AW798111.1 | EST_HUMAN | MR2-UM0025-300300-102-602 UM0025 Homo sapiens cDNA |
| 9123 | 18508 | 31254 | 0.89 | 2.0E-03 | AW798111.1 | EST_HUMAN | MR2-UM0025-300300-102-602 UM0025 Homo sapiens cDNA |
| 9164 | 21699 | 34843 | 0.85 | 2.0E-03 | AF224689.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 9445 | 21871 | 34820 | 0.99 | 2.0E-03 | H50832.1 | EST_HUMAN | yp88a09.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:184296 3' |
| 9445 | 21871 | 34821 | 0.99 | 2.0E-03 | H50832.1 | EST_HUMAN | yp88a09.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:184296 3' |
| | | | | | | | TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GNEM) (J1) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C) |
| 9477 | 21876 | 34823 | 2.57 | 2.0E-03 | P24821 | SWISSPROT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 9585 | 22085 | 35049 | 1.03 | 2.0E-03 | P48982 | SWISSPROT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |
| 9585 | 22085 | 35050 | 1.03 | 2.0E-03 | P48982 | SWISSPROT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8638 | 22139 | 35105 | 0.54 | 2.0E-03 | AF097732.1 | NT | Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds |
| 8639 | 22139 | 35106 | 0.54 | 2.0E-03 | AF097732.1 | NT | Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds |
| 8628 | 22327 | 35308 | 0.98 | 2.0E-03 | AW884288.1 | EST_HUMAN | QV3-OT0064-060400-144-e01 OT0064 Homo sapiens cDNA |
| 8655 | 22450 | | 4.55 | 2.0E-03 | AA261378.1 | EST_HUMAN | zs10s06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684764 3' |
| 10894 | 23415 | | 3.24 | 2.0E-03 | M86524.1 | NT | Human dystrophin gene |
| 11361 | 20126 | 33003 | 2.13 | 2.0E-03 | P07354 | SWISSPROT | PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP) |
| 11417 | 23868 | | 2.25 | 2.0E-03 | BF330609.1 | EST_HUMAN | RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA |
| 11424 | 23875 | 36939 | 13.97 | 2.0E-03 | Z11740.1 | NT | H. sapiens variable number tandem repeat (VNTR) locus DNA |
| 11687 | 24103 | | 3.17 | 2.0E-03 | A025745.1 | EST_HUMAN | IMAGE103.Y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283880 3' similar to SW:VATG_MANSE |
| 11705 | 24118 | 37151 | 4.77 | 2.0E-03 | AF157516.2 | NT | Q25532 VAGUOLAR ATP SYNTHASE SUBUNIT G ; Homo sapiens SEL1L (SEL1L) gene, partial cds |
| 11730 | 24135 | 37155 | 1.94 | 2.0E-03 | A084325.1 | EST_HUMAN | oy43g08.s1 Soares_parathyroid_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1688634 3' similar to |
| 11754 | 18032 | | 8.96 | 2.0E-03 | AJ245167.1 | NT | TR-P07535 P07535 PS-PLA1 PRECURSOR ; |
| 11867 | 25050 | | 2.34 | 2.0E-03 | AV697866.1 | EST_HUMAN | Carnellus dromedarius cnp19 gene for immunoglobulin heavy chain variable region |
| 12062 | 24345 | 30864 | 1.49 | 2.0E-03 | Y00508.1 | NT | AV697868 GKC Homo sapiens cDNA clone GKGXGD05 5' H. sapiens M1 gene for muscarinic acetylcholine receptor |
| 12372 | 24542 | | 2.06 | 2.0E-03 | AF129756.1 | NT | Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, |
| 12551 | 24949 | | 5.07 | 2.0E-03 | AV697868.1 | EST_HUMAN | CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds |
| 464 | 13098 | 25598 | 1.33 | 1.0E-03 | H96471.1 | EST_HUMAN | AV697868 GKC Homo sapiens cDNA clone GKGXGD05 5' y68c08.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5' |
| 862 | 13477 | 25902 | 1.47 | 1.0E-03 | A1720283.1 | EST_HUMAN | as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 |
| 862 | 13477 | 25903 | 1.47 | 1.0E-03 | A1720283.1 | EST_HUMAN | Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE ; |
| 1134 | 13737 | 26246 | 2.21 | 1.0E-03 | A085788.1 | EST_HUMAN | as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 |
| 1154 | 13757 | 26267 | 1.31 | 1.0E-03 | A054572.1 | EST_HUMAN | Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE ; |
| 1208 | 13808 | 26321 | 1.67 | 1.0E-03 | A082616.1 | EST_HUMAN | w486a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3' |
| 2074 | 14654 | 27227 | 4.05 | 1.0E-03 | P47808 | SWISSPROT | w486a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3' |
| 2189 | 14775 | 27348 | 9.98 | 1.0E-03 | AJ131016.1 | NT | w486a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3' |
| 3008 | 15624 | 28102 | 1.45 | 1.0E-03 | AB033117.1 | NT | w486a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3' |
| 3225 | 15837 | 28315 | 1.81 | 1.0E-03 | P18815 | SWISSPROT | w486a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3' w486a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3' repetitive element. HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMYWI) Homo sapiens SCL gene locus Homo sapiens mRNA for KIAA1281 protein, partial cds CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED) CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE) |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3225 | 18837 | 28316 | 1.81 | 1.0E-03 | P18915 | SWISSPROT | CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED) |
| 3341 | 15951 | 28427 | 0.79 | 1.0E-03 | P08547 | SWISSPROT | CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE) |
| 3598 | 18200 | 28683 | 0.65 | 1.0E-03 | U68081.1 | NT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 3598 | 18200 | 28684 | 0.65 | 1.0E-03 | U68081.1 | NT | Human MUC2 gene, promoter region |
| 3727 | 18328 | | 1.31 | 1.0E-03 | AB044400.1 | NT | Human MUC2 gene, promoter region |
| 3997 | 16595 | 28087 | 0.75 | 1.0E-03 | AW170532.1 | EST_HUMAN | Human sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15 |
| 4008 | 16606 | 28080 | 0.81 | 1.0E-03 | Z48649.1 | NT | xr63d07.x1 Soares_NHCC cervical tumor Homo sapiens cDNA clone IMAGE:269381 3' similar to |
| 4528 | 17112 | 28666 | 4.29 | 1.0E-03 | BE930162.1 | EST_HUMAN | contains TAR1.11 TAR1 repetitive element; |
| 4574 | 17157 | 28801 | 5.77 | 1.0E-03 | BE246538.1 | EST_HUMAN | S. cerevisiae chromosome X reading frame ORF YJR149w |
| 4770 | 17351 | 28803 | 0.83 | 1.0E-03 | U28449.1 | NT | RC1-TN0128-180800-021-g01 TN0128 Homo sapiens cDNA |
| 4850 | 17525 | 28888 | 2.83 | 1.0E-03 | A073485.1 | EST_HUMAN | TCBAP1D4809 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo |
| 4850 | 17525 | 28887 | 2.83 | 1.0E-03 | A073485.1 | EST_HUMAN | sapiens cDNA clone TCBAF-4809 |
| 4851 | 17528 | | 5.92 | 1.0E-03 | BE154087.1 | EST_HUMAN | Casorhabdilis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes |
| 5236 | 17800 | 30219 | 11.45 | 1.0E-03 | Q48408 | SWISSPROT | ow45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3' |
| 5511 | 18144 | 30556 | 2.02 | 1.0E-03 | AA280951.1 | EST_HUMAN | ow45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3' |
| 5598 | 18228 | 30878 | 2.74 | 1.0E-03 | AJ008345.1 | NT | PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA |
| 5847 | 18275 | 30749 | 1.7 | 1.0E-03 | K03332.1 | NT | APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) |
| 5847 | 18275 | 30750 | 1.7 | 1.0E-03 | K03332.1 | NT | zs44f01.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5' |
| 5761 | 18387 | 31101 | 0.92 | 1.0E-03 | BE708491.1 | EST_HUMAN | Homo sapiens KVLQ11 gene |
| 5766 | 18392 | 31105 | 1.72 | 1.0E-03 | Q02388 | SWISSPROT | Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds |
| 6171 | 18783 | | 2.62 | 1.0E-03 | X07699.1 | NT | Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds |
| 6209 | 18819 | 31580 | 1.1 | 1.0E-03 | BE983839.2 | EST_HUMAN | COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) |
| 6339 | 18945 | | 8.29 | 1.0E-03 | 11828178 | NT | Mouse nucleolin gene |
| 6476 | 19077 | 31860 | 1.21 | 1.0E-03 | T87761.1 | EST_HUMAN | 801657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3' |
| 6541 | 19140 | | 1.4 | 1.0E-03 | AW002585.1 | EST_HUMAN | Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA |
| 6852 | 19441 | 32258 | 1.31 | 1.0E-03 | L77570.1 | NT | y483a11.1 Soares fetal liver spleen TINF5 Homo sapiens cDNA clone IMAGE:115772 5' |
| 7206 | 19737 | 32580 | 2.48 | 1.0E-03 | D16828.1 | NT | QV3-NN1024-280400-171-g05 NN1024 Homo sapiens cDNA |
| 7498 | 20021 | | 1.72 | 1.0E-03 | AJ28042.1 | NT | Homo sapiens D3George syndrome critical region, centromeric end |
| | | | | | | NT | Human gene for fourth somatostatin receptor subtype |
| | | | | | | NT | Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3 |
| | | | | | | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 7635 | 20147 | 33030 | 1.7 | 1.0E-03 | U52111.2 | NT | |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7694 | 20203 | 33090 | 3.21 | 1.0E-03 | M63376.1 | NT | Human TRPM-2 protein gene, exons 1,2 and 3 |
| 7734 | 20242 | 33133 | 1.13 | 1.0E-03 | BE88044.1 | EST_HUMAN | 601461061F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893276 5' |
| 7830 | 20372 | 33279 | 0.57 | 1.0E-03 | AF274591.1 | NT | Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region |
| 7891 | 20433 | 33342 | 5.79 | 1.0E-03 | AJ261973.1 | NT | Homo sapiens partial steerin-1 gene |
| 8086 | 20627 | 33541 | 1.29 | 1.0E-03 | AA122270.1 | EST_HUMAN | z697c09.s1 Soares_pregnant_uterus_NH-IPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.1 L1 repetitive element; |
| 8186 | 20727 | 33639 | 2.03 | 1.0E-03 | AF153080.1 | NT | Homo sapiens exocyst-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds |
| 8369 | 20908 | 33828 | 0.81 | 1.0E-03 | U28397.1 | NT | Rattus norvegicus plasma membrane Ca ²⁺ ATPase isoform 3 (PMCA3) gene, 5' flanking region |
| 8530 | 21069 | 33968 | 0.52 | 1.0E-03 | AA001613.1 | EST_HUMAN | z82608.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3' |
| 8530 | 21069 | 33969 | 0.52 | 1.0E-03 | AA001613.1 | EST_HUMAN | z82608.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3' |
| 8873 | 21412 | | 1.29 | 1.0E-03 | Y11204.1 | NT | V. carteri gene encoding volvoxapain |
| 8900 | 21438 | 34361 | 0.59 | 1.0E-03 | AW840353.1 | EST_HUMAN | CM3-LT0079-170200-092-07 LT0079 Homo sapiens cDNA |
| 9008 | 21546 | | 0.68 | 1.0E-03 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca ²⁺ /calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 9047 | 21594 | 34514 | 3.37 | 1.0E-03 | M30471.1 | NT | Human class III alcohol dehydrogenase (ADH5) cH1 subunit mRNA, complete cds |
| 9047 | 21594 | 34515 | 3.37 | 1.0E-03 | M30471.1 | NT | Human class III alcohol dehydrogenase (ADH5) cH1 subunit mRNA, complete cds |
| 9525 | 22025 | 34882 | 1.98 | 1.0E-03 | AF011400.1 | NT | Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds |
| 9525 | 22025 | 34883 | 1.98 | 1.0E-03 | AF011400.1 | NT | Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds |
| 9734 | 22232 | 35210 | 0.94 | 1.0E-03 | Q01129 | SWISSPROT | BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG-40) (DERMATAN SULFATE) |
| 10068 | 22583 | 35558 | 0.57 | 1.0E-03 | AF003529.1 | NT | Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions |
| 10073 | 22598 | | 0.75 | 1.0E-03 | AF067485.1 | NT | Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds |
| 10218 | 22713 | 35705 | 1.25 | 1.0E-03 | AJ024350.1 | EST_HUMAN | ov7508.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1943175 3' similar to contains MER39.b1 |
| 10545 | 23082 | 36095 | 1.71 | 1.0E-03 | AW362393.1 | EST_HUMAN | MER39 MER39 repetitive element; |
| 10545 | 23082 | 36096 | 1.71 | 1.0E-03 | AW362393.1 | EST_HUMAN | RC1-CT0279-181098-011-a09 CT0279 Homo sapiens cDNA |
| 10628 | 23161 | 36173 | 3.2 | 1.0E-03 | BE170899.1 | EST_HUMAN | RC1-CT0279-181098-011-a09 CT0279 Homo sapiens cDNA |
| 10703 | 23232 | | 3.19 | 1.0E-03 | AJ58347.1 | EST_HUMAN | QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA |
| 11036 | 23550 | | 3.78 | 1.0E-03 | AV759949.1 | EST_HUMAN | tr73et12.x1 NCJ_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR.Q26195 Q26195 PVA1 GENE.; |
| 11882 | 24099 | 37149 | 4.46 | 1.0E-03 | BE884488.1 | EST_HUMAN | AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5' |
| 12149 | 24392 | 30874 | 1.27 | 1.0E-03 | 9507208 | NT | 601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5' |
| | | | | | | | Rattus norvegicus transformation related protein 63 (Trp63), mRNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12175 | 25030 | | 5.99 | 1.0E-03 | A347355.1 | EST_HUMAN | tc05h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element; |
| 12282 | 25052 | 30510 | 5.72 | 1.0E-03 | BE780572.1 | EST_HUMAN | 601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5' |
| 5862 | 18484 | | 1.63 | 9.0E-04 | P06727 | SWISSPROT | APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) |
| 6612 | 19209 | 32017 | 1.08 | 9.0E-04 | P02381 | SWISSPROT | MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1 |
| 9561 | 22061 | | 1.56 | 9.0E-04 | A8037203.1 | NT | Glycylhistidyl tRNA for beta-amylin synthase, complete cds |
| 1535 | 14127 | | 1.05 | 8.0E-04 | X98468.1 | NT | Xlaeids mRNA for CASR protein |
| 4259 | 16945 | | 5.17 | 8.0E-04 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 4880 | 17455 | 28808 | 2.55 | 8.0E-04 | U28185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds |
| 11024 | 23338 | | 2.15 | 8.0E-04 | AA77084.1 | EST_HUMAN | z24c10.s1 Soares_fetal_hart_NbH119W Homo sapiens cDNA clone IMAGE:377874 3' |
| 11175 | 23682 | | 2.5 | 8.0E-04 | A1571089.1 | EST_HUMAN | in85a08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3' |
| 12500 | 24026 | 30892 | 1.65 | 8.0E-04 | AW578654.1 | EST_HUMAN | PM2-HT0353-130100-002-f10 HT0353 Homo sapiens cDNA |
| 1867 | 14453 | 27012 | 0.99 | 7.0E-04 | L41825.1 | NT | Homo sapiens CYP17 gene, 5' end |
| 2442 | 16009 | 27681 | 0.92 | 7.0E-04 | U28185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds |
| 2739 | 15294 | 27861 | 1.75 | 7.0E-04 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 3319 | 15929 | 28406 | 1.23 | 7.0E-04 | 4885170 | NT | Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA |
| 6246 | 18555 | 31628 | 0.75 | 7.0E-04 | AA518212.1 | EST_HUMAN | ng65g12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:909718 similar to contains L1.b3 L1 L1 repetitive element; |
| 6636 | 19232 | | 2.63 | 7.0E-04 | A1786331.1 | EST_HUMAN | wg36f09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3' |
| 7279 | 19807 | | 0.79 | 7.0E-04 | AK024445.1 | NT | Homo sapiens mRNA for FLJ30035 protein, partial cds |
| 9719 | 22217 | 35181 | 0.57 | 7.0E-04 | P13487 | SWISSPROT | BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1) |
| 9719 | 22217 | 35182 | 0.57 | 7.0E-04 | P13487 | SWISSPROT | BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1) |
| 11440 | 23890 | | 3.42 | 7.0E-04 | U78027.1 | NT | Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 11463 | 23913 | 36880 | 2.68 | 7.0E-04 | Z40561.1 | EST_HUMAN | HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3' |
| 12222 | 24443 | | 11.57 | 7.0E-04 | BE077941.1 | EST_HUMAN | GM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA |
| 12472 | 24597 | | 4.94 | 7.0E-04 | R17336.1 | EST_HUMAN | y813c08.l1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32288 5' |
| 12505 | 24628 | | 7.97 | 7.0E-04 | 6005855 | NT | Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA |
| 2720 | 15278 | | 0.93 | 6.0E-04 | BF341380.1 | EST_HUMAN | 802013338F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149287 5' |
| 4033 | 16631 | 28100 | 1.61 | 6.0E-04 | A882525.1 | EST_HUMAN | wj15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3' |
| 4163 | 16754 | 29205 | 0.6 | 6.0E-04 | K01315.1 | NT | Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region |
| 4163 | 16754 | 29206 | 0.6 | 6.0E-04 | K01315.1 | NT | Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region |
| 4284 | 16850 | 29238 | 3.2 | 6.0E-04 | U45983.1 | NT | Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds |
| 4538 | 17122 | 29567 | 0.93 | 6.0E-04 | BE173435.1 | EST_HUMAN | RC2-HT0560-180200-011-09 HT0560 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 4538 | 17122 | 28508 | 0.93 | 6.0E-04 | BE173435.1 | EST_HUMAN | RC2-HT0560-180200-011-009 HT0560 Homo sapiens cDNA |
| 5413 | 17970 | 30378 | 0.9 | 6.0E-04 | A1806687.1 | EST_HUMAN | RC-BT122-180399-057 BT122 Homo sapiens cDNA |
| 5413 | 17970 | 30380 | 0.9 | 6.0E-04 | A1806687.1 | EST_HUMAN | RC-BT122-180399-057 BT122 Homo sapiens cDNA |
| 7807 | 20350 | | 3.04 | 6.0E-04 | P46406 | SWISSPROT | GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) |
| 7868 | 20500 | | 0.67 | 6.0E-04 | H92847.1 | EST_HUMAN | y94c11.s1 Soares_pituitary_gland_N3-HPG Homo sapiens cDNA clone IMAGE:231856 3' similar to contains LOR1 repetitive element; |
| 9890 | 22387 | | 3.74 | 6.0E-04 | AL046507.2 | EST_HUMAN | DKFZp568A2024_r1 586 (synonym: hube1) Homo sapiens cDNA clone DKFZp568A2024 |
| 9824 | 22420 | | 0.77 | 6.0E-04 | A1858286.1 | EST_HUMAN | w135p02.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2426830 3' |
| 9862 | 22487 | 35475 | 2.18 | 6.0E-04 | BE005850.1 | EST_HUMAN | RC2-BN0120-250400-012-H11 BN0120 Homo sapiens cDNA |
| 10242 | 22737 | | 0.64 | 6.0E-04 | AF287478.1 | NT | Lytecthinus variegatus embryonic blastocyst extracellular matrix protein precursor (ECM3) mRNA, complete cds |
| 11358 | 23812 | 36872 | 2.9 | 6.0E-04 | AJ228042.1 | NT | Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3 |
| 11441 | 23891 | 36958 | 5.11 | 6.0E-04 | AW013847.1 | EST_HUMAN | ULH-B10-esb-0-09-0-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 11495 | 23944 | | 2.28 | 6.0E-04 | Q01768 | SWISSPROT | NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18) |
| 11868 | 24828 | | 3.55 | 6.0E-04 | AW380519.1 | EST_HUMAN | RC1-HT0269-281189-012-008 HT0269 Homo sapiens cDNA |
| 12671 | 24739 | | 1.61 | 6.0E-04 | A1817088.1 | EST_HUMAN | w178g11.x1 NCI CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element; |
| 679 | 13303 | 25785 | 8.64 | 5.0E-04 | O10341 | SWISSPROT | HYPOTHETICAL 28.3 KD PROTEIN (ORF82) |
| 1549 | 14141 | | 1.68 | 5.0E-04 | AW851844.1 | EST_HUMAN | QV0-CT0225-021099-030-007 CT0225 Homo sapiens cDNA |
| 3460 | 18087 | 28540 | 1.53 | 5.0E-04 | AA548831.1 | EST_HUMAN | nk27e11.s1 NCI CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element; |
| 3778 | 18378 | 28843 | 1.02 | 5.0E-04 | Q8UKP4 | SWISSPROT | ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7) |
| 5664 | 18281 | 30770 | 1.98 | 5.0E-04 | AF248054.1 | NT | Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 6740 | 18334 | 32141 | 6.37 | 5.0E-04 | AA156080.1 | EST_HUMAN | 2033p08.r1 Strabagene colon (#837204) Homo sapiens cDNA clone IMAGE:588863 5' |
| 7411 | 18938 | 32801 | 16.91 | 5.0E-04 | M23604.1 | NT | Gorilla gorilla involucrin gene medium allele, complete cds |
| 7898 | 20440 | 33346 | 4.97 | 5.0E-04 | A1188382.1 | EST_HUMAN | q413f06.x1 Soares_placenta_8to9weeks_2Nbl-HPbc9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element |
| 8245 | 20786 | 33705 | 0.91 | 5.0E-04 | AA814519.1 | EST_HUMAN | cb86602.s1 NCI CGAP_GC81 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element; |
| 8201 | 21718 | 34682 | 1.37 | 5.0E-04 | AA846545.1 | EST_HUMAN | aj56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3' |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8293 | 21893 | 34840 | 0.6 | 5.0E-04 | N83785.1 | EST_HUMAN | KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT |
| 9437 | 21893 | 34912 | 0.65 | 5.0E-04 | P28128 | SWISSPROT | BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR |
| 9527 | 22027 | 34988 | 4.43 | 5.0E-04 | AW270938.1 | EST_HUMAN | xs08e02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3' |
| 10855 | 23378 | | 4.52 | 5.0E-04 | AL048507.2 | EST_HUMAN | DKFZp568M2024_r1 588 (synonym: huts1) Homo sapiens cDNA clone DKFZp568M2024 |
| 11559 | 18291 | 30770 | 11.05 | 5.0E-04 | AF248054.1 | NT | Bos taurus mitochondrial calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds |
| 11631 | 18638 | 32801 | 1.84 | 5.0E-04 | M23604.1 | NT | Gorilla gorilla involucrin gene medium allele, complete cds |
| 11809 | 24857 | | 3.21 | 5.0E-04 | AA588513.1 | EST_HUMAN | nf18r02.s1 NCI CGAP_P71 Homo sapiens cDNA clone IMAGE:913875 |
| 12353 | 24883 | | 1.77 | 5.0E-04 | U63834.1 | NT | Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds |
| 415 | 13050 | | 0.64 | 4.0E-04 | BF241482.1 | EST_HUMAN | 601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5' |
| 701 | 13323 | .25810 | 1.12 | 4.0E-04 | U32748.1 | NT | Haemophilus influenzae Rd section 63 of 163 of the complete genome |
| 880 | 13494 | 28012 | 1.46 | 4.0E-04 | AF720283.1 | EST_HUMAN | as70b08.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 |
| 880 | 13494 | 28013 | 1.46 | 4.0E-04 | AF720283.1 | EST_HUMAN | Q13825 AL-BINDING PROTEINENOL-COA HYDRATASE. ; |
| 1514 | 14108 | 28842 | 9.82 | 4.0E-04 | AW763356.1 | EST_HUMAN | as70b08.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 |
| 2130 | 14708 | 27280 | 1.59 | 4.0E-04 | AL163278.2 | NT | Q13825 AL-BINDING PROTEINENOL-COA HYDRATASE. ; |
| 2179 | 14756 | | 1.34 | 4.0E-04 | AL048704.1 | EST_HUMAN | RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA |
| 2656 | 15215 | 27787 | 1.83 | 4.0E-04 | O98815 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C078 |
| 3200 | 15912 | 28288 | 2.59 | 4.0E-04 | AF281074.1 | NT | DKFZp434D059_l1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434D059 5' |
| 3405 | 16014 | 28483 | 0.58 | 4.0E-04 | AV888624.1 | EST_HUMAN | SERPIN-2 (SILK GUM PROTEIN 2) |
| 3935 | 16533 | | 0.94 | 4.0E-04 | AL163267.2 | NT | Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced |
| 4415 | 17000 | 28442 | 3.2 | 4.0E-04 | AA576331.1 | EST_HUMAN | AV888624 GKG Homo sapiens cDNA clone GKCFH07 5' |
| 4415 | 17000 | 28443 | 3.2 | 4.0E-04 | AA576331.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C087 |
| 4635 | 17218 | 28671 | 1.94 | 4.0E-04 | AA086324.1 | EST_HUMAN | nh10a10.s1 NCI CGAP_Cor1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL |
| 5249 | 17812 | 30235 | 6.04 | 4.0E-04 | BE560860.1 | EST_HUMAN | SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN); |
| 7312 | 18940 | 32699 | 1.25 | 4.0E-04 | P48442 | SWISSPROT | nh10a10.s1 NCI CGAP_Cor1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL |
| 7541 | 20061 | | 2.42 | 4.0E-04 | AL161588.2 | NT | SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN); |
| 8473 | 21013 | 33629 | 1.42 | 4.0E-04 | BF240712.1 | EST_HUMAN | zn61c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562870 3' |
| 8481 | 21020 | 33935 | 1.85 | 4.0E-04 | NZ5507.1 | EST_HUMAN | 60184585F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5' |
| | | | | | | | EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR) |
| | | | | | | | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88 |
| | | | | | | | 601875985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089700 5' |
| | | | | | | | yc38a12.r1 Soares melanocyte 2NtHM Homo sapiens cDNA clone IMAGE:264142 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9608 | 22108 | 35070 | 2.79 | 4.0E-04 | AI025699.1 | EST_HUMAN | cr67n03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1844341 3' |
| 9754 | 22252 | | 1.22 | 4.0E-04 | AF022855.1 | NT | Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds |
| 12180 | 24833 | | 2.4 | 4.0E-04 | AF254822.1 | NT | Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced |
| 167 | 12830 | 25316 | 2.71 | 3.0E-04 | AL119428.1 | EST_HUMAN | DKFZp781J221.1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781J221 5' |
| 209 | 12870 | 25356 | 3.63 | 3.0E-04 | P49259 | SWISSPROT | 180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R) |
| 913 | 13526 | 26045 | 1.72 | 3.0E-04 | U83891.1 | NT | Human short chain acyl CoA dehydrogenase gene, exons 1 and 2 |
| 1879 | 14465 | 27022 | 5.5 | 3.0E-04 | AI282100.1 | EST_HUMAN | qz28d03.y1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2028197 5' |
| 1894 | 14479 | | 1.08 | 3.0E-04 | AI389874.1 | EST_HUMAN | h23a02.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3' |
| 3349 | 15959 | 28434 | 4.95 | 3.0E-04 | P25147 | SWISSPROT | INTERNALIN B PRECURSOR |
| 4036 | 16834 | 29103 | 3.07 | 3.0E-04 | P49448 | SWISSPROT | GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH) |
| 4131 | 16723 | | 1.37 | 3.0E-04 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 4167 | 16758 | | 1.14 | 3.0E-04 | BE140608.1 | EST_HUMAN | RC0-HT0014-310598-028 HT0014 Homo sapiens cDNA |
| 4941 | 17516 | | 5.05 | 3.0E-04 | BE153778.1 | EST_HUMAN | PM0-HT0339-180200-007-g12 HT0339 Homo sapiens cDNA |
| 6162 | 17731 | 30158 | 0.57 | 3.0E-04 | Q08472 | SWISSPROT | E1A-ASSOCIATED PROTEIN P300 |
| 6282 | 18900 | | 5.93 | 3.0E-04 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 6909 | 18568 | 32365 | 1.97 | 3.0E-04 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 7660 | 20105 | 32681 | 1.04 | 3.0E-04 | P23468 | SWISSPROT | PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA) |
| 8202 | 20743 | 33656 | 6.78 | 3.0E-04 | P22807 | SWISSPROT | FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3) |
| 9834 | 22332 | 35313 | 1.46 | 3.0E-04 | AA454055.1 | EST_HUMAN | zv48d08.l1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62782 |
| 10090 | 22575 | 35570 | 0.5 | 3.0E-04 | AB92139.1 | EST_HUMAN | wk75a11.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2513278 3' |
| 10356 | 22850 | 35844 | 8.78 | 3.0E-04 | AA781201.1 | EST_HUMAN | aj24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1391288 3' similar to gb:M36072 60S |
| 11758 | 25072 | 30514 | 3.55 | 3.0E-04 | AA228301.1 | EST_HUMAN | nc38a04.l1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010450 similar to contains L1.12 L1 repetitive element; |
| 12140 | 24909 | 30713 | 4.28 | 3.0E-04 | AB018202.1 | NT | Homo sapiens mRNA for KIAA0749 protein, partial cds |
| 12574 | 24671 | | 3.54 | 3.0E-04 | AL134483.1 | EST_HUMAN | DKFZp547L185.1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547L185 5' |
| 187 | 12848 | 25333 | 1.23 | 2.0E-04 | AF217798.1 | NT | Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds |
| 504 | 13136 | 25624 | 2.86 | 2.0E-04 | AU146707.1 | EST_HUMAN | AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3' |
| 940 | 13553 | 26068 | 5.4 | 2.0E-04 | M86524.1 | NT | Human dystrophin gene |
| 940 | 13553 | 26070 | 5.4 | 2.0E-04 | M86524.1 | NT | Human dystrophin gene |
| 1221 | 13821 | | 3.94 | 2.0E-04 | AI286021.1 | EST_HUMAN | qh98a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element; |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1228 | 13827 | | 1.95 | 2.0E-04 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 1872 | 14458 | | 1.12 | 2.0E-04 | AF224208.1 | NT | Mus musculus 5' flanking region of Pib3 gene |
| 2227 | 14802 | | 0.9 | 2.0E-04 | AA478880.1 | EST_HUMAN | HL3805.51 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element |
| 2610 | 15172 | 27740 | 6.83 | 2.0E-04 | U60091.1 | NT | Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TORBD1, TORBU1S1, TORBU1S2.> |
| 3016 | 15532 | 28109 | 1.13 | 2.0E-04 | AI124528.1 | EST_HUMAN | am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539780 3' |
| 3377 | 15986 | 28484 | 0.76 | 2.0E-04 | 6174738 | NT | Homo sapiens tubulin, beta, 4 (TUBB4) mRNA |
| 3483 | 16089 | 28561 | 2.53 | 2.0E-04 | BE082317.1 | EST_HUMAN | QV2-BT0638-070500-194-b07 BT0638 Homo sapiens cDNA |
| 3683 | 16581 | 29052 | 0.85 | 2.0E-04 | AW978441.1 | EST_HUMAN | EST390550 IMAGE resequences, MAGP Homo sapiens cDNA |
| 4224 | 16812 | | 6.34 | 2.0E-04 | U01026.1 | NT | Phaeosolus vulgaris nitrate reductase (PNR2) gene, complete cds |
| 4776 | 17357 | 28809 | 1.34 | 2.0E-04 | H86285.1 | EST_HUMAN | y01e11.1 Soares_pituitary_gland_N3H-PG Homo sapiens cDNA clone IMAGE:232558 5' |
| 4776 | 17357 | 28810 | 1.34 | 2.0E-04 | H86285.1 | EST_HUMAN | y01e11.1 Soares_pituitary_gland_N3H-PG Homo sapiens cDNA clone IMAGE:232558 5' |
| 4913 | 17488 | | 1.70 | 2.0E-04 | U09228.1 | NT | Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds |
| 5216 | 17780 | 30189 | 1.44 | 2.0E-04 | AB037697.1 | NT | Danio rerio hcgomato gene, exons 1 to 6, partial cds |
| 5733 | 18359 | 31085 | 1.92 | 2.0E-04 | AV654352.1 | EST_HUMAN | AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3' |
| 5745 | 18371 | 31079 | 1.87 | 2.0E-04 | AI690882.1 | EST_HUMAN | tp03b11.x1 NC1_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3' |
| 5924 | 18548 | 31272 | 0.87 | 2.0E-04 | AA296852.1 | EST_HUMAN | EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat |
| 6102 | 18718 | 31470 | 1.06 | 2.0E-04 | 4758178 | NT | Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA |
| 6385 | 18889 | 31769 | 0.81 | 2.0E-04 | AF140708.1 | NT | Mus musculus G protein coupled receptor gene, complete cds; and unknown gene |
| 7281 | 19809 | | 2.44 | 2.0E-04 | AU121712.1 | EST_HUMAN | AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000788 5' |
| 7616 | 20129 | | 13.08 | 2.0E-04 | P08548 | SW/ISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 7826 | 20138 | 33017 | 1.26 | 2.0E-04 | P64286 | SW/ISSPROT | MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN) |
| 7897 | 20439 | 33344 | 2.74 | 2.0E-04 | U32444.2 | NT | Solanum lycopersicum phytochrome F (PHYF) gene, partial cds |
| 7897 | 20439 | 33345 | 2.74 | 2.0E-04 | U32444.2 | NT | Solanum lycopersicum phytochrome F (PHYF) gene, partial cds |
| 8226 | 20767 | 33685 | 0.97 | 2.0E-04 | AB028898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 8226 | 20767 | 33686 | 0.97 | 2.0E-04 | AB028898.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 8500 | 21039 | 33680 | 1.77 | 2.0E-04 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5 |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8678 | 21217 | 34137 | 0.56 | 2.0E-04 | X57331.1 | NT | Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions) |
| 8257 | 21783 | 34736 | 0.47 | 2.0E-04 | AA725700.1 | EST_HUMAN | af22a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343518 3' |
| 9340 | 21854 | 34803 | 0.5 | 2.0E-04 | P18715 | SWISSPROT | GASTRULA ZINC FINGER PROTEIN XLG28.1 |
| 8885 | 22382 | 35357 | 1.4 | 2.0E-04 | BE149303.1 | EST_HUMAN | RC3-HIT0254-151098-011-b05 HT0254 Homo sapiens cDNA |
| 9830 | 22426 | 35400 | 2.39 | 2.0E-04 | AA405777.1 | EST_HUMAN | zu68c11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742884 5' |
| 10731 | 23257 | 36273 | 6.22 | 2.0E-04 | AV730373.1 | EST_HUMAN | AV730373 HTF Homo sapiens cDNA clone HTFAA01 5' |
| 11185 | 23680 | 36737 | 5.43 | 2.0E-04 | AI440282.1 | EST_HUMAN | 001f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element |
| 11303 | 23786 | 36854 | 2.72 | 2.0E-04 | AW136740.1 | EST_HUMAN | UHH-B1-adm-c-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3' |
| 789 | 13416 | 25920 | 1.41 | 1.0E-04 | H8946.1 | EST_HUMAN | y226c09.s1 Soares_melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:282884 3' similar to contains L1.1 L1 repetitive element |
| 1113 | 13717 | 26227 | 2.57 | 1.0E-04 | P11368 | SWISSPROT | RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 1153 | 13766 | 26266 | 4.04 | 1.0E-04 | AW013947.1 | EST_HUMAN | UHH-B10-eab-e-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 1153 | 13766 | 26266 | 4.04 | 1.0E-04 | AW013947.1 | EST_HUMAN | UHH-B10-eab-e-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3' |
| 1377 | 13970 | | 3.95 | 1.0E-04 | U82918.1 | NT | Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds |
| | | | | | | | Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds |
| 1658 | 14262 | 26795 | 2.57 | 1.0E-04 | AF148805.1 | NT | Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds |
| 1658 | 14262 | 26795 | 2.57 | 1.0E-04 | AF148805.1 | NT | Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds |
| 1901 | 14486 | 27047 | 2.44 | 1.0E-04 | AB048342.1 | NT | Equus caballus DNA, chromosome 24q14, microsatellite TKY38 |
| 2711 | 15288 | 27835 | 1.09 | 1.0E-04 | BE218833.1 | EST_HUMAN | hw45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3' |
| 2711 | 15288 | 27836 | 1.09 | 1.0E-04 | BE218833.1 | EST_HUMAN | hw45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3' |
| 3323 | 15933 | 28410 | 1.1 | 1.0E-04 | Q82203 | SWISSPROT | SPLICOSOME ASSOCIATED PROTEIN 62 (SAP 62) [SPLICING FACTOR 3A SUBUNIT 2] (SF3A66) |
| 3769 | 16399 | 28864 | 2.7 | 1.0E-04 | AI440282.1 | EST_HUMAN | 001f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to contains Alu repetitive element |
| 4134 | 16726 | 29180 | 1.72 | 1.0E-04 | M14042.1 | NT | Mouse alpha 1 type-IV collagen mRNA |
| 4158 | 16748 | 29201 | 1.27 | 1.0E-04 | AV647727.1 | EST_HUMAN | AV647727 GLC Homo sapiens cDNA clone GLCBBD04 3' |
| 5263 | 17825 | 30250 | 0.95 | 1.0E-04 | AI357156.1 | EST_HUMAN | q82h04.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005975 3' |
| 6021 | 18840 | 31380 | 1.5 | 1.0E-04 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 6568 | 19166 | 31902 | 0.97 | 1.0E-04 | AA177111.1 | EST_HUMAN | nc02e12.s1 NCI_CGAP_P13 Homo sapiens cDNA clone IMAGE:252 |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6825 | 19584 | 32414 | 0.78 | 1.0E-04 | AA584561.1 | EST_HUMAN | h26a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:863466 3' similar to gb:M97252 KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element; |
| 7237 | 19767 | 32823 | 14.08 | 1.0E-04 | AL251880.1 | EST_HUMAN | q157d10.x1 NCI_CGAP_OV32 Homo sapiens cDNA clone IMAGE:1985683 3' |
| 7572 | 19767 | 32823 | 14.23 | 1.0E-04 | AL251880.1 | EST_HUMAN | q157d10.x1 NCI_CGAP_OV32 Homo sapiens cDNA clone IMAGE:1985683 3' |
| 7837 | 20478 | 33389 | 1.02 | 1.0E-04 | AA630453.1 | EST_HUMAN | ab94g08.s1 Stratiogene lung (H937210) Homo sapiens cDNA clone IMAGE:854694 3' |
| 8260 | 21788 | 34738 | 2.34 | 1.0E-04 | AB06220.1 | EST_HUMAN | wf26a08.x1 Scores_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2356742 3' |
| 9270 | 21798 | 34745 | 1.71 | 1.0E-04 | Q88069 | SWISSPROT | CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8) |
| 9346 | 21880 | | 0.78 | 1.0E-04 | T77153.1 | EST_HUMAN | y472a08.l1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:113774 5' |
| 9594 | 22084 | 35023 | 2.2 | 1.0E-04 | 10963978 | NT | Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA |
| 10081 | 22578 | | 2.87 | 1.0E-04 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 10116 | 22811 | 35601 | 0.83 | 1.0E-04 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 11218 | 23721 | | 2.06 | 1.0E-04 | M26567.1 | NT | Mouse alpha leukocyte interferon gene, complete cds |
| 11503 | 23852 | 37020 | 1.98 | 1.0E-04 | AB032688.1 | NT | Homo sapiens mRNA for KIAA1142 protein, partial cds |
| 11540 | 23888 | 37050 | 2.1 | 1.0E-04 | AW269081.1 | EST_HUMAN | xx49g12.x1 Scores_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2816518 3' |
| 11570 | 24017 | 37086 | 1.87 | 1.0E-04 | Q03698 | SWISSPROT | NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM) |
| 11570 | 24017 | 37087 | 1.87 | 1.0E-04 | Q03698 | SWISSPROT | NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM) |
| 11670 | 24082 | | 1.57 | 1.0E-04 | BE886768.1 | EST_HUMAN | CM4-CT0404-130700-476-H03 CT0404 Homo sapiens cDNA |
| 11919 | 24878 | | 1.99 | 1.0E-04 | BE676398.1 | EST_HUMAN | 712a10.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3266058 3' similar to contains L1.13 L1 repetitive element; |
| 727 | 13347 | 25839 | 1.98 | 9.0E-05 | AA718833.1 | EST_HUMAN | at45c11.s1 Scores_beslie_NHT Homo sapiens cDNA clone 1292468 3' |
| 2047 | 14029 | 27198 | 0.92 | 9.0E-05 | AW868218.1 | EST_HUMAN | QV4-SN0023-070400-168-H04 SN0023 Homo sapiens cDNA |
| 8117 | 18733 | 31486 | 1.45 | 9.0E-05 | Q80716 | SWISSPROT | PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR |
| 9397 | 21820 | | 2.71 | 9.0E-05 | D85606.1 | NT | Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds |
| 9399 | 21822 | 34771 | 2.79 | 9.0E-05 | AF120882.1 | NT | Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b |
| 11017 | 23531 | 36567 | 2.86 | 9.0E-05 | AW073078.1 | EST_HUMAN | xs34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element; |
| 11121 | 23629 | 36671 | 1.99 | 9.0E-05 | A297878.1 | EST_HUMAN | q123f08.x1 NCI_CGAP_Lyn8 Homo sapiens cDNA clone IMAGE:1882435 3' similar to contains element |
| 11483 | 18733 | 31486 | 3.89 | 9.0E-05 | Q80716 | SWISSPROT | MIR repetitive element; |
| | | | | | | | PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR |
| 11974 | 24839 | | 4.26 | 9.0E-05 | AF129758.1 | NT | Homo sapiens MSH55 gene, partial cds; and CLIC1, DD4H, G8b, G8c, G8d, G8e, G8f, BAT5, G9b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds |
| 854 | 13470 | 25681 | 1.21 | 8.0E-05 | AJ251648.1 | NT | Pisum sativum mRNA for beta-1,3 glucanase (gms2 gene) |
| 897 | 13511 | | 9.89 | 8.0E-05 | AJ251648.1 | NT | Pisum sativum mRNA for beta-1,3 glucanase (gms2 gene) |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2677 | 15583 | | 0.71 | 8.0E-05 | M85575.1 | NT | Human platelet-derived growth factor A chain (PDGFA) gene, exons only |
| 4579 | 17162 | 29604 | 1.87 | 8.0E-05 | AW044605.1 | EST_HUMAN | wy78a04.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3' |
| 8883 | 21222 | 34142 | 0.49 | 8.0E-05 | Y11686.1 | NT | Mus musculus gene for hexokinase II, exon 1 (end joined CDS) |
| 11030 | 23544 | 36591 | 2.32 | 8.0E-05 | M88197.1 | NT | Human heptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds |
| 12613 | 24621 | | 2.72 | 8.0E-05 | AA278333.1 | EST_HUMAN | z888h01.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:704583 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ; |
| 369 | 13018 | 25501 | 8.81 | 7.0E-05 | AW847445.1 | EST_HUMAN | RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA |
| 369 | 13018 | 25502 | 8.81 | 7.0E-05 | AW847445.1 | EST_HUMAN | RC3-CT0208-220989-011-E04 CT0208 Homo sapiens cDNA |
| 593 | 13223 | 25697 | 3.82 | 7.0E-05 | L48075.1 | EST_HUMAN | HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HFD072014 |
| 593 | 13223 | 25698 | 3.82 | 7.0E-05 | L48075.1 | EST_HUMAN | HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HFD072014 |
| 1063 | 13698 | 26208 | 1.41 | 7.0E-05 | Q22949 | SWISSPROT | PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT) |
| 2744 | 15286 | 27865 | 3.67 | 7.0E-05 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 3194 | 15808 | 28279 | 4.69 | 7.0E-05 | AB009080.1 | NT | Dicyostelium discoideum gene for TRFA, complete cds |
| 4462 | 17048 | 29492 | 1.73 | 7.0E-05 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 4543 | 17127 | 29570 | 0.58 | 7.0E-05 | U60680.1 | NT | Caenorhabditis elegans Skp1p homolog mRNA, complete cds |
| 8167 | 20708 | 33624 | 1.11 | 7.0E-05 | AA505582.1 | EST_HUMAN | nh93g01.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966098 3' |
| 9472 | 21871 | 34820 | 3.74 | 7.0E-05 | T07065.1 | EST_HUMAN | EST04984 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBED80 |
| 11040 | 23554 | | 7.95 | 7.0E-05 | 10835048 | NT | Homo sapiens sarcoglycan, epsilon (SGCE), mRNA |
| 2073 | 14653 | 27225 | 2.03 | 6.0E-05 | 4885170 | NT | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA |
| 2073 | 14653 | 27226 | 2.03 | 6.0E-05 | 4885170 | NT | Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA |
| 2624 | 15186 | 27753 | 1.34 | 6.0E-05 | A1855241.1 | EST_HUMAN | w654h08.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA |
| 2709 | 15288 | 27833 | 0.9 | 6.0E-05 | Z84506.1 | NT | TOPOISOMERASE I (HUMAN); |
| 2709 | 15288 | 27834 | 0.9 | 6.0E-05 | Z84506.1 | NT | H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28810 |
| 2840 | 13328 | 25815 | 2.88 | 6.0E-05 | AF053630.1 | NT | H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28810 |
| 5352 | 17812 | 30327 | 1.3 | 6.0E-05 | AW962309.1 | EST_HUMAN | Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds |
| 6071 | 18688 | 31432 | 3.12 | 6.0E-05 | Q12860 | SWISSPROT | EST1374382 MAGE resequences, MAGG Homo sapiens cDNA |
| 6071 | 18688 | 31433 | 3.12 | 6.0E-05 | Q12860 | SWISSPROT | CONTACTIN PRECURSOR (GLYCOPROTEIN GP135) |
| 6335 | 19135 | 31928 | 1.45 | 6.0E-05 | N72829.1 | SWISSPROT | CONTACTIN PRECURSOR (GLYCOPROTEIN GP135) |
| 7013 | 19511 | 32332 | 0.79 | 6.0E-05 | AA897880.1 | EST_HUMAN | y50g11.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:246212 5' |
| 8029 | 20571 | 33475 | 0.97 | 6.0E-05 | BE064410.1 | EST_HUMAN | q8ba03.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3' |
| 8029 | 20571 | 33476 | 0.97 | 6.0E-05 | BE064410.1 | EST_HUMAN | RC4-BT0311-141198-011-h08 BT0311 Homo sapiens cDNA |
| 8029 | 20571 | 33478 | 0.97 | 6.0E-05 | BE064410.1 | EST_HUMAN | RC4-BT0311-141198-011-h08 BT0311 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8381 | 20821 | 33841 | 0.85 | 6.0E-05 | AA150482.1 | EST_HUMAN | 208c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491728 3' similar to contains element MER28 repetitive element; |
| 8385 | 20825 | 33845 | 2.3 | 6.0E-05 | AW886828.1 | EST_HUMAN | PMA-NIN0050-310300-001-110 NN0050 Homo sapiens cDNA |
| 8516 | 21055 | 33978 | 0.62 | 6.0E-05 | Q80401 | SWISSPROT | COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR |
| 9176 | 21753 | 34699 | 1.09 | 6.0E-05 | P08607 | SWISSPROT | C4B-BINDING PROTEIN PRECURSOR (C4BP) |
| 9176 | 21753 | 34700 | 1.09 | 6.0E-05 | P08607 | SWISSPROT | C4B-BINDING PROTEIN PRECURSOR (C4BP) |
| 9440 | 21988 | 34815 | 1.13 | 6.0E-05 | T94149.1 | EST_HUMAN | ye28c12.11 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:119062 5' |
| 9637 | 22137 | 35103 | 0.57 | 6.0E-05 | AW627885.1 | EST_HUMAN | h37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3' |
| 10627 | 23159 | 36172 | 3.98 | 6.0E-05 | R75639.1 | EST_HUMAN | ye6d08.s1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:119062 5' repetitive element; contains LTR7 repetitive element; |
| 11394 | 23848 | 36811 | 4.18 | 6.0E-05 | AA044015.1 | EST_HUMAN | 2k58f02.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5' |
| 12183 | 24919 | 30716 | 10.28 | 6.0E-05 | AW890110.1 | EST_HUMAN | MR0-NT0038-250400-001-409 NT0038 Homo sapiens cDNA |
| 1449 | 14041 | 26569 | 18.37 | 5.0E-05 | AW392088.1 | EST_HUMAN | QV4-ST0234-241189-040-111 ST0234 Homo sapiens cDNA |
| 1903 | 14488 | | 1.75 | 6.0E-05 | 89228691 | NT | Homo sapiens 220a peroxisomal membrane protein-like (LOC55895), mRNA |
| 4051 | 18048 | 29116 | 3.86 | 5.0E-05 | AJ251884.1 | NT | Homo sapiens partial SLG22A3 gene for extraneuronal monoamine transporter (EMT), exon 1 |
| 5716 | 18342 | 30848 | 11.26 | 5.0E-05 | X59855.1 | NT | Human MLG1emb gene for embryonic myosin alkaline light chain, 3'UTR |
| 6144 | 18758 | 31518 | 2.97 | 6.0E-05 | AV863544.1 | EST_HUMAN | AV863544 GLC Homo sapiens cDNA clone GLCDMA08 3' |
| 6316 | 18923 | 31700 | 0.97 | 5.0E-05 | AF280225.1 | NT | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 7370 | 19698 | | 1.22 | 5.0E-05 | AB037984.1 | NT | Mus musculus gene for calretinin, exon 1 |
| 11971 | 24460 | | 5.73 | 5.0E-05 | P49183 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 12248 | 24460 | | 9.18 | 5.0E-05 | P49183 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 2833 | 12806 | | 3.49 | 4.0E-05 | U12821.1 | NT | Human retin (REN) gene, 5' flanking region |
| 4580 | 17163 | 29605 | 1.37 | 4.0E-05 | P49183 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 4580 | 17163 | 29606 | 1.37 | 4.0E-05 | P49183 | SWISSPROT | RETINAL-BINDING PROTEIN (RALBP) |
| 5166 | 17735 | 30162 | 0.58 | 4.0E-05 | AF212313.1 | NT | Drosophila melanogaster senseless protein (sens) gene, complete cds |
| 7020 | 19518 | 32340 | 0.75 | 4.0E-05 | U01947.1 | NT | Macaca mulatta hemoglobin (HP) gene, 5' region |
| 9442 | 21988 | | 7.26 | 4.0E-05 | AF202635.1 | NT | Homo sapiens PP1200 mRNA, complete cds |
| | | | | | | | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; |
| | | | | | | | ENDONUCLEASE] |
| 9912 | 22408 | 35384 | 0.55 | 4.0E-05 | P11369 | SWISSPROT | BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE) |
| 10305 | 22788 | 35790 | 0.73 | 4.0E-05 | P23780 | SWISSPROT | h38c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element; |
| 10648 | 23180 | 36183 | 5.05 | 4.0E-05 | AW627948.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C052 |
| 11850 | 24210 | 31041 | 3.27 | 4.0E-05 | AL163252.2 | NT | h383e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3' |
| 11929 | 24264 | | 1.38 | 4.0E-05 | AW117580.1 | EST_HUMAN | |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 709 | 13330 | 25817 | 0.64 | 3.0E-05 | AI248061.1 | EST_HUMAN | qf84c10.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element; |
| 1097 | 13702 | 26212 | 1.49 | 3.0E-05 | AW273851.1 | EST_HUMAN | xv24g03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3' |
| 1170 | 13772 | 26280 | 1.51 | 3.0E-05 | BF037688.1 | EST_HUMAN | 601461463F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3865142 5' |
| 1170 | 13772 | 26281 | 1.51 | 3.0E-05 | BF037688.1 | EST_HUMAN | 601461463F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3865142 5' |
| 2748 | 15301 | 27867 | 1.17 | 3.0E-05 | Q62234 | SWISSPROT | SKELEMIN |
| 3331 | 15941 | | 0.69 | 3.0E-05 | AI288819.1 | EST_HUMAN | qf91g11.x1 Scores_NHIMPJ_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632 |
| 4471 | 17057 | 29503 | 7.22 | 3.0E-05 | BE168211.1 | EST_HUMAN | O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN ; |
| 4471 | 17057 | 29504 | 7.22 | 3.0E-05 | BE168211.1 | EST_HUMAN | PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA |
| 4565 | 17148 | 29594 | 1.06 | 3.0E-05 | AA368678.1 | EST_HUMAN | PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA |
| 4565 | 17148 | 29595 | 1.06 | 3.0E-05 | AA368678.1 | EST_HUMAN | EST178986 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein |
| 4682 | 17274 | | 0.71 | 3.0E-05 | AL163302.2 | NT | EST178986 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein |
| 4728 | 17307 | 29751 | 0.75 | 3.0E-05 | AF149773.1 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 4963 | 13330 | 25817 | 0.65 | 3.0E-05 | AI248061.1 | EST_HUMAN | Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3 |
| 5746 | 18372 | 31080 | 1.73 | 3.0E-05 | 11072102 | NT | qf04c10.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element; |
| 6854 | 19442 | 32257 | 1.28 | 3.0E-05 | AJ225782.1 | NT | Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myo2pl), mRNA |
| 6854 | 19442 | 32258 | 1.28 | 3.0E-05 | AJ225782.1 | NT | Homo sapiens SYBL1 gene, exons 6-8 |
| 7839 | 20381 | 33286 | 1.9 | 3.0E-05 | BE733167.1 | EST_HUMAN | Homo sapiens SYBL1 gene, exons 6-8 |
| 8283 | 20634 | 33756 | 1.28 | 3.0E-05 | AA284049.1 | EST_HUMAN | 601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5' |
| 8824 | 21383 | 34288 | 1.78 | 3.0E-05 | AW770862.1 | EST_HUMAN | zs60605.s1 Stratiene echizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3' |
| 8828 | 21387 | 34291 | 1.22 | 3.0E-05 | AW770862.1 | EST_HUMAN | h194608.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3' |
| 8832 | 21371 | 34286 | 0.47 | 3.0E-05 | P43361 | SWISSPROT | Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA |
| 9058 | 21595 | | 0.88 | 3.0E-05 | X03273.1 | NT | MELANOMA-ASSOCIATED ANTIGEN 8 (IMAGE-8 ANTIGEN) |
| 9244 | 21770 | 34718 | 1.3 | 3.0E-05 | AA372562.1 | EST_HUMAN | Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene |
| 9581 | 22081 | | 2.97 | 3.0E-05 | AJ169331.1 | EST_HUMAN | EST184475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end |
| 10428 | 22922 | 35925 | 0.85 | 3.0E-05 | Q62818 | SWISSPROT | w93609.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3' |
| 10428 | 22922 | 35926 | 0.85 | 3.0E-05 | Q62818 | SWISSPROT | PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2) |
| 12055 | 24338 | | 1.48 | 3.0E-05 | AJ271735.1 | NT | PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NEL-LIKE PROTEIN 2) |
| 12387 | 25101 | | 1.52 | 3.0E-05 | AW518689.1 | EST_HUMAN | Homo sapiens Xq pseudautosomal region, segment 1/2 |
| 2362 | 14933 | 27508 | 1.55 | 2.0E-05 | AI286021.1 | EST_HUMAN | zs89406.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2776811 3' |
| 2619 | 15181 | 27747 | 10.28 | 2.0E-05 | M13792.1 | NT | qf88e11.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element; |
| | | | | | | | Human adenosine deaminase (ADA) gene, complete cds |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2738 | 15283 | | 0.76 | 2.0E-05 | AA160562.1 | EST_HUMAN | zq46a12.1 Stratagene hNT neuron (#337233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element; |
| 3171 | 15785 | 28257 | 1.59 | 2.0E-05 | BE066038.1 | EST_HUMAN | RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA |
| 3391 | 15889 | 28477 | 0.63 | 2.0E-05 | AF184614.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 3416 | 16024 | 28506 | 1.04 | 2.0E-05 | X89211.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 3541 | 16148 | | 0.72 | 2.0E-05 | X95465.1 | NT | S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV |
| 3880 | 16478 | | 0.67 | 2.0E-05 | AL039107.1 | EST_HUMAN | DKFZp5681084_r1 668 (synonym: hfxd2) Homo sapiens cDNA clone DKFZp5681084 5' |
| 5010 | 17583 | 30028 | 0.63 | 2.0E-05 | AJ131018.1 | NT | Homo sapiens SCL gene locus |
| 5176 | 17743 | | 2.42 | 2.0E-05 | L77589.1 | NT | Homo sapiens DiGeorge syndrome critical region, telomeric end |
| 5633 | 18555 | 31282 | 1.64 | 2.0E-05 | AJ011712.1 | NT | Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS) |
| 6125 | 18740 | 31482 | 1.4 | 2.0E-05 | Q13183 | SWISSPROT | RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) |
| 6125 | 18740 | 31483 | 1.4 | 2.0E-05 | Q13183 | SWISSPROT | RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER) |
| 6305 | 18912 | 31688 | 0.73 | 2.0E-05 | A1148272.1 | EST_HUMAN | qc72a02.x1 Soares_placenta_86dweeks_2hbpP89W Homo sapiens cDNA clone IMAGE:1715114 3' similar to contains L1 L3 L1 repetitive element; |
| 6736 | 18330 | 32138 | 2.12 | 2.0E-05 | AA714330.1 | EST_HUMAN | hw08d12.s1 NCJ CGAP_SST1 Homo sapiens cDNA clone IMAGE:1238519 3' |
| 6882 | 19480 | 32301 | 2.2 | 2.0E-05 | Y08928.1 | NT | P. falciparum mRNA for AARP1 protein, partial |
| 6894 | 19482 | 32313 | 1.34 | 2.0E-05 | A1482980.1 | EST_HUMAN | qc47b08.x1 NCJ CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:002711 |
| 7002 | 19500 | | 8.08 | 2.0E-05 | A891025.1 | EST_HUMAN | O02711 PRO-POL-DUTPASE POLYPROTEIN; |
| | | | | | | | wu35h07.x1 Soares_Dieckgreffe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3' |
| 7207 | 19736 | 32591 | 2.2 | 2.0E-05 | AF224282.1 | NT | Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds |
| 7207 | 19738 | 32592 | 2.2 | 2.0E-05 | AF224282.1 | NT | Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds |
| 7403 | 19828 | | 0.91 | 2.0E-05 | AF128947.1 | NT | Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds |
| 7828 | 20368 | 33276 | 1.41 | 2.0E-05 | A361040.1 | EST_HUMAN | h20h05.x1 NCJ CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2108389 3' |
| 9191 | 21708 | 34651 | 0.49 | 2.0E-05 | P49457 | SWISSPROT | COMPLEMENT DECAY-ACCELERATING FACTOR (CD55) |
| 9191 | 21708 | 34652 | 0.49 | 2.0E-05 | P49457 | SWISSPROT | COMPLEMENT DECAY-ACCELERATING FACTOR (CD55) |
| 9837 | 22335 | 35317 | 0.48 | 2.0E-05 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 10041 | 22536 | 35632 | 0.74 | 2.0E-05 | BF055839.1 | EST_HUMAN | 775g09.y1 NCJ CGAP_Bim20 Homo sapiens cDNA clone IMAGE:3340576 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10482 | 22978 | 35984 | 2.62 | 2.0E-05 | N41751.1 | EST_HUMAN | yw81a06.r1 Soares_placenta_8to9weeks_2NkHP8a09W Homo sapiens cDNA clone IMAGE:256570 5' |
| 10482 | 22978 | 35985 | 2.62 | 2.0E-05 | N41751.1 | EST_HUMAN | yw81a06.r1 Soares_placenta_8to9weeks_2NkHP8a09W Homo sapiens cDNA clone IMAGE:256570 5' |
| 10524 | 19500 | | 2.44 | 2.0E-05 | A1891025.1 | EST_HUMAN | wu35r07.x1 Soares_Dickgreffe_cdon_NHCO Homo sapiens cDNA clone IMAGE:2522077 3' |
| 11327 | 23025 | 36034 | 2.74 | 2.0E-05 | BE175801.1 | EST_HUMAN | RCS-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA |
| 11983 | 24844 | | 4.81 | 2.0E-05 | BE346228.1 | EST_HUMAN | hw21a03.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2; |
| 12080 | 25018 | | 13.02 | 2.0E-05 | AW074804.1 | EST_HUMAN | xs89a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 repetitive element; |
| 12144 | 24831 | | 2.54 | 2.0E-05 | AF275948.1 | NT | Homo sapiens ABCA1 (ABCA1) gene, complete cds |
| 12655 | 24727 | | 2.35 | 2.0E-05 | A1200970.1 | EST_HUMAN | qf69g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755236 3' |
| 2719 | 15475 | 27841 | 1.45 | 1.0E-05 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 3711 | 16312 | 28780 | 1.91 | 1.0E-05 | AF088273.1 | NT | Drosophila melanogaster strain Larinto 120 Suppressor of Hairless (Su(H)) gene, partial cds |
| 4039 | 16637 | 29105 | 11.9 | 1.0E-05 | P81274 | SWISSPROT | MOSAIC PROTEIN LGN |
| 4252 | 16840 | 29289 | 0.88 | 1.0E-05 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 4364 | 16951 | 29391 | 1.89 | 1.0E-05 | AA431119.1 | EST_HUMAN | zw68g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781464 5' |
| 4876 | 17550 | 29982 | 2.24 | 1.0E-05 | AW419134.1 | EST_HUMAN | xy48g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2656548 3' |
| 5395 | 17953 | | 0.94 | 1.0E-05 | A1733568.1 | EST_HUMAN | cs64d07.x5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1610125 3' similar to contains Alu repetitive element; |
| 5428 | 17983 | 30389 | 0.91 | 1.0E-05 | L27595.1 | NT | Mus musculus bradykinin B2 receptor (B2R) gene, complete cds |
| 6848 | 19438 | 32252 | 1.32 | 1.0E-05 | AJ246003.1 | NT | Homo sapiens Spast gene for spastin protein |
| 7140 | 19520 | 32342 | 3.96 | 1.0E-05 | AA841846.1 | EST_HUMAN | ns19g02.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 L1 repetitive element; |
| 7142 | 19675 | 32515 | 14.32 | 1.0E-05 | 4505844 | NT | Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products |
| 7655 | 20167 | 33054 | 0.76 | 1.0E-05 | BF222846.1 | EST_HUMAN | 7p57d01.x1 NCI_CGAP_P-28 Homo sapiens cDNA clone IMAGE:3649045 3' similar to contains MER10.b3 MER10 repetitive element; |
| 7754 | 20282 | | 2.22 | 1.0E-05 | P19474 | SWISSPROT | S2 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) |
| 8846 | 21385 | | 2.56 | 1.0E-05 | AL163227.2 | NT | Homo sapiens chromosome 21 segment HS21C027 |
| 8890 | 21528 | 34457 | 2.18 | 1.0E-05 | AA452578.1 | EST_HUMAN | z35h12.x1 Soares_tet_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:L02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); |
| 9211 | 21728 | 34671 | 13.74 | 1.0E-05 | AA236110.1 | EST_HUMAN | zs05a11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:384332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element; |
| 9288 | 21888 | 34834 | 0.6 | 1.0E-05 | AV732190.1 | EST_HUMAN | AV732190 HTF Homo sapiens cDNA clone HTEBIL-H01 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 9752 | 22250 | 35232 | 0.76 | 1.0E-05 | AW510902.1 | EST_HUMAN | h411b02.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element: |
| 9752 | 22250 | 35233 | 0.76 | 1.0E-05 | AW510902.1 | EST_HUMAN | h411b02.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element: |
| 9830 | 22328 | 35309 | 1.58 | 1.0E-05 | AW291521.1 | EST_HUMAN | UH-B12-egk-a-08-0-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724388 3' |
| 9830 | 22328 | 35310 | 1.58 | 1.0E-05 | AW291521.1 | EST_HUMAN | UH-B12-egk-a-08-0-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724388 3' |
| 10087 | 22582 | | 1.73 | 1.0E-05 | AW468995.1 | EST_HUMAN | h407c10.x1 NCI CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1 L2 L1 repetitive element: |
| 10798 | 23322 | 36332 | 2.32 | 1.0E-05 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds |
| 10798 | 23322 | 36333 | 2.32 | 1.0E-05 | U91328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds |
| 12483 | 25011 | 30616 | 1.67 | 1.0E-05 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21G103 |
| 2698 | 15253 | 27824 | 4.74 | 9.0E-06 | AI583811.1 | EST_HUMAN | h73a06.x1 NCI CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246388 3' |
| 3130 | 15744 | 28213 | 5.23 | 9.0E-06 | AI218983.1 | EST_HUMAN | qg11b08.x1 Soares_placenta_8to9weeks_2NtHP8tc8W Homo sapiens cDNA clone IMAGE:1759191 3' |
| 3670 | 16271 | | 3.37 | 9.0E-06 | M61755.1 | NT | Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2 |
| 6064 | 18881 | 31423 | 2.25 | 9.0E-06 | L23416.1 | NT | Homo sapiens differentiation antigen CD20 gene, exons 5, 6 |
| 6947 | 19524 | 32346 | 0.84 | 9.0E-06 | BE065042.1 | EST_HUMAN | RC1-BT0313-110500-017-e07 BT0313 Homo sapiens cDNA |
| 7466 | 19888 | 32853 | 0.85 | 9.0E-06 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 7751 | 20259 | 33156 | 12.47 | 9.0E-06 | AI094370.1 | EST_HUMAN | cc20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element: |
| 8400 | 20940 | 33863 | 1.18 | 9.0E-06 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 8913 | 21451 | 34372 | 2.48 | 9.0E-06 | Q63769 | SWISSPROT | SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC) |
| 8913 | 21451 | 34373 | 2.48 | 9.0E-06 | Q63769 | SWISSPROT | SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC) |
| 9149 | 21884 | 34628 | 4.8 | 9.0E-06 | U35114.1 | NT | Human apolipoprotein E (APOE) gene, hepatic control region HCR-2 |
| 10616 | 23339 | 36353 | 3.76 | 9.0E-06 | Q10384 | SWISSPROT | PUTATIVE SERINE/THREONINE-PROTEIN KINASE GZE12.14C |
| 2569 | 15469 | 27701 | 1.48 | 8.0E-06 | AW362539.1 | EST_HUMAN | RC3-CT0283-201189-011-r11 CT0283 Homo sapiens cDNA |
| 10424 | 22018 | 35919 | 0.64 | 8.0E-06 | P34083 | SWISSPROT | FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II) |
| 10424 | 22018 | 35920 | 0.64 | 8.0E-06 | P34083 | SWISSPROT | FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II) |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1015 | 13825 | | 1.71 | 7.0E-08 | AA689728.1 | EST_HUMAN | ab60710.x1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains |
| 1487 | 14080 | 26819 | 3.38 | 7.0E-08 | 7882177 | NT | MER20.11 MER20 repetitive element; |
| 2177 | 14754 | 27324 | 1.55 | 7.0E-08 | AW593215.1 | EST_HUMAN | Homo sapiens KIAA0555 gene product (KIAA0555), mRNA |
| 2897 | 15514 | | 7.94 | 7.0E-08 | A1388252.1 | EST_HUMAN | hg11b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845279 3' similar to |
| 3620 | 16223 | | 1 | 7.0E-08 | AA395542.1 | EST_HUMAN | gb:XB2048_cds1 WEE1-LIKE PROTEIN KINASE (HUMAN); |
| 5874 | 18486 | | 5.81 | 7.0E-08 | AW883141.1 | EST_HUMAN | qw16g08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1891288 3' similar to contains Alu repetitive |
| 5972 | 18593 | 31327 | 0.94 | 7.0E-08 | N98845.1 | EST_HUMAN | element; |
| 8724 | 21283 | 34183 | 0.72 | 7.0E-08 | 11420708 | NT | EST189205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat |
| 9814 | 22312 | | 2.32 | 7.0E-08 | Q61147 | SWISSPROT | QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA |
| 11710 | 25043 | 30508 | 1.82 | 7.0E-08 | BF215972.1 | EST_HUMAN | y65c07.1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:278412 5' |
| 2942 | 15558 | 28032 | 1.29 | 8.0E-08 | BE089189.1 | EST_HUMAN | Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF08S1E), mRNA |
| 4885 | 15594 | 28085 | 2.03 | 8.0E-08 | Q01456 | SWISSPROT | CERULOPLASMIN PRECURSOR (FERROXIDASE) |
| 4875 | 17450 | 28901 | 1.47 | 8.0E-08 | A1040099.1 | EST_HUMAN | 601881622F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083972 5' |
| 5552 | 18184 | 30599 | 1.3 | 8.0E-08 | AF167441.1 | NT | QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA |
| 5805 | 18234 | 30885 | 1.15 | 8.0E-08 | Q02040 | SWISSPROT | OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN) |
| 9770 | 22288 | | 1.67 | 8.0E-08 | AW801912.1 | EST_HUMAN | aa08a02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to |
| 12802 | 24888 | 30881 | 1.47 | 8.0E-08 | 11418157 | NT | contains MER8.12 MER8 repetitive element; |
| 5361 | 17921 | 30335 | 1.02 | 5.0E-08 | AL163288.2 | NT | Mus musculus E-cadherin binding protein E7 mRNA, complete cds |
| 6211 | 18821 | 31592 | 3.73 | 5.0E-08 | AL163246.2 | NT | PROTEIN XE7 |
| 6479 | 19080 | 31883 | 2.04 | 5.0E-08 | U07581.1 | NT | IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA |
| 7284 | 18812 | 32888 | 1.11 | 5.0E-08 | AB007546.1 | NT | Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA |
| 10013 | 22508 | 35499 | 6.57 | 5.0E-08 | AA313820.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C088 |
| 10408 | 22800 | 35895 | 0.54 | 5.0E-08 | P06881 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C048 |
| 12482 | 24615 | 30890 | 13.8 | 5.0E-08 | A1065045.1 | EST_HUMAN | Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds |
| 675 | 13288 | 25780 | 6.05 | 4.0E-08 | R18287.1 | EST_HUMAN | Homo sapiens gene for LECT2, complete cds |
| 879 | 13493 | 26011 | 6.94 | 4.0E-08 | AW103354.1 | EST_HUMAN | EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1379 | 13872 | 28489 | 3.92 | 4.0E-06 | AF334928.1 | EST_HUMAN | h33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' |
| 1379 | 13872 | 28500 | 3.92 | 4.0E-06 | AF334928.1 | EST_HUMAN | h33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3' |
| 1522 | 14114 | 28851 | 3.17 | 4.0E-06 | BF365612.1 | EST_HUMAN | QV2-NT0046-200800-250-107 NT0046 Homo sapiens cDNA |
| 2305 | 14878 | 27454 | 1.68 | 4.0E-06 | AW015401.1 | EST_HUMAN | U1-H-BIO-est-4-05-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3' |
| 3099 | 15714 | 28186 | 1.26 | 4.0E-06 | AF198349.1 | NT | Gallus gallus Dact2 protein (Dact2) mRNA, complete cds |
| 3953 | 16561 | 28030 | 1.35 | 4.0E-06 | AW848285.1 | EST_HUMAN | IL3-CT0214-150200-074-803 CT0214 Homo sapiens cDNA |
| 4930 | 17505 | 28851 | 1.86 | 4.0E-06 | AB88839.1 | EST_HUMAN | w84c10.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element |
| 5053 | 17628 | 30070 | 2.12 | 4.0E-06 | AL163279.2 | NT | MER22 repetitive element; |
| 8438 | 20878 | 33890 | 0.53 | 4.0E-06 | OT16393 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C079 |
| 8735 | 21274 | 34195 | 2.68 | 4.0E-06 | AF008660.1 | NT | TRANSMEMBRANE PROTEASE, SERINE 2 |
| 9824 | 22124 | 35088 | 1.11 | 4.0E-06 | AJ272265.1 | NT | Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region |
| 11324 | 23022 | 36031 | 3.84 | 4.0E-06 | AB007055.1 | NT | Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8 |
| 2208 | 14784 | 27357 | 1.31 | 3.0E-06 | AA700562.1 | EST_HUMAN | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486 |
| 2208 | 14784 | 27358 | 1.31 | 3.0E-06 | AA700562.1 | EST_HUMAN | z54b08.s1 Scores_fetal_liver_spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1.t1 L1 repetitive element; |
| 2307 | 14879 | | 1.54 | 3.0E-06 | AF202635.1 | NT | z54b08.s1 Scores_fetal_liver_spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1.t1 L1 repetitive element; |
| 2948 | 15584 | 28038 | 1.02 | 3.0E-06 | AA868218.1 | EST_HUMAN | Homo sapiens PP1200 mRNA, complete cds |
| 3304 | 15915 | | 2.41 | 3.0E-06 | AB577778.1 | EST_HUMAN | ak48g11.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13 |
| 3651 | 16449 | 28911 | 1.08 | 3.0E-06 | BE047094.1 | EST_HUMAN | LTR1 repetitive element; |
| 3651 | 16449 | 28912 | 1.08 | 3.0E-06 | BE047094.1 | EST_HUMAN | wf22a05.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2425816 3' similar to TR:O60734 O60734 |
| 4573 | 17156 | 28600 | 0.68 | 3.0E-06 | T50288.1 | EST_HUMAN | LINE-1 LIKE PROTEIN :contains L1.12 L1 repetitive element; |
| 4661 | 17243 | 28697 | 4.82 | 3.0E-06 | X54816.1 | NT | h64412.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3' |
| 5045 | 17618 | 30063 | 0.94 | 3.0E-06 | J04038.1 | NT | h64412.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3' |
| 5045 | 17618 | 30064 | 0.94 | 3.0E-06 | J04038.1 | NT | h64412.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3' |
| 6308 | 18915 | 31689 | 0.78 | 3.0E-06 | AU159412.1 | EST_HUMAN | y678b10.1 Strabagene ovary (#637217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element |
| 7280 | 18908 | | 2.79 | 3.0E-06 | P08548 | SWISSPROT | Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.) |
| 8027 | 20569 | 33473 | 0.72 | 3.0E-06 | BE562864.1 | EST_HUMAN | Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds |
| 8618 | 21157 | 34070 | 0.69 | 3.0E-06 | P07743 | SWISSPROT | Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12162 | 24394 | | 13.37 | 3.0E-06 | AW365262.1 | EST_HUMAN | RCO-LT0001:261169-011-A03 LT0001 Homo sapiens cDNA |
| 216 | 12877 | | 2.91 | 2.0E-06 | P54366 | SWISSPROT | HOMEOBOX PROTEIN GOOSECOID |
| 1614 | 14207 | | 4.48 | 2.0E-06 | P21414 | SWISSPROT | POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE] |
| 2418 | 14980 | 27530 | 2.2 | 2.0E-06 | A1672138.1 | EST_HUMAN | w804603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element; |
| 2508 | 15070 | 27643 | 1.79 | 2.0E-06 | P04629 | SWISSPROT | HISTIDINE-RICH GLYCOPROTEIN PRECURSOR |
| 2601 | 15163 | 27731 | 1.34 | 2.0E-06 | P06719 | SWISSPROT | KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP) |
| 3570 | 16174 | 28656 | 1.04 | 2.0E-06 | AV657555.1 | EST_HUMAN | AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3' |
| 3825 | 16425 | 28887 | 1.85 | 2.0E-06 | AA173518.1 | EST_HUMAN | zp02605.11 Stratiotes ovata cancer (#637219) Homo sapiens cDNA clone IMAGE:595232 5' |
| 3838 | 16435 | 28897 | 0.63 | 2.0E-06 | AW450215.1 | EST_HUMAN | U-H-B13-alky-9-05-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3' |
| 3844 | 16443 | 28904 | 1.74 | 2.0E-06 | AB030898.1 | NT | Mus musculus gene for odorant receptor A18, complete cds |
| 6239 | 18848 | | 0.79 | 2.0E-06 | AA974632.1 | EST_HUMAN | on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element; |
| 6267 | 18875 | 31643 | 0.87 | 2.0E-06 | A1539448.1 | EST_HUMAN | ts5105.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13637 Q13637 MER37 TRANSDUCIBLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.; |
| 6570 | 19168 | 31965 | 4.94 | 2.0E-06 | A1819424.1 | EST_HUMAN | w80804.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3' |
| 7858 | 20400 | | 0.89 | 2.0E-06 | AW869223.1 | EST_HUMAN | MR3-SN0067-120400-002-02 SN0067 Homo sapiens cDNA |
| 8033 | 20575 | 33480 | 0.75 | 2.0E-06 | T12238.1 | EST_HUMAN | A447R Heart Homo sapiens cDNA clone A447 |
| 8770 | 21309 | | 0.59 | 2.0E-06 | AA772497.1 | EST_HUMAN | zh27c11.s1 Soares_pined_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to TR:P70467 P70467 REVERSE TRANSCRIPTASE; |
| 8782 | 21321 | 34245 | 1.54 | 2.0E-06 | H62051.1 | EST_HUMAN | yv37c04.r1 Soares ovary NBHOT Homo sapiens cDNA clone IMAGE:235674 5' similar to gb:X74929 KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN); |
| 9143 | 21678 | 34621 | 0.91 | 2.0E-06 | AF003529.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 9143 | 21678 | 34622 | 0.91 | 2.0E-06 | AF003529.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 9817 | 22117 | 35080 | 0.72 | 2.0E-06 | N30576.1 | EST_HUMAN | yw69d03.s1 Soares_placenta_8to9weeks_2NBHP609W Homo sapiens cDNA clone IMAGE:267212 3' |
| 9833 | 22331 | | 0.63 | 2.0E-06 | AV748969.1 | EST_HUMAN | AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5' |
| 12052 | 25046 | 30508 | 1.61 | 2.0E-06 | P23249 | SWISSPROT | PROTEIN MOV-10 |
| 12210 | 24434 | | 6.63 | 2.0E-06 | BE328232.1 | EST_HUMAN | hs20202.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.12 L1 repetitive element; |
| 36 | 12715 | 25174 | 1.77 | 1.0E-06 | O76082 | SWISSPROT | ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER) |
| 685 | 13309 | 25794 | 1.45 | 1.0E-06 | AF084384.1 | NT | Mus musculus D6M45E protein (D6M45e) mRNA, complete cds |
| 1500 | 14092 | 26631 | 2.08 | 1.0E-06 | P09125 | SWISSPROT | MEROZOITE SURFACE PROTEIN GMZ-8 |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 1571 | 14164 | 26895 | 1.12 | 1.0E-06 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 1627 | 14220 | | 1.54 | 1.0E-06 | P27625 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT |
| 2037 | 14619 | 27186 | 8.38 | 1.0E-06 | AF184614.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 2037 | 14619 | 27187 | 8.38 | 1.0E-06 | AF184614.1 | NT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 4459 | 17045 | 29488 | 14.7 | 1.0E-06 | U07561.1 | NT | Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds |
| 5269 | 17831 | 30256 | 0.99 | 1.0E-06 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 5269 | 17831 | 30257 | 0.99 | 1.0E-06 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 5494 | 18128 | 30536 | 4.64 | 1.0E-06 | BF333015.1 | EST_HUMAN | MIR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA |
| 5518 | 18150 | 30563 | 1.08 | 1.0E-06 | BE834518.1 | EST_HUMAN | MIR3-FN0004-080600-001-c04 FN0004 Homo sapiens cDNA |
| 5518 | 18150 | 30564 | 1.08 | 1.0E-06 | BE834518.1 | EST_HUMAN | MIR3-FN0004-080600-001-c04 FN0004 Homo sapiens cDNA |
| 5687 | 18294 | 30774 | 1.13 | 1.0E-06 | O60613 | SWISSPROT | 15 KDA SELENOPROTEIN PRECURSOR |
| 6854 | 19631 | 32258 | 5.98 | 1.0E-06 | P02871 | SWISSPROT | FIBRINOGEN ALPHA2(A)ALPHA-E CHAIN PRECURSOR |
| 7943 | 20485 | | 0.68 | 1.0E-06 | AA012823.1 | EST_HUMAN | d23-08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3' |
| 8216 | 20757 | 33671 | 1.21 | 1.0E-06 | AS47010.1 | EST_HUMAN | qp54-02.k1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1928842 3' |
| 8425 | 20985 | 33879 | 1.23 | 1.0E-06 | AL287878.1 | EST_HUMAN | q23-08.k1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element |
| 9228 | 21950 | 34889 | 0.88 | 1.0E-06 | N74635.1 | EST_HUMAN | MIR repetitive element; |
| 9301 | 21901 | 34850 | 0.5 | 1.0E-06 | Q39575 | SWISSPROT | zs55-01.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:286472 3' |
| 9600 | 22100 | 35062 | 3.34 | 1.0E-06 | U82668.1 | NT | DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM |
| 9600 | 22100 | 35063 | 3.34 | 1.0E-06 | U82668.1 | NT | Homo sapiens shox gene, alternatively spliced products, complete cds |
| 9843 | 22143 | 35111 | 4.36 | 1.0E-06 | AA132611.1 | EST_HUMAN | Homo sapiens shox gene, alternatively spliced products, complete cds |
| 9703 | 22202 | | 3.84 | 1.0E-06 | AA448257.1 | EST_HUMAN | zo17-08.r1 Strategene colon (8637204) Homo sapiens cDNA clone IMAGE:587174 5' |
| 10382 | 22876 | | 1.61 | 1.0E-06 | AL163203.2 | NT | zo04411.s1 Soares fetal spleen 1NFSL Homo sapiens cDNA clone IMAGE:587174 5' |
| 11502 | 23951 | | 6.24 | 1.0E-06 | AW890941.1 | EST_HUMAN | gb:D28128 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN); |
| 12087 | 24356 | 30966 | 7.83 | 1.0E-06 | L78810.1 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 12185 | 14619 | 27186 | 1.67 | 1.0E-06 | AF184614.1 | NT | RC4-NT0054-120500-012-503 NT0054 Homo sapiens cDNA |
| 12185 | 14619 | 27187 | 1.67 | 1.0E-06 | AF184614.1 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 12803 | 14220 | | 1.38 | 1.0E-06 | P27625 | SWISSPROT | Homo sapiens p47-phox (NCF1) gene, complete cds |
| 383 | 13030 | 25618 | 2.01 | 9.0E-07 | AF003528.1 | NT | DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT |
| 383 | 13030 | 25619 | 2.01 | 9.0E-07 | AF003528.1 | NT | Homo sapiens gypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 8346 | 20887 | | 0.57 | 9.0E-07 | AL163280.2 | NT | Homo sapiens gypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 11126 | 23634 | 36075 | 2.95 | 9.0E-07 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| | | | | | | NT | Homo sapiens chromosome 21 segment HS21C081 |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4885 | 17460 | 28912 | 5.02 | 8.0E-07 | AI288588.1 | EST_HUMAN | q82g07.x1 Soares_NH-MIPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3' |
| 4885 | 17460 | 28913 | 5.02 | 8.0E-07 | AI288588.1 | EST_HUMAN | q82g07.x1 Soares_NH-MIPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3' |
| 6047 | 18686 | | 7.48 | 8.0E-07 | P21414 | SWISSPROT | POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE] |
| 7044 | 20486 | | 9.51 | 8.0E-07 | AF135418.1 | NT | Homo sapiens UDP-glucuronosyltransferase gene, complete cds |
| 11488 | 23835 | | 8.73 | 8.0E-07 | T07770.1 | EST_HUMAN | EST056860 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBEN89 |
| 11680 | 24106 | | 7.98 | 8.0E-07 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 1806 | 14481 | 27052 | 1.14 | 7.0E-07 | AF167341.1 | NT | Homo sapiens membrane Interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11 |
| 5710 | 18336 | 30841 | 0.89 | 7.0E-07 | 6005700 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA |
| 5710 | 18336 | 30842 | 0.89 | 7.0E-07 | 6005700 | NT | Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA |
| 10942 | 23174 | 36188 | 1.59 | 7.0E-07 | BE676848.1 | EST_HUMAN | 733g01.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:3288468 3' similar to TR-Q96897 Q96897 |
| 1856 | 14540 | 27036 | 2.56 | 8.0E-07 | AW855558.1 | EST_HUMAN | ENDOGENOUS RETROVIRUS-K, LTR U5 AND GAG GENE. ; |
| | | | | | | | CN3-CT0277-221068-024-611 CT0277 Homo sapiens cDNA |
| 2534 | 15036 | 27671 | 2.3 | 6.0E-07 | AF018413.1 | NT | Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytchrome P-450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, > |
| 4044 | 16842 | | 1.78 | 8.0E-07 | P41479 | SWISSPROT | HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION |
| 9068 | 21605 | 34536 | 1.94 | 6.0E-07 | BF001867.1 | EST_HUMAN | 7g84f07.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR-O75620 O75620 4F5L ; |
| 11625 | 24067 | 37131 | 1.83 | 6.0E-07 | AI782850.1 | EST_HUMAN | om87f05.y6 NCI_CGAP_Ki63 Homo sapiens cDNA clone IMAGE:1554177 5' |
| 11949 | 24989 | | 2.85 | 6.0E-07 | AW903222.1 | EST_HUMAN | OM4-NH1029-260300-121-h12 NH1029 Homo sapiens cDNA |
| 348 | 12889 | | 1.19 | 5.0E-07 | AU831883.1 | EST_HUMAN | wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3' |
| 1095 | 13700 | | 2.21 | 5.0E-07 | AA380630.1 | EST_HUMAN | EST183615 Supt cells Homo sapiens cDNA 5' end |
| 3068 | 15881 | | 0.94 | 5.0E-07 | AU831883.1 | EST_HUMAN | wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3' |
| 4751 | 17332 | 29775 | 1.32 | 5.0E-07 | AF149774.1 | NT | Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds |
| 6268 | 18876 | 31644 | 1.13 | 5.0E-07 | U85067.1 | NT | Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds |
| 7124 | 19464 | 32281 | 1.56 | 5.0E-07 | A1893981.1 | EST_HUMAN | tg08f05.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alu repetitive element/contains element A3R repetitive element ; |
| 7124 | 19464 | 32282 | 1.56 | 5.0E-07 | A1893981.1 | EST_HUMAN | tg08f05.x1 NCI_CGAP_CL11 Homo sapiens cDNA clone IMAGE:2107853 3' similar to contains Alu repetitive element/contains element A3R repetitive element ; |
| 7386 | 18812 | 32776 | 16.07 | 5.0E-07 | AW070885.1 | EST_HUMAN | xx31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2588342 3' similar to gb.X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN); |
| 8217 | 20758 | 33672 | 0.82 | 5.0E-07 | Q9WUQ1 | SWISSPROT | ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1) |

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Table 4
Single Exon Probes Expressed In Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8427 | 20967 | | 1.06 | 5.0E-07 | P09583 | SWISSPROT | S-ANTIGEN PROTEIN PRECURSOR |
| 10270 | 22765 | 35752 | 4.46 | 5.0E-07 | A1808597.1 | EST_HUMAN | CM-BT178-220468-014 BT178 Homo sapiens cDNA |
| 10542 | 23079 | 36093 | 1.56 | 5.0E-07 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 11391 | 23843 | 36907 | 4.94 | 5.0E-07 | P11087 | SWISSPROT | COLLAGEN ALPHA 1(I) CHAIN PRECURSOR |
| 11452 | 23902 | | 2.43 | 5.0E-07 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 12391 | 24889 | | 2.85 | 5.0E-07 | AW882537.1 | EST_HUMAN | QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA |
| 4071 | 16867 | 28129 | 1.94 | 4.0E-07 | AW009602.1 | EST_HUMAN | ws84h05.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2504697 3' |
| 7230 | 19761 | | 0.88 | 4.0E-07 | AJ272265.1 | NT | Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8 |
| 7311 | 19839 | 32697 | 1.35 | 4.0E-07 | Q8Z2V6 | SWISSPROT | HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1) |
| 7311 | 19839 | 32698 | 1.35 | 4.0E-07 | Q8Z2V6 | SWISSPROT | HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1) |
| 7863 | 20405 | 33312 | 0.65 | 4.0E-07 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 8681 | 21519 | 34445 | 5.37 | 4.0E-07 | AW419134.1 | EST_HUMAN | xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3' |
| 10228 | 22723 | 35715 | 0.5 | 4.0E-07 | AL163218.2 | NT | Homo sapiens chromosome 21 segment HS21C018 |
| 10617 | 23338 | 36351 | 4.05 | 4.0E-07 | AJ765528.1 | EST_HUMAN | wf81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2389703 3' |
| 10817 | 23338 | 36352 | 4.05 | 4.0E-07 | AJ765528.1 | EST_HUMAN | wf81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2389703 3' |
| 11100 | 23610 | | 2.08 | 4.0E-07 | BE001828.1 | EST_HUMAN | PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA |
| 486 | 13100 | 25591 | 4.51 | 3.0E-07 | U19718.1 | NT | Human microfilament-associated glycoprotein (MIFAP2) gene, putative promoter region and alternatively spliced untranslated exons |
| 609 | 13237 | 25711 | 2.84 | 3.0E-07 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 1417 | 14010 | 28539 | 1.65 | 3.0E-07 | M89149.1 | NT | Human polymorphic microsatellite DNA |
| 1667 | 14260 | | 1.85 | 3.0E-07 | M84857.1 | NT | Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele |
| 2080 | 14670 | | 3.87 | 3.0E-07 | AA528763.1 | EST_HUMAN | nt56b09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1.13 L1 repetitive element; |
| 2327 | 14898 | 27471 | 1.72 | 3.0E-07 | M89149.1 | NT | Human polymorphic microsatellite DNA |
| 2508 | 15072 | 27845 | 6.56 | 3.0E-07 | BE005077.1 | EST_HUMAN | MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA |
| 2508 | 15072 | 27846 | 6.56 | 3.0E-07 | BE005077.1 | EST_HUMAN | MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA |
| 3089 | 15684 | 28156 | 0.79 | 3.0E-07 | T84704.1 | EST_HUMAN | y450f12.l1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:111695 5' |
| 3195 | 15907 | 28280 | 2.03 | 3.0E-07 | P38739 | SWISSPROT | HYPOHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR |
| 4788 | 17368 | | 0.58 | 3.0E-07 | P20740 | SWISSPROT | OVOSTATIN PRECURSOR (OVOMACROGLOBULIN) |
| 4834 | 17412 | 28865 | 7.74 | 3.0E-07 | AV650201.1 | EST_HUMAN | AV650201 GLC Homo sapiens cDNA clone GLC00001 3' |
| 4878 | 17453 | 28865 | 0.71 | 3.0E-07 | AJ797236.1 | EST_HUMAN | ws86b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3' |
| 5222 | 17787 | 30205 | 1.81 | 3.0E-07 | T57850.1 | EST_HUMAN | jc14f09.s1 Strathene lung (8837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb-M82982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN) |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 5222 | 17787 | 30208 | 1.81 | 3.0E-07 | T57850.1 | EST_HUMAN | yc14h09.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:1462382 ARACHIDONATE 12-LIPOXYGENASE (HUMAN) |
| 5847 | 18471 | 31197 | 12.78 | 3.0E-07 | O88807 | SWISSPROT | PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) |
| 6128 | 18743 | 31488 | 0.71 | 3.0E-07 | O42280 | SWISSPROT | (PEPTIDYLARGININE DEIMINASE TYPE ALPHA) |
| 6804 | 18395 | | 5.41 | 3.0E-07 | AA815175.1 | EST_HUMAN | WNT-14 PROTEIN PRECURSOR |
| 7519 | 20039 | 32808 | 3.22 | 3.0E-07 | AW787168.1 | EST_HUMAN | cc04c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1330890 3' |
| 7659 | 20171 | | 1.6 | 3.0E-07 | AI591065.1 | EST_HUMAN | QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA |
| 11373 | 23825 | | 1.88 | 3.0E-07 | BE439409.1 | EST_HUMAN | tw28f11.x1 NCI_CGAP_OV35 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ; |
| 12841 | 24716 | | 6.74 | 3.0E-07 | AJ132352.1 | NT | HTMH-025F1 HTM1 Homo sapiens cDNA |
| 31 | 12710 | 25168 | 3.36 | 2.0E-07 | AF262888.1 | NT | Rattus norvegicus mRNA for 45 kDa secretory protein, partial |
| 165 | 12828 | 25314 | 7.91 | 2.0E-07 | L77589.1 | NT | Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds |
| 165 | 12828 | 25315 | 7.91 | 2.0E-07 | L77589.1 | NT | Homo sapiens DRGeorge syndrome critical region, telomeric end |
| 194 | 12854 | 25338 | 45.53 | 2.0E-07 | U38949.1 | NT | Homo sapiens DRGeorge syndrome critical region, telomeric end |
| 778 | 13397 | 25898 | 2.58 | 2.0E-07 | AF003530.1 | NT | Fugu rubripes beta-cytoplasmic (vascular) actin gene, complete cds |
| 778 | 13397 | 25898 | 2.58 | 2.0E-07 | AF003530.1 | NT | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions |
| | | | | | | | Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions |
| | | | | | | | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; |
| 791 | 13409 | | 0.81 | 2.0E-07 | P11369 | SWISSPROT | ENDONUCLEASE] |
| 979 | 13591 | 26108 | 2.56 | 2.0E-07 | AA223280.1 | EST_HUMAN | z08b07.s1 Stragene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:650868 3' similar to gb:131880 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element |
| 980 | 13592 | 26107 | 6.66 | 2.0E-07 | T63042.1 | EST_HUMAN | yc15g04.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80780 3' similar to contains L1 repetitive element ; |
| 1205 | 13805 | 26318 | 0.76 | 2.0E-07 | Q26768 | SWISSPROT | I68 AUTOANTIGEN |
| 1644 | 14236 | 26771 | 1.88 | 2.0E-07 | Q08701 | SWISSPROT | HYPOPHYSICAL 72.6 KD PROTEIN C2F7.10 IN CHROMOSOME 1 |
| 3679 | 16280 | | 0.65 | 2.0E-07 | BF131397.1 | EST_HUMAN | 801818818F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5' |
| 3751 | 16352 | 28820 | 22.38 | 2.0E-07 | AF125348.1 | NT | Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds |
| 5547 | 18179 | 30563 | 1.81 | 2.0E-07 | AW890066.1 | EST_HUMAN | RC3-NIN0068-260400-021-g11 NIN0068 Homo sapiens cDNA |
| 6769 | 19382 | 32171 | 1.59 | 2.0E-07 | AI208715.1 | EST_HUMAN | qq56d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3' |
| 8405 | 20946 | | 3.67 | 2.0E-07 | AV728390.1 | EST_HUMAN | AV728390 HTC Homo sapiens cDNA clone HTCAEG02 5' |
| 8528 | 21167 | 34082 | 1.1 | 2.0E-07 | AA035198.1 | EST_HUMAN | z427g09.s1 Soares_pregnant_uterus_Nht-IPU Homo sapiens cDNA clone IMAGE:471808 3' |
| 8978 | 22175 | | 2.27 | 2.0E-07 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 10168 | 22863 | 35658 | 5.85 | 2.0E-07 | AW892507.1 | EST_HUMAN | GM4-NIN003-280300-124-e08 NIN003 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10383 | 22877 | 35888 | 0.76 | 2.0E-07 | P00751 | SWISSPROT | COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2) |
| 10383 | 22877 | 35888 | 0.75 | 2.0E-07 | P00751 | SWISSPROT | COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2) |
| 11642 | 24603 | | 2.67 | 2.0E-07 | BE153717.1 | EST_HUMAN | PMO-HT03339-260100-008-H07 HT0339 Homo sapiens cDNA |
| 11734 | 24890 | | 3.56 | 2.0E-07 | A1732462.1 | EST_HUMAN | z185h11.x6 Strabegene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565028 3' similar to contains THR.b2 THR repetitive element: |
| 1141 | 13744 | | 1.17 | 1.0E-07 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 2013 | 14595 | 27157 | 0.97 | 1.0E-07 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 2013 | 14595 | 27158 | 0.97 | 1.0E-07 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 2424 | 14892 | 27565 | 0.93 | 1.0E-07 | P10283 | SWISSPROT | RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1) |
| 2654 | 14162 | 26893 | 2.94 | 1.0E-07 | P08266 | SWISSPROT | GLYCOPROTEIN GPV |
| 3807 | 13744 | | 1.22 | 1.0E-07 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 4380 | 16987 | 29413 | 2.75 | 1.0E-07 | AV718682.1 | EST_HUMAN | AV718682 GLC Homo sapiens cDNA clone GLCFNF04.6 |
| 4380 | 16987 | 29414 | 2.75 | 1.0E-07 | AV718682.1 | EST_HUMAN | AV718682 GLC Homo sapiens cDNA clone GLCFNF04.5 |
| 6627 | 19223 | 32028 | 1.57 | 1.0E-07 | U82871.2 | NT | Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1> |
| 6850 | 19527 | 32349 | 4.57 | 1.0E-07 | BE047871.1 | EST_HUMAN | bx43d06.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2291339.5 |
| 6850 | 19527 | 32350 | 4.57 | 1.0E-07 | BE047871.1 | EST_HUMAN | bx43d06.y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2291339.5 |
| 7504 | 20028 | 32890 | 8.62 | 1.0E-07 | N55081.1 | EST_HUMAN | y43607.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484.3 |
| 7644 | 20156 | 33042 | 0.82 | 1.0E-07 | BF375809.1 | EST_HUMAN | PM4-TN0024-030800-002-005 TN0024 Homo sapiens cDNA |
| 7644 | 20156 | 33043 | 0.82 | 1.0E-07 | BF375809.1 | EST_HUMAN | PM4-TN0024-030800-002-005 TN0024 Homo sapiens cDNA |
| 7669 | 20181 | 33068 | 1.35 | 1.0E-07 | AL163281.2 | NT | Homo sapiens chromosome 21 segment HS21C081 |
| 8157 | 20688 | 33611 | 2.52 | 1.0E-07 | P97435 | SWISSPROT | ENTEROPEPTIDASE (ENTEROKINASE) |
| 8157 | 20688 | 33612 | 2.52 | 1.0E-07 | P97435 | SWISSPROT | ENTEROPEPTIDASE (ENTEROKINASE) |
| 8884 | 21422 | 34347 | 2.7 | 1.0E-07 | AA683578.1 | EST_HUMAN | z51e10.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone IMAGE:434346.3 |
| 9104 | 21711 | 34654 | 1.05 | 1.0E-07 | P57110 | SWISSPROT | ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2) |
| 9535 | 22035 | 34995 | 0.49 | 1.0E-07 | BE327843.1 | EST_HUMAN | huz28r06.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419.3 similar to contains MER18.13 |
| 9849 | 22347 | 35329 | 2.51 | 1.0E-07 | BF674524.1 | EST_HUMAN | MER18 repetitive element: |
| 9855 | 22353 | 35334 | 1.19 | 1.0E-07 | AA396311.1 | EST_HUMAN | 602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274428.5 |
| 10362 | 22856 | | 3.53 | 1.0E-07 | AL163282.2 | NT | EST185054 Brain IV Homo sapiens cDNA |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C082 |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 12013 | 24860 | 30704 | 2.42 | 1.0E-07 | BE048770.1 | EST_HUMAN | h53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:065722 O95722 |
| 7325 | 19852 | 32714 | 0.87 | 9.0E-08 | A1530362.1 | EST_HUMAN | DJ116311.1; |
| 9802 | 22300 | 35285 | 2.1 | 9.0E-08 | AV734818.1 | EST_HUMAN | le51b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3' |
| 11091 | 23573 | 36610 | 3.41 | 9.0E-08 | A1891052.1 | EST_HUMAN | AV734819 cdA Homo sapiens cDNA clone cdaBF808 5' |
| 11519 | 23967 | 37039 | 4.51 | 9.0E-08 | AL163301.2 | NT | wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446832 3' similar to contains OFR.12 |
| 11981 | 24283 | | 2.98 | 9.0E-08 | AJ251973.1 | NT | OFR repetitive element; |
| 635 | 15420 | | 2.27 | 8.0E-08 | A1811352.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C101 |
| 1068 | 13693 | | 0.79 | 8.0E-08 | BE795468.1 | EST_HUMAN | Homo sapiens partial steerin-1 gene |
| 3598 | 16202 | | 1.05 | 8.0E-08 | BE795468.1 | EST_HUMAN | wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3' |
| 8674 | 21213 | 34133 | 3.54 | 8.0E-08 | A1752367.1 | EST_HUMAN | 601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5' |
| 8674 | 21213 | 34134 | 3.54 | 8.0E-08 | A1752367.1 | EST_HUMAN | 601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5' |
| 8545 | 22045 | 35008 | 3.32 | 8.0E-08 | AW1970683.1 | EST_HUMAN | cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH1BC_cn15c02 random |
| 11124 | 23632 | | 2.81 | 8.0E-08 | AF253417.1 | NT | cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH1BC_cn15c02 random |
| 84 | 12780 | 25243 | 2.82 | 7.0E-08 | Q02357 | SWISSPROT | EST382778 MAGE resequences, MAGK Homo sapiens cDNA |
| 1405 | 13968 | 26527 | 11.08 | 7.0E-08 | X04808.1 | NT | Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds |
| 3635 | 16238 | 28713 | 0.7 | 7.0E-08 | P15305 | SWISSPROT | ANKYRIN 1 (ERYTHROCYTE ANKYRIN) |
| 3635 | 16238 | 28714 | 0.7 | 7.0E-08 | P15305 | SWISSPROT | Rat mRNA for ribosomal protein L31 |
| 4002 | 16600 | 29073 | 0.89 | 7.0E-08 | P01806 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 4002 | 16600 | 29074 | 0.89 | 7.0E-08 | P01806 | SWISSPROT | DYNEIN HEAVY CHAIN (DYHC) |
| 10693 | 23223 | | 6.5 | 7.0E-08 | A1535743.1 | EST_HUMAN | IG KAPPA CHAIN V4 REGION OU |
| 11523 | 23971 | 37041 | 6.1 | 7.0E-08 | U24070.1 | NT | IG KAPPA CHAIN V4 REGION OU |
| 12450 | 16238 | 28713 | 3.59 | 7.0E-08 | P15305 | SWISSPROT | cong3.P11.A5 conom Homo sapiens cDNA 3' |
| 12450 | 16238 | 28714 | 3.59 | 7.0E-08 | P15305 | SWISSPROT | Rattus norvegicus Munc13-1 mRNA, complete cds |
| 850 | 13466 | 25974 | 3.81 | 6.0E-08 | AL163248.2 | NT | DYNEIN HEAVY CHAIN (DYHC) |
| 850 | 13466 | 25975 | 3.81 | 6.0E-08 | AL163248.2 | NT | DYNEIN HEAVY CHAIN (DYHC) |
| 2401 | 14969 | 27543 | 2.01 | 6.0E-08 | BE144308.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C048 |
| 4334 | 16921 | 28363 | 1.14 | 6.0E-08 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 7892 | 20434 | | 0.68 | 6.0E-08 | P08547 | SWISSPROT | MRO-HT0168-191189-004-g09 HT0168 Homo sapiens cDNA |
| 9251 | 21777 | | 0.6 | 6.0E-08 | AA827075.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C048 |
| | | | | | | | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| | | | | | | | cb56605.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains |
| | | | | | | | MER12.b3 MER12 repetitive element; |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|-----------------------------|-------------------------------|--|
| 11283 | 23745 | 36802 | 2.61 | 6.0E-08 | P11368 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 11407 | 23858 | | 1.77 | 6.0E-08 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 88 | 12784 | 26247 | 2.33 | 5.0E-08 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2277 | 14851 | 27429 | 1.23 | 5.0E-08 | AA469351.1 | EST_HUMAN | nr033609.at1 NC1_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element; |
| 11692 | 24107 | | 7.32 | 5.0E-08 | P06681 | SWISSPROT | COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE) |
| 11689 | 24233 | 31004 | 1.48 | 5.0E-08 | AW851878.1 | EST_HUMAN | QV0-CT0225-131088-034-412 CT0225 Homo sapiens cDNA |
| 1787 | 14387 | 26831 | 1.53 | 4.0E-08 | P25723 | SWISSPROT | DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR |
| 1787 | 14387 | 26832 | 1.53 | 4.0E-08 | P25723 | SWISSPROT | DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR |
| 2810 | 15527 | | 1.49 | 4.0E-08 | AL079681.1 | EST_HUMAN | DKFZp434J0428_r1_434 (synonym: lites3) Homo sapiens cDNA clone DKFZp434J0428_5' |
| 3100 | 15715 | | 1.01 | 4.0E-08 | AI078417.1 | EST_HUMAN | cd05402.x1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element; |
| 3886 | 16584 | 29055 | 0.67 | 4.0E-08 | UB2668.1 | NT | Homo sapiens short gene, alternatively spliced products, complete cds |
| 6537 | 19136 | 31929 | 1.14 | 4.0E-08 | P52624 | SWISSPROT | URIDINE PHOSPHORYLASE (UDRPASE) |
| 8733 | 21272 | 34182 | 0.57 | 4.0E-08 | O15383 | SWISSPROT | TRANSMEMBRANE PROTEASE, SERINE 2 |
| 9068 | 21803 | 34533 | 0.92 | 4.0E-08 | L42571.1 | NT | Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds |
| 9563 | 22063 | | 0.87 | 4.0E-08 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 10233 | 22728 | | 0.71 | 4.0E-08 | AI016342.1 | EST_HUMAN | cd78d12.at1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622903 3' |
| 10287 | 22782 | 35774 | 3.59 | 4.0E-08 | AI050027.1 | EST_HUMAN | an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1689411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element; |
| 10782 | 23306 | | 1.7 | 4.0E-08 | AJ238617.1 | NT | Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene) |
| 10868 | 23483 | 36510 | 3.7 | 4.0E-08 | BF682493.1 | EST_HUMAN | 602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5' |
| 10868 | 23483 | 36511 | 3.7 | 4.0E-08 | BF682493.1 | EST_HUMAN | 602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5' |
| 11697 | 25022 | | 1.4 | 4.0E-08 | W76159.1 | EST_HUMAN | z885g03.r1 Scores_fetal_liver_NBH-H19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element; |
| 12378 | 24546 | | 3.48 | 4.0E-08 | AJ343353.1 | EST_HUMAN | tb85a11.x1 NC1_CGAP_Cor16 Homo sapiens cDNA clone IMAGE:2062078 3' similar to contains MER18.b3 MER18 MER18 repetitive element; |
| 5785 | 18420 | 31136 | 3.12 | 3.0E-08 | BE018348.1 | EST_HUMAN | b678a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TRC92158 Q82158 |
| 7052 | 18071 | 30462 | 3.77 | 3.0E-08 | AJ792737.1 | EST_HUMAN | SYNTAXIN 17.; |
| 7545 | 20065 | 32939 | 1.41 | 3.0E-08 | AL163246.2 | NT | qs78f11.y6 NC1_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1944045 5' |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C046 |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7730 | 20238 | | 4.17 | 3.0E-08 | AK36352.1 | EST_HUMAN | tr03008.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ; |
| 8812 | 22310 | | 0.51 | 3.0E-08 | AF055086.1 | NT | Homo sapiens MHC class 1 region |
| 11852 | 24087 | | 38.65 | 3.0E-08 | R18420.1 | EST_HUMAN | y02804.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element; |
| 220 | 12881 | | 6.74 | 2.0E-08 | AW302886.1 | EST_HUMAN | tr87006.x1 NCI CGAP_L1281 Homo sapiens cDNA clone IMAGE:2767139 3' |
| 247 | 12007 | | 6.48 | 2.0E-08 | AA425568.1 | EST_HUMAN | zw4807.r1 Soares fetal_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element/contains element MER15 repetitive element ; |
| 522 | 13154 | 25637 | 2.59 | 2.0E-08 | AF198348.1 | NT | Gallus gallus Dach2 protein (Dach2) mRNA, complete cds |
| 688 | 13312 | 25786 | 10.98 | 2.0E-08 | AW889438.1 | EST_HUMAN | MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA |
| 688 | 13312 | 25797 | 10.98 | 2.0E-08 | AW889438.1 | EST_HUMAN | MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA |
| 1027 | 13638 | | 22.68 | 2.0E-08 | BE280477.1 | EST_HUMAN | 60115321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138868 5' |
| 1387 | 13981 | 26508 | 2.09 | 2.0E-08 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 1777 | 14387 | | 1.3 | 2.0E-08 | BET34871.1 | EST_HUMAN | 601670463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845189 5' |
| 1895 | 14480 | | 4.65 | 2.0E-08 | AW270271.1 | EST_HUMAN | tr43F11.x1 NCI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3' |
| 2402 | 15028 | 27587 | 0.97 | 2.0E-08 | AA731948.1 | EST_HUMAN | tr64H01.s1 NCI CGAP_G081 Homo sapiens cDNA clone IMAGE:1261408 3' similar to contains L1.L3 L1 repetitive element ; |
| 2580 | 15143 | | 2.21 | 2.0E-08 | K00218.1 | NT | Sheep His-RNA-GUG |
| 3243 | 15855 | 28337 | 6.85 | 2.0E-08 | O42280 | SWISSPROT | WNT-14 PROTEIN PRECURSOR |
| 3243 | 15855 | 28338 | 6.85 | 2.0E-08 | O42280 | SWISSPROT | WNT-14 PROTEIN PRECURSOR |
| 3928 | 16524 | | 1.93 | 2.0E-08 | AW813820.1 | EST_HUMAN | RC3-ST0187-161089-012-503 ST0187 Homo sapiens cDNA |
| 4152 | 16744 | 28188 | 0.57 | 2.0E-08 | U82888.1 | NT | Homo sapiens af06 gene, alternatively spliced products, complete cds |
| 4494 | 17079 | | 1.74 | 2.0E-08 | AA459040.1 | EST_HUMAN | tr28c07.r1 NCI CGAP_G081 Homo sapiens cDNA clone IMAGE:814980 5' similar to contains L1.L2 L1 repetitive element ; |
| 5082 | 17885 | | 3.83 | 2.0E-08 | AW572881.1 | EST_HUMAN | tr17H08.x2 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element; |
| 5817 | 18441 | 31163 | 0.87 | 2.0E-08 | AA613204.1 | EST_HUMAN | tr60H11.s1 Soares testis_NHT Homo sapiens cDNA clone 1377189 3' |
| 5898 | 18618 | 31354 | 0.87 | 2.0E-08 | AW088924.1 | EST_HUMAN | tr32c04.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595482 3' similar to contains MER18.b3 |
| 7845 | 20488 | 33388 | 1.07 | 2.0E-08 | P10272 | SWISSPROT | MER18 MER18 repetitive element ; |
| 8054 | 20598 | 33503 | 1.2 | 2.0E-08 | AA490121.1 | EST_HUMAN | POL POLYPROTEIN [CONTAINS: PROTEASE, REVERSE TRANSCRIPTASE, ENDONUCLEASE] |
| 8014 | 21551 | | 1.41 | 2.0E-08 | AU139978.1 | EST_HUMAN | tr02p06.s1 Stratiene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839874 3' |
| | | | | | | | AU139978 PLACE1 Homo sapiens cDNA clone PLACE101719 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10413 | 22807 | 35804 | 0.78 | 2.0E-08 | N78087.1 | EST_HUMAN | w7202.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contig... |
| 10413 | 22807 | 35805 | 0.78 | 2.0E-08 | N78087.1 | EST_HUMAN | LTR1.63 LTR1 repetitive element; |
| 11882 | 24283 | | 1.74 | 2.0E-08 | AL163284.2 | NT | w7202.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains |
| | | | | | | | LTR1.63 LTR1 repetitive element; |
| | | | | | | | Homo sapiens chromosome 21 segment HS21C084 |
| 12559 | 25073 | | 1.44 | 2.0E-08 | AF280107.1 | NT | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide |
| 1812 | 14402 | 26947 | 0.98 | 1.0E-08 | AF125348.1 | EST_HUMAN | 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 |
| 2095 | 14674 | | 2.74 | 1.0E-08 | BE141658.1 | EST_HUMAN | polypeptide 5 (CYP3A5) gene, partial cds |
| 5785 | 18410 | 31128 | 4.23 | 1.0E-08 | AJ010770.1 | NT | Homo sapiens carotid 1 (CAV1) gene, exon 3 and partial cds |
| 7748 | 20254 | 33148 | 1.14 | 1.0E-08 | P19474 | SWISSPROT | PM2-HT0130-150888-001-112 HT0130 Homo sapiens cDNA |
| 7978 | 20520 | 33428 | 0.55 | 1.0E-08 | AL163302.2 | NT | Homo sapiens hyperion gene, exons 1-50 |
| | | | | | | | 82 KD RO PROTEIN (SJOJREN SYNDROME TYPE A ANTIGEN (SS-A)) (RQ(SS-A)) |
| 8070 | 20612 | 33525 | 0.85 | 1.0E-08 | AF224688.1 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| | | | | | | | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 |
| | | | | | | | (UBE2D3) genes, complete cds |
| 8070 | 20612 | 33528 | 0.85 | 1.0E-08 | AF224688.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 |
| 8484 | 21023 | 33940 | 1.84 | 1.0E-08 | AJ015304.1 | EST_HUMAN | (UBE2D3) genes, complete cds |
| 9132 | 21687 | 34808 | 0.75 | 1.0E-08 | BE072572.1 | EST_HUMAN | cd35a05.s1 Scores_beta_NHT Homo sapiens cDNA clone IMAGE:1618738 3' |
| | | | | | | | PM2-BT0546-210100-004-002 BT0546 Homo sapiens cDNA |
| 9878 | 22373 | 35350 | 1.16 | 1.0E-08 | P78110 | SWISSPROT | TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) |
| 10449 | 22943 | 35833 | 0.84 | 1.0E-08 | P98083 | SWISSPROT | (TRICARBOXYLATE CARRIER PROTEIN) |
| 11195 | 23700 | 36751 | 3.79 | 1.0E-08 | AF044083.1 | NT | BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1) |
| 12081 | 24353 | | 2.27 | 1.0E-08 | X51755.1 | NT | Homo sapiens major histocompatibility locus class III region |
| 4327 | 16813 | 28356 | 3.93 | 9.0E-08 | AL163278.2 | NT | Human lambda-immunoglobulin constant region complex (germline) |
| 4327 | 16813 | 28357 | 3.93 | 9.0E-08 | AL163279.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 8974 | 22469 | | 0.49 | 9.0E-09 | T97950.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C079 |
| | | | | | | | ye58a12.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121818 3' |
| 7308 | 19839 | 32894 | 8.83 | 8.0E-08 | AI183500.1 | EST_HUMAN | qq42a07.x1 Scores_fetal_Heart_NbHH18W Homo sapiens cDNA clone IMAGE:1732164 3' similar to |
| 7942 | 20484 | 33396 | 2.88 | 8.0E-09 | AW600159.1 | EST_HUMAN | contains MSR1.11 MSR1 repetitive element; |
| 8919 | 21457 | | 2.77 | 8.0E-08 | AA838882.1 | EST_HUMAN | CARD-NN1004-100300-273-c08 NN1004 Homo sapiens cDNA |
| | | | | | | | op74d08.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3' |
| 3687 | 16288 | | 1.87 | 7.0E-08 | D68842.1 | NT | Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3 |
| 4080 | 16678 | | 1 | 7.0E-09 | U50871.1 | NT | [Human familial Alzheimer's disease (STM2) gene, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 7843 | 20385 | | 0.5 | 7.0E-08 | BF108755.1 | EST_HUMAN | 745e10.x1 Soares NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element; |
| 7991 | 20533 | | 0.78 | 7.0E-08 | AA256200.1 | EST_HUMAN | zf60c05.r1 Soares NIHMFu_S1 Homo sapiens cDNA clone IMAGE:681882 5' similar to contains L1.12 L1 repetitive element; |
| 8184 | 21701 | 34844 | 2.88 | 7.0E-09 | L09709.1 | NT | Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region |
| 10088 | 22581 | 35574 | 1.3 | 7.0E-09 | BE264850.1 | EST_HUMAN | 601111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5' |
| 10248 | 22743 | | 0.63 | 7.0E-08 | AA058826.1 | EST_HUMAN | zf58e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381158 3' similar to contains L1.12 L1 repetitive element; |
| 10552 | 23088 | | 2.78 | 7.0E-08 | T97950.1 | EST_HUMAN | ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121818 3' |
| 2188 | 14774 | | 1.16 | 6.0E-08 | AL040438.1 | EST_HUMAN | DKFZp434C0514_1 434 (synonym: hbas3) Homo sapiens cDNA clone DKFZp434C0514 5' |
| 5118 | 17688 | 30128 | 5.44 | 6.0E-08 | BE188421.1 | EST_HUMAN | PM1-HT0527-160200-001-005 HT0527 Homo sapiens cDNA |
| 5246 | 17810 | 30232 | 1 | 6.0E-09 | AW593471.1 | EST_HUMAN | hg18f12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2945807 3' similar to gb:53743 FIBULIN-1, ISOFORM C PRECURSOR (HUMAN); |
| 5248 | 17810 | 30233 | 1 | 6.0E-09 | AW593471.1 | EST_HUMAN | hg18f12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2945807 3' similar to gb:53743 FIBULIN-1, ISOFORM C PRECURSOR (HUMAN); |
| 5582 | 18213 | 30662 | 12.11 | 6.0E-09 | AW185784.1 | EST_HUMAN | xn85h08.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2701311 3' |
| 8512 | 21051 | 33973 | 0.81 | 6.0E-09 | BE161653.1 | EST_HUMAN | MR3-HT0448-280300-201-h12 HT0448 Homo sapiens cDNA |
| 8103 | 21638 | 34578 | 2.37 | 6.0E-09 | | NT | Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA |
| 10177 | 22872 | | 3.89 | 6.0E-09 | AF200823.2 | NT | Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds |
| 10910 | 23143 | 36154 | 1.88 | 6.0E-09 | BF108755.1 | EST_HUMAN | 745e10.x1 Soares NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element; |
| 1480 | 14052 | 26584 | 3.95 | 5.0E-09 | BE149284.1 | EST_HUMAN | RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA |
| 1893 | 14478 | 27038 | 0.93 | 5.0E-09 | AL163284.2 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 6542 | 18141 | 31833 | 2.28 | 5.0E-09 | AA359454.1 | EST_HUMAN | EST168746 Fetal lung II Homo sapiens cDNA 5' end |
| 8521 | 21060 | 33983 | 0.59 | 5.0E-09 | P37071 | SWISSPROT | OLFACTORY RECEPTOR-LIKE PROTEIN COR5 |
| 10007 | 22502 | 35483 | 2.27 | 5.0E-09 | AW798687.1 | EST_HUMAN | PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA |
| 547 | 13178 | | 1.69 | 4.0E-09 | AL163282.2 | NT | Homo sapiens chromosome 21 segment HS21C082 |
| 1000 | 13611 | | 1.89 | 4.0E-09 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 1518 | 14110 | 28648 | 1.81 | 4.0E-09 | 9558718 | NT | Homo sapiens hypothetical protein (AF038169), mRNA |
| 2473 | 15040 | 27608 | 4.54 | 4.0E-09 | AA350878.1 | EST_HUMAN | EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa |
| 7788 | 20331 | 33237 | 0.72 | 4.0E-09 | AA495747.1 | EST_HUMAN | zn04c08.r1 Soares NIHMFu_S1 Homo sapiens cDNA clone IMAGE:788298 5' |
| 8458 | 20688 | 33915 | 0.62 | 4.0E-09 | TC4942.1 | EST_HUMAN | yd11a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:68804 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 10896 | 23510 | | 1.73 | 4.0E-09 | AA195142.1 | EST_HUMAN | z344r12.1 Scores_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:985278 5' similar to gb:L07807 |
| 2390 | 14958 | 27530 | 6.83 | 3.0E-09 | BE222239.1 | EST_HUMAN | DYNAMIN-1 (HUMAN); |
| 2589 | 15151 | 27717 | 0.86 | 3.0E-09 | BE222239.1 | EST_HUMAN | h09009.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 |
| 2677 | 15235 | 27802 | 1.22 | 3.0E-09 | P23249 | EST_HUMAN | MER18 repetitive element; |
| | | | | | | SWISSPROT | h09009.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 |
| | | | | | | SWISSPROT | PROTEIN MOV-10 |
| 3372 | 15980 | 28457 | 1.05 | 3.0E-09 | BE222239.1 | EST_HUMAN | h09009.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 |
| 3423 | 16031 | | 3.13 | 3.0E-09 | AA44272.1 | EST_HUMAN | MER18 repetitive element; |
| 4172 | 16763 | | 3.54 | 3.0E-09 | X16874.1 | NT | z65404.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5' |
| 4517 | 17101 | 29548 | 5.18 | 3.0E-09 | AF175325.1 | NT | H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase |
| 4610 | 17193 | 29639 | 1.52 | 3.0E-09 | Q8Y3R5 | SWISSPROT | Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds |
| | | | | | | SWISSPROT | 258.1 KDA PROTEIN C21ORF5 (KIAA0893) |
| 7841 | 20363 | 33287 | 1.28 | 3.0E-09 | BE465780.1 | EST_HUMAN | h080402.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091 |
| 10146 | 22641 | 35631 | 1.98 | 3.0E-09 | AL163247.2 | NT | O55091 IMPACT PROTEIN.; |
| 10900 | 23420 | 36437 | 3.87 | 3.0E-09 | BF108943.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C047 |
| 10900 | 23420 | 36438 | 3.87 | 3.0E-09 | BF108943.1 | EST_HUMAN | 717208.x1 Scores_NSF_F8_9W_OT_PA_P S1 Homo sapiens cDNA clone IMAGE:3527030 3' |
| 845 | 13461 | | 1.01 | 2.0E-09 | X16874.1 | NT | 717208.x1 Scores_NSF_F8_9W_OT_PA_P S1 Homo sapiens cDNA clone IMAGE:3527030 3' |
| 1301 | 13885 | 28417 | 6.02 | 2.0E-09 | AL163284.2 | NT | H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase |
| 1698 | 14291 | | 10.31 | 2.0E-09 | AL118573.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C084 |
| 2364 | 14835 | 27507 | 2.79 | 2.0E-09 | Q8Y3R5 | SWISSPROT | DKFZp781B1710_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781B1710 5' |
| 4011 | 16909 | 29082 | 4.13 | 2.0E-09 | O60241 | SWISSPROT | 258.1 KDA PROTEIN C21ORF5 (KIAA0893) |
| 4083 | 16378 | 28139 | 0.94 | 2.0E-09 | AI283478.1 | EST_HUMAN | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR |
| 6676 | 19610 | | 0.74 | 2.0E-09 | AA357407.1 | EST_HUMAN | q07009.x1 Scores_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3' |
| | | | | | | EST_HUMAN | EST168142 Kidney IX Homo sapiens cDNA 5' and similar to EST containing L1 repeat |
| 7474 | 19986 | 32861 | 8.48 | 2.0E-09 | AA481430.1 | EST_HUMAN | z63106.r1 Scores_tad_fetus_Nb23-IF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains |
| 7532 | 20052 | 32925 | 0.88 | 2.0E-09 | W28634.1 | EST_HUMAN | Alu repetitive element; |
| 8646 | 21185 | 34104 | 1.72 | 2.0E-09 | AJ271735.1 | NT | 52411 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA |
| 11634 | 24074 | | 1.72 | 2.0E-09 | AF111168.2 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 12238 | 13461 | | 27.08 | 2.0E-09 | X16874.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| | | | | | | NT | Homo sapiens sarine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| | | | | | | NT | H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase |
| 12310 | 25084 | | 2.25 | 2.0E-09 | AA226070.1 | EST_HUMAN | nc11602.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element; |

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Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 1032 | 13642 | | 1.14 | 1.0E-09 | W78152.1 | EST_HUMAN | z078003.s1 Scores_fetal_heart_NIH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to |
| 1148 | 13751 | 26280 | 2.3 | 1.0E-09 | 5031824 | NT | gb1.02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); |
| 1148 | 13751 | 26281 | 2.3 | 1.0E-09 | 5031824 | NT | Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA |
| 2914 | 15531 | 28003 | 1.74 | 1.0E-09 | U80017.1 | NT | Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA |
| 2952 | 15568 | 28042 | 3.98 | 1.0E-09 | M28699.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p-44) gene, partial cds, neuronal apoptosis inhibitory |
| 2952 | 15568 | 28043 | 3.98 | 1.0E-09 | M28699.1 | NT | protein (nlp) and survival motor neuron protein (smn) genes, complete cds |
| 3073 | 15688 | 28160 | 0.77 | 1.0E-09 | BE535440.1 | EST_HUMAN | Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds |
| | | | | | | | Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds |
| 4816 | 17491 | | 5.48 | 1.0E-09 | AA719287.1 | EST_HUMAN | 601058802F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5' |
| 5694 | 18320 | 30819 | 0.87 | 1.0E-09 | AL163283.2 | NT | z035003.s1 Scores_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:414028 3' similar to contains |
| 5998 | 18816 | 31352 | 1.48 | 1.0E-09 | U07000.1 | NT | Alu repetitive element; contains element MER22 repetitive element ; |
| 6283 | 18901 | 31871 | 3.17 | 1.0E-09 | P28694 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C083 |
| 8328 | 20870 | 33794 | 0.87 | 1.0E-09 | A089474.1 | EST_HUMAN | Human breakpoint cluster region (BCR) gene, complete cds |
| 10216 | 22711 | | 2.57 | 1.0E-09 | AL163283.2 | NT | CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS) |
| 12136 | 25032 | 30820 | 3.3 | 1.0E-09 | 11418127 | NT | w038005.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains |
| 12593 | 24944 | | 1.82 | 1.0E-09 | AF260225.1 | NT | MER25.11 MER25 repetitive element ; |
| 1352 | 13947 | 26471 | 1.48 | 9.0E-10 | AW867740.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C083 |
| | | | | | | | Homo sapiens GTP binding protein 1 (GTPBP1), mRNA |
| 2860 | 15479 | 27955 | 6.87 | 9.0E-10 | A0870071.1 | EST_HUMAN | Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced |
| 6922 | 19581 | 32410 | 4.35 | 9.0E-10 | A452982.1 | EST_HUMAN | MPO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA |
| 158 | 12821 | 25309 | 10.47 | 8.0E-10 | U63630.2 | NT | we78h03.x1 Scores_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to |
| 3368 | 15985 | 28472 | 0.69 | 8.0E-10 | BE080748.1 | EST_HUMAN | SW_RL28_HUMAN P47914 60S RIBOSOMAL PROTEIN L28 ; contains element PTR5 repetitive element ; |
| 4279 | 18865 | 28311 | 4.11 | 8.0E-10 | AA376832.1 | EST_HUMAN | 448b09.x1 Scores_NSIF_FB_PW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to |
| 9875 | 22372 | | 2.34 | 8.0E-10 | U36308.2 | NT | TR-C00372 C00372 PUTATIVE P150. ; |
| 730 | 13350 | 25844 | 24.84 | 7.0E-10 | 7706225 | NT | Homo sapiens MCMA4 (MCMA) and DNA-PKcs (PRKDC) genes, partial cds |
| 730 | 13350 | 25845 | 24.84 | 7.0E-10 | 7706225 | NT | QV1-BT0831-150200-071-01 BT0831 Homo sapiens cDNA |
| 1893 | 14256 | 26791 | 2.13 | 7.0E-10 | Q13342 | SWISSPROT | EST188564 Small intestine [Homo sapiens cDNA 5' end |
| 2067 | 14847 | | 1.31 | 7.0E-10 | P08548 | SWISSPROT | Homo sapiens lens major intrinsic protein (MIP) gene, complete cds |
| 2594 | 15156 | | 13 | 7.0E-10 | P08547 | SWISSPROT | Homo sapiens TPA inducible protein (LOC51586), mRNA |
| | | | | | | | Homo sapiens TPA inducible protein (LOC51586), mRNA |
| | | | | | | | LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100) |
| | | | | | | | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| | | | | | | | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3124 | 15738 | 28208 | 2.84 | 7.0E-10 | X00858.1 | NT | H.sapiens DHFR gene, exon 3 |
| 6332 | 18938 | 31714 | 5.26 | 7.0E-10 | AA345220.1 | EST_HUMAN | EST51247 Gall bladder II Homo sapiens cDNA 5' end |
| 7446 | 18970 | 32838 | 1.2 | 7.0E-10 | BF352883.1 | EST_HUMAN | IL3-HT0619-110700-208-D12 HT0619 Homo sapiens cDNA |
| 7652 | 20184 | | 1.43 | 7.0E-10 | P35084 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT |
| 7916 | 20458 | 33364 | 1.68 | 7.0E-10 | AF029701.2 | NT | Homo sapiens presenilin-1 gene, exons 1 and 2 |
| 7916 | 20458 | 33365 | 1.68 | 7.0E-10 | AF029701.2 | NT | Homo sapiens presenilin-1 gene, exons 1 and 2 |
| 10212 | 22707 | 35701 | 0.57 | 7.0E-10 | L08885.1 | NT | Homo sapiens MAD5MEF2-family transcription factor (MEF2C) mRNA, complete cds |
| 11511 | 23858 | 37030 | 1.54 | 7.0E-10 | AW778789.1 | EST_HUMAN | h012602.x1 NCI_CGAP_C014 Homo sapiens cDNA clone IMAGE:3037202 3' similar to contains Alu repetitive element; contains MER7.b1 MER7 repetitive element; |
| 948 | 13558 | 28072 | 3.68 | 6.0E-10 | AJ400877.1 | NT | Homo sapiens ASQL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene |
| 2702 | 15258 | 27827 | 1.89 | 6.0E-10 | AJ424405.1 | EST_HUMAN | h02007.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2085021 3' |
| 4847 | 17425 | | 2.15 | 6.0E-10 | AW653718.1 | EST_HUMAN | RC3-C10254-031088-012-g12 C10254 Homo sapiens cDNA |
| 8718 | 21257 | 34177 | 0.94 | 6.0E-10 | P33730 | SWISSPROT | E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) |
| 8718 | 21257 | 34178 | 0.94 | 6.0E-10 | P33730 | SWISSPROT | E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 2) (LECAM2) (CD62E) |
| 9552 | 22052 | 35015 | 0.52 | 6.0E-10 | P38073 | SWISSPROT | E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 2) (LECAM2) (CD62E) |
| 11731 | 24136 | | 1.47 | 6.0E-10 | AW971923.1 | EST_HUMAN | ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE) |
| 782 | 13410 | | 5.2 | 6.0E-10 | AL046804.1 | EST_HUMAN | EST384012 MAGE reassortment, MAGL Homo sapiens cDNA |
| 3522 | 16127 | 28607 | 0.86 | 5.0E-10 | Q01033 | SWISSPROT | OKFZp434N219_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N219 5' |
| 5002 | 17575 | 30018 | 1.05 | 5.0E-10 | AW028877.1 | EST_HUMAN | HYPOTHETICAL GENE 48 PROTEIN |
| 5002 | 17575 | 30019 | 1.05 | 5.0E-10 | AW028877.1 | EST_HUMAN | OKFZp434N219_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N219 5' |
| 5128 | 17700 | 30134 | 1.37 | 5.0E-10 | AF181897.1 | NT | HYPOTHETICAL GENE 48 PROTEIN |
| 7363 | 18888 | | 1.84 | 5.0E-10 | BF105159.1 | EST_HUMAN | OKFZp434N219_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N219 5' |
| 9455 | 21881 | 34832 | 1.66 | 5.0E-10 | P34878 | SWISSPROT | HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III |
| 9455 | 21881 | 34833 | 1.65 | 5.0E-10 | P34878 | SWISSPROT | HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III |
| 116 | 12787 | | 1.02 | 4.0E-10 | A1221083.1 | EST_HUMAN | OKFZp434N219_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N219 5' |
| 607 | 13235 | 25708 | 0.73 | 4.0E-10 | AA515280.1 | EST_HUMAN | HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III |
| 2039 | 14821 | 27189 | 1.17 | 4.0E-10 | AW594709.1 | EST_HUMAN | HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2608 | 15171 | 27739 | 4.19 | 4.0E-10 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 7228 | 19759 | 32614 | 22.35 | 4.0E-10 | AF224998.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 10097 | 22582 | 35584 | 0.82 | 4.0E-10 | AW263243.1 | EST_HUMAN | UH-H-B12-af4-a-07-Q-UJ.s1 NC1_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3' |
| 10342 | 22638 | 35831 | 1.01 | 4.0E-10 | AI287342.1 | EST_HUMAN | ex3h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653 |
| 948 | 13560 | 26074 | 1.85 | 3.0E-10 | N38113.1 | EST_HUMAN | y92708.s1 Soares melanocyte ZN1H1M Homo sapiens cDNA clone IMAGE:272863 3' similar to contains L1 H L1 repetitive element ; |
| 1395 | 13989 | | 4.43 | 3.0E-10 | AY006150.1 | NT | Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds |
| 4633 | 17216 | 28667 | 1.07 | 3.0E-10 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 4633 | 17216 | 28668 | 1.07 | 3.0E-10 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 5846 | 18274 | 30748 | 0.92 | 3.0E-10 | N50109.1 | EST_HUMAN | yz1g08.s1 Soares_multiple_sclerosis_ZN1H1MSP Homo sapiens cDNA clone IMAGE:282782 3' |
| 6350 | 18855 | 31734 | 1.87 | 3.0E-10 | P20350 | SWISSPROT | RHOMBOID PROTEIN (VEINLET PROTEIN) |
| 6492 | 19093 | 31877 | 2.86 | 3.0E-10 | BE302870.1 | EST_HUMAN | ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806319 5' |
| 7737 | 20245 | 33136 | 2.3 | 3.0E-10 | AV743302.1 | EST_HUMAN | AV743302 CB1 Homo sapiens cDNA clone CBFBGD08 5' |
| 7737 | 20245 | 33137 | 2.3 | 3.0E-10 | AV743302.1 | EST_HUMAN | AV743302 CB1 Homo sapiens cDNA clone CBFBGD08 5' |
| 8695 | 21204 | 34122 | 1.08 | 3.0E-10 | H87208.1 | EST_HUMAN | y874b12.s1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER28 repetitive element ; |
| 8979 | 21517 | 34442 | 1.81 | 3.0E-10 | AW850731.1 | EST_HUMAN | IL3-CT0219-160200-064-B08 CT0219 Homo sapiens cDNA |
| 8979 | 21517 | 34443 | 1.81 | 3.0E-10 | AW850731.1 | EST_HUMAN | IL3-CT0219-160200-064-B08 CT0219 Homo sapiens cDNA |
| 9284 | 21790 | | 0.86 | 3.0E-10 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5 |
| 10359 | 22853 | | 2.13 | 3.0E-10 | T65991.1 | EST_HUMAN | ye11e12.r1 Stragene lung (8837210) Homo sapiens cDNA clone IMAGE:80308 5' |
| 10485 | 22879 | | 1.71 | 3.0E-10 | AA788294.1 | EST_HUMAN | n28g03.s1 NC1_CGAP_CCB1 Homo sapiens cDNA clone IMAGE:1289908 3' |
| 12415 | 24598 | 30911 | 3.44 | 3.0E-10 | BE178517.1 | EST_HUMAN | IL3-H10618-110500-139-E07 HT0618 Homo sapiens cDNA |
| 38 | 12717 | 25178 | 92.79 | 2.0E-10 | P48988 | SWISSPROT | MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) |
| 38 | 12717 | 25177 | 92.79 | 2.0E-10 | P48988 | SWISSPROT | MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) |
| 1942 | 14528 | | 2.33 | 2.0E-10 | U80017.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds |
| 3015 | 15631 | | 0.66 | 2.0E-10 | BF875047.1 | EST_HUMAN | 602136840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5' |
| 5971 | 18582 | | 7.24 | 2.0E-10 | Q28840 | SWISSPROT | (HPRG) |
| 6398 | 18001 | 31779 | 1.42 | 2.0E-10 | AF280107.1 | NT | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds |
| 7414 | 18639 | 32803 | 7.79 | 2.0E-10 | BE791082.1 | EST_HUMAN | 601568208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3840824 5' |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7958 | 20468 | 33407 | 0.54 | 2.0E-10 | P28809 | SWISSPROT | POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H] |
| 7958 | 20468 | 33408 | 0.54 | 2.0E-10 | P28809 | SWISSPROT | POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H] |
| 8228 | 21742 | | 0.85 | 2.0E-10 | BF434585.1 | EST_HUMAN | 7078d08.x1 NCL_CGAP_Kd111 Homo sapiens cDNA clone IMAGE:3842303 3' similar to contains L1.13 L1 repetitive element: |
| 1556 | 14148 | | 2.28 | 1.0E-10 | AW867787.1 | EST_HUMAN | NR0-SN0038-280300-001-401 SN0038 Homo sapiens cDNA |
| 1650 | 14242 | 26776 | 2.41 | 1.0E-10 | AW652123.1 | EST_HUMAN | AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3' |
| 2618 | 15180 | | 1.78 | 1.0E-10 | AW852001.1 | EST_HUMAN | QV0-CT0225-191189-058-e08 CT0225 Homo sapiens cDNA |
| 3548 | 16152 | 28634 | 0.73 | 1.0E-10 | AW832812.1 | EST_HUMAN | QV2-TT0003-161189-013-g10 TT0003 Homo sapiens cDNA |
| 3593 | 16197 | | 0.62 | 1.0E-10 | AL041685.1 | EST_HUMAN | DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5' |
| 3911 | 16197 | | 0.80 | 1.0E-10 | AL041685.1 | EST_HUMAN | DKFZp434N1317_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5' |
| 4087 | 16883 | | 6.83 | 1.0E-10 | AF213884.1 | NT | Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds |
| 4207 | 16786 | 28243 | 5.77 | 1.0E-10 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 4207 | 16786 | 28244 | 5.77 | 1.0E-10 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 4214 | 16803 | 28253 | 1.86 | 1.0E-10 | AB031069.1 | NT | Homo sapiens PCCX1 mRNA for protein containing COXC domain 1, complete cds |
| 4249 | 16837 | | 2.53 | 1.0E-10 | MA30628.1 | NT | Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, test exon |
| 5343 | 17904 | | 1 | 1.0E-10 | AF797745.1 | EST_HUMAN | we82704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.1 MER31 repetitive element: |
| 8182 | 20723 | 33637 | 1.08 | 1.0E-10 | AW408980.1 | EST_HUMAN | FB_9A4 Fetal brain library Homo sapiens cDNA |
| 8589 | 21128 | | 1.03 | 1.0E-10 | AL288340.1 | EST_HUMAN | qtn04610.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element: |
| 10103 | 22588 | | 4.16 | 1.0E-10 | AA081888.1 | EST_HUMAN | zn23p06.r1 Stratiogene neuroepithelium NT2RAM1 637234 Homo sapiens cDNA clone IMAGE:548314 5' |
| 10793 | 23316 | 36325 | 3.47 | 1.0E-10 | AL038280.1 | EST_HUMAN | cy65f03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672861 3' |
| 11672 | 18038 | | 1.58 | 1.0E-10 | X87344.1 | NT | H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 283 | 12839 | 25425 | 0.98 | 9.0E-11 | BE145600.1 | EST_HUMAN | IL2-HT0203-281099-016-c08 HT0203 Homo sapiens cDNA |
| 2152 | 14729 | 27302 | 6.73 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225_1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5' |
| 2152 | 14729 | 27303 | 6.73 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225_1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5' |
| 3430 | 16038 | 28520 | 2.33 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225_1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5' |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3430 | 16038 | 28521 | 2.33 | 9.0E-11 | AL134395.1 | EST_HUMAN | DKFZp547D225_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5' |
| 4588 | 17182 | 29828 | 0.89 | 9.0E-11 | AA775985.1 | EST_HUMAN | ae7801.s1 Strategene echizo brain S11 Homo sapiens cDNA clone IMAGE:970287 3' |
| 5763 | 18389 | | 3.77 | 9.0E-11 | BE079780.1 | EST_HUMAN | RC8-BT0827-140200-011-E08 BT0827 Homo sapiens cDNA |
| 10058 | 22553 | 35548 | 0.98 | 9.0E-11 | AA324960.1 | EST_HUMAN | EST17872 Cerebellum II Homo sapiens cDNA 5' end |
| 10058 | 22553 | 35549 | 0.98 | 9.0E-11 | AA324960.1 | EST_HUMAN | EST17872 Cerebellum II Homo sapiens cDNA 5' end |
| 12059 | 24342 | 30889 | 3.52 | 9.0E-11 | C16835.1 | EST_HUMAN | C16835 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-506808 5' |
| 3150 | 15764 | | 0.38 | 8.0E-11 | H19071.1 | EST_HUMAN | yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element; |
| 4035 | 16833 | 20102 | 0.68 | 8.0E-11 | AA778817.1 | EST_HUMAN | hm54c08.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2101838 3' |
| 4117 | 16711 | 29165 | 5.2 | 8.0E-11 | N23712.1 | EST_HUMAN | yw46c06.s1 Wellmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255288 3' |
| 1487 | 14088 | 26829 | 2.94 | 7.0E-11 | AA330842.1 | EST_HUMAN | EST134382 Embryo, 8 week I Homo sapiens cDNA 5' end |
| 3938 | 16537 | 28004 | 0.84 | 7.0E-11 | AJ277546.2 | NT | Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor |
| 8435 | 20875 | 33889 | 2.91 | 7.0E-11 | AF163864.1 | NT | Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced |
| 10129 | 22824 | | 1.1 | 7.0E-11 | P11389 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 12208 | 24430 | | 1.52 | 7.0E-11 | AV701856.1 | EST_HUMAN | AV701856 ADB Homo sapiens cDNA clone ADBABC08 5' |
| 437 | 13070 | 25568 | 5.57 | 8.0E-11 | M55270.1 | NT | Human matrix Gla protein (MGP) gene, complete cds |
| 437 | 13070 | 25567 | 5.57 | 8.0E-11 | M55270.1 | NT | Human matrix Gla protein (MGP) gene, complete cds |
| 8822 | 19412 | 32228 | 1.03 | 6.0E-11 | L44140.1 | NT | Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's |
| 7880 | 20191 | 33080 | 3.29 | 8.0E-11 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 8305 | 20848 | 33789 | 3.25 | 6.0E-11 | AV727859.1 | EST_HUMAN | AV727859 HTC Homo sapiens cDNA clone HTCA5C08 5' |
| 12 | 12891 | 25147 | 0.9 | 5.0E-11 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 3411 | 12891 | 25147 | 1.29 | 5.0E-11 | AL163283.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 4312 | 16898 | 26343 | 1.04 | 5.0E-11 | P48034 | SWISSPROT | ALDEHYDE OXIDASE |
| 8638 | 18235 | 32037 | 3.02 | 5.0E-11 | AL163213.2 | NT | Homo sapiens chromosome 21 segment HS21C013 |
| 7537 | 20057 | 32831 | 12.3 | 5.0E-11 | 11418798 | NT | Homo sapiens protocadherin beta 3 (PCDH3), mRNA |
| 1448 | 14038 | | 1.41 | 4.0E-11 | AA436042.1 | EST_HUMAN | zn01b12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559 5' |
| 2818 | 15368 | 27937 | 8.36 | 4.0E-11 | BE885600.1 | EST_HUMAN | 601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908285 5' |
| 2897 | 15613 | 28093 | 1.17 | 4.0E-11 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 4725 | 17308 | 29750 | 0.93 | 4.0E-11 | D44686.1 | EST_HUMAN | HUMSUP068 Human brain cDNA Homo sapiens cDNA clone 069 |
| 6802 | 19189 | 32005 | 3.5 | 4.0E-11 | P20095 | SWISSPROT | PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2 |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 7409 | 19934 | | 4.08 | 4.0E-11 | AF224669.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 9316 | 21830 | | 1.44 | 4.0E-11 | BE149425.1 | EST_HUMAN | RC1-HT0256-210100-013-008 HT0256 Homo sapiens cDNA |
| 9580 | 22080 | 35045 | 0.91 | 4.0E-11 | AI6009763.1 | EST_HUMAN | H82g12.x1 NCI_CGAP_Bmt23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP-ZK353.1 |
| 12275 | 24478 | 30937 | 1.36 | 4.0E-11 | 11545732 | NT | CE00385; Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA |
| 1538 | 14130 | 28866 | 3.79 | 3.0E-11 | 6678077 | NT | Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA |
| 4363 | 16950 | | 1.47 | 3.0E-11 | AA309248.1 | EST_HUMAN | EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end |
| 895 | 13607 | 26121 | 1.64 | 2.0E-11 | AI150502.1 | EST_HUMAN | q30c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13 |
| 1227 | 13626 | 26342 | 5.04 | 2.0E-11 | R24807.1 | EST_HUMAN | MER10 repetitive element; |
| 1227 | 13626 | 26343 | 5.04 | 2.0E-11 | R24807.1 | EST_HUMAN | Y943a12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5' |
| 1655 | 14247 | 26780 | 6.04 | 2.0E-11 | L17432.1 | NT | Y943a12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5' |
| 1655 | 14247 | 26781 | 6.04 | 2.0E-11 | L17432.1 | NT | Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and effector receptor-like protein |
| 1659 | 14252 | 26786 | 1.09 | 2.0E-11 | AI126371.1 | EST_HUMAN | COR3beta (COR3beta) genes, complete cds |
| 3230 | 15842 | 26323 | 6.98 | 2.0E-11 | P10263 | SWISSPROT | Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and effector receptor-like protein |
| 3368 | 15978 | 26453 | 0.78 | 2.0E-11 | AI478617.1 | EST_HUMAN | COR3beta (COR3beta) genes, complete cds |
| 3409 | 18018 | 28487 | 0.65 | 2.0E-11 | Q10473 | SWISSPROT | q51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:U02832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.11 L1 repetitive element; |
| 3544 | 19148 | | 1.01 | 2.0E-11 | AF20503.1 | NT | RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1) |
| 4539 | 17123 | | 0.89 | 2.0E-11 | BE065537.1 | EST_HUMAN | tm54c09.x1 NCI_CGAP_K411 Homo sapiens cDNA clone IMAGE:2161836 3' |
| 4711 | 17203 | | 0.65 | 2.0E-11 | AI163227.2 | EST_HUMAN | POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP |
| 5070 | 17643 | | 1.37 | 2.0E-11 | BE062558.1 | EST_HUMAN | ACETYL GALACTOSAMINYL TRANSFERASE (UDP-GALNAc:POLYPEPTIDE, N- |
| 6294 | 18892 | 31661 | 1.2 | 2.0E-11 | AW877808.1 | EST_HUMAN | ACETYL GALACTOSAMINYL TRANSFERASE (GALNAc-T1) |
| 6452 | 19053 | 31838 | 2.02 | 2.0E-11 | AA591028.1 | EST_HUMAN | Homo sapiens FRA3B common fragile region, diadenosine triphosphatase hydrolase (FHT) gene, exon 5 |
| 7246 | 19775 | 32832 | 0.78 | 2.0E-11 | BF592845.1 | EST_HUMAN | RC3-BT0316-170200-014-e05 BT0316 Homo sapiens cDNA |
| 7823 | 20365 | | 0.68 | 2.0E-11 | P37072 | SWISSPROT | Homo sapiens chromosome 21 segment HS21C027 |
| | | | | | | | QV2-BT0256-261089-014-e01 BT0256 Homo sapiens cDNA |
| | | | | | | | QV2-P10073-280300-109-H08 PT0073 Homo sapiens cDNA |
| | | | | | | | nc83M05.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW-PR18_YEAST |
| | | | | | | | P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP18; |
| | | | | | | | 797c03.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3442565 3' |
| | | | | | | | QLFACTORY RECEPTOR-LIKE PROTEIN COR6 |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 9150 | 21685 | | 1.27 | 2.0E-11 | AF028308.1 | NT | Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families |
| 10184 | 22678 | 35671 | 4.6 | 2.0E-11 | Q13608 | SWISSPROT | OLFACTORY RECEPTOR 61 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1) |
| 10409 | 22803 | 35889 | 0.79 | 2.0E-11 | AW885874.1 | EST_HUMAN | RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA |
| 10409 | 22803 | 35900 | 0.79 | 2.0E-11 | AW885874.1 | EST_HUMAN | RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA |
| 10982 | 23506 | 36538 | 2.41 | 2.0E-11 | AA035398.1 | EST_HUMAN | z427g02.s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3' |
| 10982 | 23508 | 36539 | 2.41 | 2.0E-11 | AA035398.1 | EST_HUMAN | z427g02.s1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471784 3' |
| 11805 | 25020 | | 2.8 | 2.0E-11 | AA704195.1 | EST_HUMAN | z177e03.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:480824 3' |
| 11836 | 24200 | | 2.48 | 2.0E-11 | AW842143.1 | EST_HUMAN | RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA |
| 11880 | 24218 | 31043 | 2.25 | 2.0E-11 | BF377859.1 | EST_HUMAN | CM2-TN0140-070800-372-g01 TN0140 Homo sapiens cDNA |
| 12135 | 24388 | | 2.03 | 2.0E-11 | D25217.2 | NT | Homo sapiens mRNA for KIAA0027 protein, partial cds |
| 12283 | 24492 | | 5.24 | 2.0E-11 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 12628 | 24707 | | 3.57 | 2.0E-11 | 11417866 | NT | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 704 | 13325 | 25812 | 2.83 | 1.0E-11 | AJ131016.1 | NT | Homo sapiens SCL gene locus |
| 816 | 13434 | 25839 | 0.84 | 1.0E-11 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C009 |
| 1259 | 13856 | 26372 | 2.96 | 1.0E-11 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 1546 | 14138 | | 1.66 | 1.0E-11 | AF118974.1 | NT | Homo sapiens PRO3078 mRNA, complete cds |
| 2171 | 14748 | 27317 | 2.61 | 1.0E-11 | AF000573.1 | NT | Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds |
| 3546 | 16150 | 28630 | 0.83 | 1.0E-11 | BE004315.1 | EST_HUMAN | GM0-BN0105-170300-262-d12 BN0105 Homo sapiens cDNA |
| 4005 | 17480 | | 0.97 | 1.0E-11 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 5535 | 18167 | 30581 | 15.03 | 1.0E-11 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 5997 | 18617 | 31353 | 0.8 | 1.0E-11 | BF222846.1 | EST_HUMAN | 7p57d01.x1 NC1_OGAP_P128 Homo sapiens cDNA clone IMAGE:3648945 3' similar to contains MER10.b3 |
| 8143 | 20684 | 33598 | 3.16 | 1.0E-11 | 4885646 | NT | MER10 repetitive element; |
| 8517 | 21056 | 33979 | 4.69 | 1.0E-11 | R13174.1 | EST_HUMAN | Homo sapiens PHD finger protein 2 (PHIF2), mRNA |
| 8978 | 21518 | 34440 | 1.38 | 1.0E-11 | BF365119.1 | EST_HUMAN | YF73d08.1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:28168 5' |
| 8978 | 21518 | 34441 | 1.38 | 1.0E-11 | BF365119.1 | EST_HUMAN | QV4-NN1148-250900-423-e03 NN1148 Homo sapiens cDNA |
| 11187 | 23674 | 36721 | 2.46 | 1.0E-11 | BF680078.1 | EST_HUMAN | QV4-NN1149-250900-423-e03 NN1149 Homo sapiens cDNA |
| 2879 | 15595 | 28075 | 0.67 | 9.0E-12 | P20742 | SWISSPROT | 602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285977 5' |
| 9713 | 22211 | 35184 | 5.63 | 9.0E-12 | AL163300.2 | NT | PREGNANCY ZONE PROTEIN PRECURSOR |
| 9713 | 22211 | 35185 | 5.63 | 9.0E-12 | AL163300.2 | NT | Homo sapiens chromosome 21 segment HS21C100 |
| 9261 | 21787 | | 1 | 8.0E-12 | BE074720.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C100 |
| 11911 | 24249 | | 4.51 | 8.0E-12 | AJ271736.1 | NT | IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA |
| 4766 | 17347 | 28796 | 1.88 | 7.0E-12 | Q05904 | SWISSPROT | Homo sapiens Xq pseudautosomal region; segment 2/2 34 KD SPIGULE MATRIX PROTEIN PRECURSOR (LSM34) |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11228 | 23759 | 36815 | 12.18 | 7.0E-12 | AA704735.1 | EST_HUMAN | z223g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3' |
| 3601 | 16205 | | 0.72 | 6.0E-12 | AV730554.1 | EST_HUMAN | AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5' |
| 4440 | 17026 | 29468 | 10.25 | 8.0E-12 | AA732516.1 | EST_HUMAN | nz88111.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element |
| 8828 | 21464 | 34380 | 0.82 | 6.0E-12 | AF003249.1 | NT | Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds |
| 8895 | 21818 | | 1.8 | 6.0E-12 | AA847898.1 | EST_HUMAN | cd10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1387588 similar to contains MER29.12 MER29 repetitive element |
| 1081 | 13688 | 28188 | 2.85 | 5.0E-12 | T06573.1 | EST_HUMAN | EST04462 Fetal brain, Striatogene (cat836208) Homo sapiens cDNA clone HFB0V33 |
| 3437 | 16045 | 28528 | 1.19 | 5.0E-12 | BE047779.1 | EST_HUMAN | tz42805.y1 NCI_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2281217 5' |
| 3780 | 16390 | 28555 | 6.68 | 5.0E-12 | AJ271736.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 6172 | 18784 | 31550 | 5.56 | 5.0E-12 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 6172 | 18784 | 31551 | 5.59 | 5.0E-12 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 6817 | 19214 | 32019 | 9.82 | 5.0E-12 | AW974780.1 | EST_HUMAN | EST388350 IMAGE resequences, MAGN Homo sapiens cDNA |
| 7089 | 19448 | 32264 | 1.12 | 5.0E-12 | AL040739.1 | EST_HUMAN | DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3' |
| 7108 | 19448 | 32264 | 1.14 | 5.0E-12 | AL040739.1 | EST_HUMAN | DKFZp434B1615_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3' |
| 8171 | 20712 | 33628 | 1.43 | 5.0E-12 | AA033745.1 | EST_HUMAN | z01612.s1 Soares_fetal_heart_NIH19W Homo sapiens cDNA clone IMAGE:376718 3' similar to contains L1.13 L1 repetitive element |
| 8802 | 21141 | | 0.7 | 5.0E-12 | AW887037.1 | EST_HUMAN | RC1-OT0088-220300-011-b07 OT0088 Homo sapiens cDNA |
| 8925 | 21453 | | 0.56 | 5.0E-12 | AL078581.1 | EST_HUMAN | DKFZp434J0428_j1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0428 5' |
| 8937 | 21574 | 34504 | 2.42 | 5.0E-12 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 9344 | 21858 | 34808 | 1.04 | 5.0E-12 | P34882 | SWISSPROT | OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HCMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4) |
| 10176 | 22871 | | 4.17 | 5.0E-12 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 10266 | 22761 | 35748 | 0.87 | 5.0E-12 | AL163302.2 | NT | Homo sapiens chromosome 21 segment HS21C102 |
| 10461 | 22855 | 35968 | 2.12 | 5.0E-12 | 6978754 | NT | Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA |
| 265 | 12923 | 25408 | 3.53 | 4.0E-12 | AA700326.1 | EST_HUMAN | z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3' |
| 268 | 12923 | 25409 | 4.43 | 4.0E-12 | AA700326.1 | EST_HUMAN | z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3' |
| 4727 | 17308 | 28752 | 0.82 | 4.0E-12 | A068984.1 | EST_HUMAN | b28805.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR-Q13539 Q13539 MARINER TRANSPOSASE; |
| 7615 | 20128 | | 0.7 | 4.0E-12 | BF445140.1 | EST_HUMAN | rad21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3368077 3' similar to contains MER7.b2 MER7 repetitive element |
| 8185 | 20726 | | 2.2 | 4.0E-12 | AF108907.1 | NT | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 8821 | 21160 | 34075 | 1.2 | 4.0E-12 | AB042816.1 | NT | Bos taurus Mch2 mRNA for mitochondrial carrier homolog 2, complete cds |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 10961 | 23476 | 36501 | 4.25 | 4.0E-12 | AJ228043.1 | NT | Homo sapiens 958 kb contig between AM1.1 and CBR1 on chromosome 21q22, segment 3/3 |
| 12180 | 24416 | | 1.61 | 4.0E-12 | U78027.1 | NT | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 644 | 13267 | 25744 | 2.73 | 3.0E-12 | AW341683.1 | EST_HUMAN | h13401.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:2808377 3' similar to TR-O14517 O14517 SMRP.; |
| 644 | 13267 | 25745 | 2.73 | 3.0E-12 | AW341683.1 | EST_HUMAN | h13401.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:2808377 3' similar to TR-O14517 O14517 SMRP.; |
| 5643 | 18272 | 30746 | 1.18 | 3.0E-12 | AF111168.2 | NT | Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes |
| 8316 | 20857 | 33783 | 0.52 | 3.0E-12 | O35453 | SWISSPROT | SERINE PROTEASE HEPSIN |
| 9035 | 21572 | 34501 | 0.56 | 3.0E-12 | O35453 | SWISSPROT | SERINE PROTEASE HEPSIN |
| 10535 | 23072 | 36085 | 3.26 | 3.0E-12 | U37672.1 | NT | Human prostate specific antigen gene, 5' flanking region |
| 10535 | 23072 | 36086 | 3.26 | 3.0E-12 | U37672.1 | NT | Human prostate specific antigen gene, 5' flanking region |
| 1693 | 14265 | 28820 | 1.05 | 2.0E-12 | AW802131.1 | EST_HUMAN | IL5-UM0071-120400-065-e05 UM0071 Homo sapiens cDNA |
| 3513 | 16118 | 28598 | 0.67 | 2.0E-12 | 6754495 | NT | Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA |
| 4192 | 16781 | 26229 | 0.9 | 2.0E-12 | J01884.1 | NT | Rat U3A small nuclear RNA |
| 4192 | 16781 | 26230 | 0.9 | 2.0E-12 | J01884.1 | NT | Rat U3A small nuclear RNA |
| 4512 | 17096 | | 2.58 | 2.0E-12 | BE063509.1 | EST_HUMAN | CMO-BT0281-031169-087-e03 BT0281 Homo sapiens cDNA |
| 6603 | 19200 | | 1.54 | 2.0E-12 | AW971857.1 | EST_HUMAN | EST383948 IMAGE resequences, MAGL Homo sapiens cDNA |
| 7227 | 19758 | 32613 | 2.97 | 2.0E-12 | T08180.1 | EST_HUMAN | EST06060 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBA13 5' end |
| 7382 | 18908 | 32773 | 1.21 | 2.0E-12 | BE173035.1 | EST_HUMAN | MFR0-HT0659-200400-016-e08 HT0559 Homo sapiens cDNA |
| 7656 | 20168 | 33055 | 2.38 | 2.0E-12 | 11422228 | NT | Homo sapiens Ac-like transposable element (AL TE), mRNA |
| 7894 | 20436 | | 0.6 | 2.0E-12 | AV683827.1 | EST_HUMAN | AV683827 GKC Homo sapiens cDNA clone GKCFZB04 5' |
| 9232 | 21954 | | 2.18 | 2.0E-12 | AF198884.1 | NT | Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds |
| 9898 | 22393 | | 11.42 | 2.0E-12 | BE165960.1 | EST_HUMAN | MFR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA |
| 10408 | 22902 | 35888 | 0.69 | 2.0E-12 | AJ334130.1 | EST_HUMAN | qq07702.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR-Q13538 Q13538 ORF2: FUNCTION UNKNOWN.; |
| 11820 | 24190 | | 2.46 | 2.0E-12 | AL163263.2 | NT | Homo sapiens chromosome 21 segment HS21C083 |
| 128 | 12796 | 25282 | 2.78 | 1.0E-12 | AW627674.1 | EST_HUMAN | h180a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.1 MER18 repetitive element; |
| 2031 | 14613 | | 1.53 | 1.0E-12 | AJ871726.1 | EST_HUMAN | wm51f07.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2439463 3' similar to contains L1.b3 L1 repetitive element; |
| 3106 | 15721 | 28191 | 1.33 | 1.0E-12 | AF000991.1 | NT | Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds |
| 3106 | 15721 | 28192 | 1.33 | 1.0E-12 | AF000991.1 | NT | Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds |
| 3943 | 16541 | 26007 | 38.65 | 1.0E-12 | AU132248.1 | EST_HUMAN | AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 3943 | 16541 | 28008 | 38.85 | 1.0E-12 | AU132248.1 | EST_HUMAN | AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' |
| 6121 | 18736 | | 1.85 | 1.0E-12 | U82828.1 | NT | Homo sapiens ataxia telangiectasia (ATM) gene, complete cds |
| 6192 | 18802 | | 1.95 | 1.0E-12 | Q8Y2G7 | SWISSPROT | HYPOTHETICAL ZINC FINGER PROTEIN KIA0861 |
| 6653 | 19249 | 32051 | 0.7 | 1.0E-12 | AF22843.1 | NT | Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene |
| 7170 | 19702 | 32549 | 1.74 | 1.0E-12 | AF196884.1 | NT | Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds |
| 7204 | 19735 | 32587 | 9.7 | 1.0E-12 | AI248533.1 | EST_HUMAN | qh68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849014 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element; |
| 7204 | 19735 | 32588 | 9.7 | 1.0E-12 | AI248533.1 | EST_HUMAN | qh68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849014 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element; |
| | | | | | | | Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV8S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV8S2A2PT, TCRBV7S2A1N4T, TCRBV13S3P13S3> |
| 8426 | 20986 | 33880 | 0.54 | 1.0E-12 | U68059.1 | NT | ec28d05.s1 Stragene ovary (#837217) Homo sapiens cDNA clone IMAGE:857577 3' |
| 8639 | 21178 | 34098 | 1.18 | 1.0E-12 | AA782323.1 | EST_HUMAN | EST374237 IMAGE resequences, MAGG Homo sapiens cDNA |
| 11723 | 24130 | 37154 | 4.65 | 1.0E-12 | AW962164.1 | EST_HUMAN | w83308.x1 NCI CGAP Cor16 Homo sapiens cDNA clone IMAGE:2392095 3' |
| 11941 | 24273 | | 1.6 | 1.0E-12 | AI738592.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C068 |
| 12097 | 24990 | | 2.72 | 1.0E-12 | AL163289.2 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 12424 | 24909 | | 2.02 | 1.0E-12 | AF224699.1 | NT | Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5 |
| 4019 | 16617 | 28092 | 0.91 | 9.0E-13 | AB072600.1 | NT | z28506.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:283651 3' |
| 9519 | 22019 | | 3.1 | 9.0E-13 | N88693.1 | EST_HUMAN | Homo sapiens prion protein (PrP) gene, complete cds |
| 746 | 13366 | 25860 | 4.58 | 8.0E-13 | U28185.1 | NT | Homo sapiens prion protein (PrP) gene, complete cds |
| 746 | 13366 | 25861 | 4.58 | 8.0E-13 | U28185.1 | NT | Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds |
| 1878 | 14464 | 27021 | 3.95 | 8.0E-13 | U90017.1 | NT | wm3109.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3' |
| 8056 | 20598 | 33505 | 0.68 | 8.0E-13 | AI894398.1 | EST_HUMAN | wm3109.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3' |
| 8056 | 20598 | 33506 | 0.68 | 8.0E-13 | AI894398.1 | EST_HUMAN | Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds |
| 10051 | 22546 | | 2.58 | 8.0E-13 | U78027.1 | NT | |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11609 | 24052 | 37117 | 2.51 | 8.0E-13 | U68080.1 | NT | Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S6A3N2T, TCRBV13S8A2T, TCRBV6S8P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV6S2, TCRBV6S8A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12P |
| 8178 | 20717 | | 0.63 | 7.0E-13 | Q85155 | SWISSPROT | OLFACTORY RECEPTOR-LIKE PROTEIN OLF2 |
| 12212 | 24435 | | 37.61 | 7.0E-13 | BE78223.1 | EST_HUMAN | 001403285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866613 5' |
| 12448 | 24563 | | 1.71 | 7.0E-13 | Q10473 | SWISSPROT | POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1) |
| 2149 | 14728 | 27290 | 6.02 | 6.0E-13 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 3384 | 16972 | | 0.78 | 5.0E-13 | R78338.1 | EST_HUMAN | y6204.1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:145759 5' |
| 3444 | 16952 | | 1.84 | 5.0E-13 | AA435773.1 | EST_HUMAN | z177a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Abu repetitive element; contains element MER22 repetitive element; |
| 6958 | 19535 | 32359 | 0.68 | 5.0E-13 | P08983 | SWISSPROT | GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30) |
| 10739 | 23264 | 36279 | 2.49 | 5.0E-13 | P07313 | SWISSPROT | MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK) |
| 1908 | 14493 | | 3.69 | 4.0E-13 | AW378614.1 | EST_HUMAN | PM2-HT0224-221069-001-e11 HT0224 Homo sapiens cDNA |
| 2500 | 15084 | | 1.71 | 4.0E-13 | AF003529.1 | NT | Homo sapiens glycylalanine 3 (GPC3) gene, partial cds and flanking repeat regions |
| 4858 | 17438 | | 1.03 | 4.0E-13 | AA454054.1 | EST_HUMAN | z149d07.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:785489 5' |
| 5774 | 18368 | 31113 | 5.09 | 4.0E-13 | BE169131.1 | EST_HUMAN | PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA |
| 7257 | 19785 | 32841 | 1.07 | 4.0E-13 | AB037750.1 | NT | Homo sapiens mRNA for KIAA1329 protein, partial cds |
| 7807 | 20120 | 32897 | 0.81 | 4.0E-13 | AA431529.1 | EST_HUMAN | z178g12.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763 G452763 COR1 MRNA. |
| 7705 | 20214 | | 1.84 | 4.0E-13 | N44281.1 | EST_HUMAN | y633g05.1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:273080 5' similar to PIRJA32895 A32895 t complex sterility protein - mouse; |
| 8775 | 21314 | 34236 | 0.94 | 4.0E-13 | AL043810.1 | EST_HUMAN | DKFZp434A0128_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434A0128 5' |
| 9833 | 22429 | 35403 | 4.28 | 4.0E-13 | AL289831.1 | EST_HUMAN | q132d05.x1 NC1_CGAP_K145 Homo sapiens cDNA clone IMAGE:1898945 3' similar to contains Abu repetitive element; |
| 11048 | 23559 | 36585 | 1.91 | 4.0E-13 | AA435819.1 | EST_HUMAN | z178g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3' |
| 11048 | 23559 | 36586 | 1.91 | 4.0E-13 | AA435819.1 | EST_HUMAN | z178g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3' |
| 192 | 12852 | | 4.5 | 3.0E-13 | AF003528.1 | NT | Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions |
| 898 | 13512 | | 4.67 | 3.0E-13 | AA430310.1 | EST_HUMAN | z168g08.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781408 5' |
| 2408 | 14976 | 27550 | 1.06 | 3.0E-13 | ALJ21738.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 2519 | 15083 | | 6.72 | 3.0E-13 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2687 | 15245 | 27812 | 2.75 | 3.0E-13 | BF372682.1 | EST_HUMAN | CM3-FT0100-140700-242-M08 FT0100 Homo sapiens cDNA |
| 3221 | 15633 | | 3.1 | 3.0E-13 | AA745844.1 | EST_HUMAN | cb18d02.a1 NCI_QGAP_Kd5 Homo sapiens cDNA clone IMAGE:1324035 3' |
| 3551 | 16155 | 28637 | 1.04 | 3.0E-13 | P18616 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1) |
| 3551 | 16155 | 28638 | 1.04 | 3.0E-13 | P18616 | SWISSPROT | DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1) |
| 5730 | 18356 | 31060 | 0.7 | 3.0E-13 | AA134017.1 | EST_HUMAN | zn88h10.1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR 12 THR repetitive element ; |
| 5730 | 18356 | 31061 | 0.7 | 3.0E-13 | AA134017.1 | EST_HUMAN | zn88h10.1 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR 12 THR repetitive element ; |
| 6143 | 18757 | 31515 | 0.88 | 3.0E-13 | AW005639.1 | EST_HUMAN | wz88c02.x1 NCI_QGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139 O75139 KIAA0644 PROTEIN. ; |
| 7824 | 20366 | 33274 | 9.98 | 3.0E-13 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 8021 | 20563 | 33464 | 0.66 | 3.0E-13 | AA352487.1 | EST_HUMAN | EST60487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Re-reactive factor |
| 8021 | 20563 | 33465 | 0.66 | 3.0E-13 | AA352487.1 | EST_HUMAN | EST60487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Re-reactive factor |
| 10558 | 23092 | | 4.07 | 3.0E-13 | AJ084768.1 | EST_HUMAN | HA0536 Human fetal liver cDNA library Homo sapiens cDNA |
| 10924 | 23443 | 36464 | 2.91 | 3.0E-13 | BE063506.1 | EST_HUMAN | CM0-BT0281-031169-087-a03 BT0281 Homo sapiens cDNA |
| 11469 | 23919 | 36868 | 2.49 | 3.0E-13 | AL163248.2 | NT | Homo sapiens chromosome 21 segment HS21C048 |
| 161 | 12824 | 25312 | 2.56 | 2.0E-13 | U52111.2 | NT | Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein > |
| 260 | 12919 | 25406 | 2.22 | 2.0E-13 | U23839.1 | NT | Dario ratio fibroblast growth factor receptor 4 mRNA, complete cds |
| 1313 | 13907 | 26427 | 8.94 | 2.0E-13 | AF239710.1 | NT | Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds |
| 3038 | 15654 | 26133 | 0.58 | 2.0E-13 | 8824119 | NT | Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA |
| 3038 | 15654 | 26134 | 0.58 | 2.0E-13 | 8824119 | NT | Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA |
| 3320 | 15630 | 28407 | 1.2 | 2.0E-13 | BF431898.1 | EST_HUMAN | ncb76005.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' |
| 3555 | 16156 | 28842 | 1.14 | 2.0E-13 | AF108907.1 | NT | Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds |
| 4188 | 16776 | | 1.9 | 2.0E-13 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C078 |
| 6271 | 18879 | 31647 | 5.27 | 2.0E-13 | Q06852 | SWISSPROT | CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1) |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6805 | 18639 | 32475 | 7.42 | 2.0E-13 | X16912.1 | NT | Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2 |
| 10355 | 22649 | 35943 | 4.58 | 2.0E-13 | 5031868 | NT | Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA |
| 11683 | 24236 | | 20.31 | 2.0E-13 | AW882155.1 | EST_HUMAN | CMD-NIN0001-100300-274-e11 NN0001 Homo sapiens cDNA |
| 313 | 12967 | 25455 | 1.8 | 1.0E-13 | S74128.1 | NT | FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2] |
| 821 | 13534 | 26052 | 4.35 | 1.0E-13 | AJ007973.1 | NT | Homo sapiens LGMD2B gene |
| 1381 | 13974 | 26502 | 1.01 | 1.0E-13 | X87344.1 | NT | H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 2068 | 14648 | 27220 | 1.8 | 1.0E-13 | AA720574.1 | EST_HUMAN | nm21g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 |
| 4116 | 16710 | | 2.21 | 1.0E-13 | AA324394.1 | EST_HUMAN | THR repetitive element; |
| 4698 | 17278 | 28724 | 1.51 | 1.0E-13 | BF340887.1 | EST_HUMAN | EST127235 Carabellum II Homo sapiens cDNA 5' end similar to EST containing L1 repeat |
| 7851 | 20383 | 33296 | 0.77 | 1.0E-13 | AA577812.1 | EST_HUMAN | 602038008F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4185966 5' |
| 7851 | 20383 | 33297 | 0.77 | 1.0E-13 | AA577812.1 | EST_HUMAN | nm24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu |
| 10002 | 22497 | | 0.9 | 1.0E-13 | Q15481 | SWISSPROT | repetitive element;contains element MER24 repetitive element; |
| 10202 | 22697 | 35681 | 0.52 | 1.0E-13 | AF300701.1 | NT | nm24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu |
| 11256 | 23786 | 36842 | 15.07 | 1.0E-13 | BF108755.1 | EST_HUMAN | repetitive element;contains element MER24 repetitive element; |
| 11714 | 24124 | | 1.87 | 1.0E-13 | AV19377.1 | EST_HUMAN | MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN) |
| 12393 | 24553 | | 4.28 | 1.0E-13 | AJ271735.1 | NT | Mus musculus osteoblastic protein tyrosine phosphatase mRNA, complete cds |
| 355 | 13004 | 25488 | 4.61 | 9.0E-14 | AA781159.1 | EST_HUMAN | 745e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29 b2 MER29 repetitive element; |
| 359 | 13005 | 25489 | 2.07 | 9.0E-14 | AA781159.1 | EST_HUMAN | AV19377 DC8 Homo sapiens cDNA clone DCBAIE03 5' |
| 2545 | 15109 | | 3.84 | 9.0E-14 | AW861577.1 | EST_HUMAN | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 2627 | 15189 | 27757 | 1.41 | 9.0E-14 | AJ133127.1 | NT | qj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 |
| 2627 | 15189 | 27758 | 1.41 | 9.0E-14 | AJ133127.1 | NT | repetitive element; |
| 2782 | 15335 | 27905 | 3.29 | 9.0E-14 | AB038162.1 | NT | qj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 |
| 3145 | 15759 | 28225 | 4.32 | 9.0E-14 | AW513286.1 | EST_HUMAN | repetitive element; |
| 3275 | 13004 | 25488 | 0.71 | 9.0E-14 | AA781159.1 | EST_HUMAN | RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA |
| 3886 | 16464 | 28928 | 7.24 | 9.0E-14 | D14547.1 | NT | Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene) |
| 4870 | 17448 | 28997 | 1.77 | 9.0E-14 | AJ002153.1 | NT | Homo sapiens TFF gene cluster for trefoil factor, complete cds |
| | | | | | | | nm24d05.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707833 3' |
| | | | | | | | qj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 |
| | | | | | | | repetitive element; |
| | | | | | | | Human DNA, SINE repetitive element |
| | | | | | | | Sagittarius oedipus gene for seminal vesicle secreted protein semenogelin I |

Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 3545 | 16149 | | 0.97 | 8.0E-14 | BE468263.1 | EST_HUMAN | h271c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3' |
| 4028 | 16627 | | 3.29 | 8.0E-14 | R76269.1 | EST_HUMAN | Y72a03.r1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:144786 3' |
| 9369 | 20308 | 33211 | 36.57 | 8.0E-14 | X89211.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 9479 | 21878 | 34826 | 4.61 | 8.0E-14 | AA218316.1 | EST_HUMAN | zq17c10.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:628870 3' |
| 11310 | 23803 | | 4.45 | 8.0E-14 | BE062556.1 | EST_HUMAN | QV2-BT0258-261089-014-401 BT0258 Homo sapiens cDNA |
| 12106 | 24368 | 30972 | 2.07 | 8.0E-14 | A1688118.1 | EST_HUMAN | wc92h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3' |
| | | | | | | | x467a10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823146 3' similar to contains MER10.12 |
| 1671 | 15447 | | 2.78 | 7.0E-14 | AW151973.1 | EST_HUMAN | MER10 repetitive element; |
| 8851 | 21390 | | 0.54 | 7.0E-14 | AL163265.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 390 | 13036 | 25526 | 14.21 | 6.0E-14 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 9736 | 22234 | 35212 | 3.27 | 6.0E-14 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 9736 | 22234 | 35213 | 3.27 | 6.0E-14 | AF020503.1 | NT | Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 |
| 646 | 13269 | 25747 | 5.26 | 5.0E-14 | Q63120 | SWISSPROT | CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) |
| | | | | | | | x403b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1 |
| 5209 | 17774 | 30197 | 1.53 | 5.0E-14 | AW073781.1 | EST_HUMAN | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 5724 | 18350 | 31053 | 4.91 | 5.0E-14 | P08547 | SWISSPROT | S-ANTIGEN PROTEIN PRECURSOR |
| 1162 | 15434 | | 1.81 | 4.0E-14 | P04828 | SWISSPROT | Homo sapiens LGMD2B gene |
| 1920 | 14505 | 27062 | 3.86 | 4.0E-14 | AJ007873.1 | NT | 2k67a06.r1 Soares_pregnant_luteus_NH-IPU Homo sapiens cDNA clone IMAGE:487858 5' |
| 3816 | 16416 | | 0.84 | 4.0E-14 | AA048502.1 | EST_HUMAN | yy73c12.s1 Soares_multiple_sclerosis_2NHIMSP Homo sapiens cDNA clone IMAGE:278180 3' similar to contains L1.13 L1 repetitive element; |
| 4379 | 16866 | 28412 | 0.9 | 4.0E-14 | N46328.1 | EST_HUMAN | H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 7899 | 20441 | | 0.49 | 4.0E-14 | X87344.1 | NT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 11633 | 24073 | 37135 | 1.91 | 4.0E-14 | P08548 | SWISSPROT | wm08c03.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element; |
| 12457 | 25107 | | 4.37 | 4.0E-14 | A1886224.1 | EST_HUMAN | R. norvegicus mRNA for GPC2 protein |
| 985 | 13597 | 28110 | 1.28 | 3.0E-14 | X85466.1 | NT | xp45f12.x1 NCI_CGAP_JH11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element; |
| 5059 | 17632 | 30075 | 0.74 | 3.0E-14 | AW285354.1 | EST_HUMAN | |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 6832 | 19422 | 32237 | 1.08 | 3.0E-14 | AI420786.1 | EST_HUMAN | ta91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 O00519 FATTY ACID AMIDE HYDROLASE.; |
| 6832 | 19422 | 32238 | 1.08 | 3.0E-14 | AI420786.1 | EST_HUMAN | ta91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 O00519 FATTY ACID AMIDE HYDROLASE.; |
| 8722 | 21281 | 34181 | 0.96 | 3.0E-14 | N42165.1 | EST_HUMAN | y07b10.1 Scores melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:270523 5' |
| 10872 | 23383 | 38408 | 2.75 | 3.0E-14 | BE88016.1 | EST_HUMAN | 601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5' |
| 11118 | 17832 | 30076 | 9.84 | 3.0E-14 | AW285354.1 | EST_HUMAN | xp45f12.x1 NCI_CGAP_H111 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element; |
| 12689 | 24884 | | 1.64 | 3.0E-14 | AL163285.2 | NT | Homo sapiens chromosome 21 segment HS21C085 |
| 413 | 13048 | 25539 | 2.51 | 2.0E-14 | AJ271738.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 413 | 13048 | 25540 | 2.51 | 2.0E-14 | AJ271738.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 719 | 15422 | 25828 | 9.8 | 2.0E-14 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2431 | 14898 | | 1.48 | 2.0E-14 | AW372888.1 | EST_HUMAN | RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA |
| 2504 | 15068 | | 1.07 | 2.0E-14 | 7657528 | NT | Homo sapiens rhadoid tumor deletion region protein 1 (RTDR1), mRNA |
| 2567 | 15131 | 27689 | 1.03 | 2.0E-14 | AL163209.2 | NT | Homo sapiens chromosome 21 segment HS21C008 |
| 2689 | 15256 | | 0.88 | 2.0E-14 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 5715 | 18341 | 30847 | 0.95 | 2.0E-14 | BF380861.1 | EST_HUMAN | IL2-JT0072-240800-142-D07 UT0072 Homo sapiens cDNA |
| 5804 | 18428 | 31148 | 0.8 | 2.0E-14 | AI312351.1 | EST_HUMAN | ta78h01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element; |
| 5895 | 18517 | 31242 | 2.86 | 2.0E-14 | U01317.1 | NT | Human beta globin region on chromosome 11 |
| 6863 | 18540 | | 0.88 | 2.0E-14 | BE000550.1 | EST_HUMAN | RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA |
| 7329 | 18856 | 32719 | 1.12 | 2.0E-14 | P56163 | SWISSPROT | ZINC-FINGER PROTEIN NEURO-Q4 |
| 7518 | 20038 | 32808 | 20.34 | 2.0E-14 | BE158761.1 | EST_HUMAN | IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA |
| 7518 | 20038 | 32807 | 20.34 | 2.0E-14 | BE158761.1 | EST_HUMAN | IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA |
| 9831 | 22328 | 35311 | 0.54 | 2.0E-14 | AI878795.1 | EST_HUMAN | wf58g10.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2482034 3' similar to contains Alu repetitive element |
| 10659 | 23191 | 36206 | 4.65 | 2.0E-14 | AW139800.1 | EST_HUMAN | U1-H-B11-adv-a-10-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3' |
| 12668 | 24968 | | 3.3 | 2.0E-14 | AF008191.1 | NT | Homo sapiens putative G6 protein (GR6) gene, complete cds |
| 12817 | 15068 | | 1.99 | 2.0E-14 | 7657528 | NT | Homo sapiens rhadoid tumor deletion region protein 1 (RTDR1), mRNA |
| 1105 | 13708 | 28218 | 1.89 | 1.0E-14 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 1452 | 14044 | 28572 | 6.88 | 1.0E-14 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 1452 | 14044 | 28573 | 6.88 | 1.0E-14 | AL163268.2 | NT | Homo sapiens chromosome 21 segment HS21C068 |
| 2044 | 14628 | 27195 | 7.63 | 1.0E-14 | L44140.1 | NT | Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 2228 | 14803 | 27374 | 5.33 | 1.0E-14 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 2453 | 15020 | 27591 | 5.89 | 1.0E-14 | A001689.1 | NT | Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds |
| 2971 | 15597 | 28069 | 1.51 | 1.0E-14 | P05227 | SWISSPROT | HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHIRP-II) |
| 3203 | 15816 | 28280 | 3.91 | 1.0E-14 | BF335227.1 | EST_HUMAN | RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA |
| 3203 | 15815 | 28291 | 3.91 | 1.0E-14 | BF335227.1 | EST_HUMAN | RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA |
| 3955 | 16553 | 29022 | 2.1 | 1.0E-14 | AA882984.1 | EST_HUMAN | ae88c12.s1 Striatogene schizob brain S11 Homo sapiens cDNA clone IMAGE:371350 3' |
| 4572 | 17155 | 29599 | 1.71 | 1.0E-14 | AW275852.1 | EST_HUMAN | xq39h10.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2733059 3' |
| 5977 | 18597 | 31332 | 2.03 | 1.0E-14 | AF126145.1 | NT | Bos taurus xenobiotic/medium-chain fatty acid-CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds |
| 6778 | 24770 | 32183 | 12 | 1.0E-14 | 11437150 | NT | Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA |
| 6778 | 24770 | 32184 | 12 | 1.0E-14 | 11437150 | NT | Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA |
| 1620 | 14213 | 28744 | 1.19 | 9.0E-15 | 7427522 | NT | Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA |
| 2217 | 14782 | | 1.39 | 9.0E-15 | AF196778.1 | NT | Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel α) |
| 7507 | 20029 | 32892 | 3.77 | 9.0E-15 | P21416 | SWISSPROT | GAG POLYPEPTIDE [CONTAINS: CORE PROTEINS P15, P12, P30, P10] |
| 7969 | 20501 | 33410 | 1.38 | 9.0E-15 | BE603559.1 | EST_HUMAN | 601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3980158 5' |
| 12580 | 24690 | | 1.78 | 9.0E-15 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 2837 | 13138 | | 1.17 | 8.0E-15 | BE261482.1 | EST_HUMAN | 601149832F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3184023 5' |
| 7233 | 19783 | 32819 | 1.29 | 7.0E-15 | BF035327.1 | EST_HUMAN | 60145831F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882088 5' |
| 10331 | 22825 | | 2.53 | 7.0E-15 | AW241958.1 | EST_HUMAN | nt77d02.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element: |
| 11776 | 24164 | | 1.78 | 7.0E-15 | AA284485.1 | EST_HUMAN | zs57d08.r1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gb.L21834 STEROL O-ACYLTRANSFERASE (HUMAN); contains L1.1 L1 repetitive element: |
| 1031 | 13641 | 26156 | 6.29 | 6.0E-15 | AJ271738.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 6077 | 18694 | 31440 | 1.18 | 6.0E-15 | X73462.1 | NT | O.aries mRNA for hair keratin cysteine-rich protein |
| 6077 | 18694 | 31441 | 1.18 | 6.0E-15 | X73462.1 | NT | O.aries mRNA for hair keratin cysteine-rich protein |
| 11182 | 25128 | | 1.86 | 6.0E-15 | AW636843.1 | EST_HUMAN | QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA |
| 12648 | 24722 | | 1.3 | 6.0E-15 | BF432200.1 | EST_HUMAN | ne881c12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' |
| 435 | 13068 | 25563 | 5.19 | 5.0E-15 | AL163208.2 | NT | Homo sapiens chromosome 21 segment HS21C008 |
| 2789 | 15342 | 27912 | 2.35 | 6.0E-15 | U691328.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 3515 | 16120 | | 1.08 | 5.0E-15 | AW286817.1 | EST_HUMAN | UIH-BW0-qib-g-10-Q-UJ.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731219 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 5289 | 17881 | | 1.28 | 5.0E-15 | P11389 | SWISSPROT | RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE] |
| 10555 | 23091 | | 2.72 | 5.0E-15 | AV730056.1 | EST_HUMAN | AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5' |
| 452 | 12881 | 25137 | 2.33 | 4.0E-15 | AL163303.2 | NT | Homo sapiens chromosome 21 segment HS21C103 |
| 6771 | 18384 | 32173 | 0.79 | 4.0E-15 | AB007970.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501 |
| 10940 | 20287 | 33184 | 2.54 | 4.0E-15 | AJ130894.1 | NT | Homo sapiens mRNA for transcription factor |
| 10940 | 20287 | 33185 | 2.54 | 4.0E-15 | AJ130894.1 | NT | Homo sapiens mRNA for transcription factor |
| 4287 | 16883 | | 7.28 | 3.0E-15 | N89452.1 | EST_HUMAN | LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN) |
| 5060 | 17833 | | 0.57 | 3.0E-15 | P92485 | SWISSPROT | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 |
| 5178 | 17748 | 30175 | 0.72 | 3.0E-15 | AA078097.1 | EST_HUMAN | 7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03 |
| 5179 | 17748 | 30176 | 0.72 | 3.0E-15 | AA078097.1 | EST_HUMAN | 7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03 |
| 6804 | 18638 | | 1.41 | 3.0E-15 | Q84825 | SWISSPROT | GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1) |
| 7323 | 18650 | 32711 | 3.48 | 3.0E-15 | M27685.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| 7323 | 18650 | 32712 | 3.48 | 3.0E-15 | M27685.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| 9839 | 22337 | | 2.32 | 3.0E-15 | AA807128.1 | EST_HUMAN | cc38a07.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11 MER19 repetitive element ; |
| 10673 | 23205 | 36218 | 3.36 | 3.0E-15 | AB026888.1 | NT | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 12114 | 24987 | | 1.36 | 3.0E-15 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 271 | 12928 | 25415 | 4.1 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 391 | 13037 | 25528 | 3.78 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 391 | 13037 | 25527 | 3.78 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 2410 | 14978 | 27552 | 1.44 | 2.0E-15 | BE350127.1 | EST_HUMAN | ht08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER28.b3 MER28 repetitive element ; |
| 2410 | 14978 | 27553 | 1.44 | 2.0E-15 | BE350127.1 | EST_HUMAN | ht08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER28.b3 MER28 repetitive element ; |
| 3558 | 16163 | 28845 | 0.73 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 3559 | 16163 | 28848 | 0.73 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 4142 | 16734 | 28188 | 0.85 | 2.0E-15 | AW238468.1 | EST_HUMAN | xp28801.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521 3' similar to contains L1.83 L1 repetitive element ; |
| 4729 | 17310 | | 2.72 | 2.0E-15 | A1808335.1 | EST_HUMAN | wf07708.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2349823 3' similar to TR:Q61043 Q61043 NINEIN ; |
| 5332 | 17883 | 30306 | 0.83 | 2.0E-15 | P13983 | SWISSPROT | REPEPTITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR |
| 5332 | 17893 | 30307 | 0.83 | 2.0E-15 | P13983 | SWISSPROT | REPEPTITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR |
| 6329 | 18935 | 31711 | 1.02 | 2.0E-15 | BE562352.1 | EST_HUMAN | 601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877268 5' |
| 6329 | 18935 | 31712 | 1.02 | 2.0E-15 | BE562352.1 | EST_HUMAN | 601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877268 5' |
| 7168 | 19700 | | 1.37 | 2.0E-15 | AJ400877.1 | NT | Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene |
| 7315 | 18842 | 32703 | 2.51 | 2.0E-15 | AA704195.1 | EST_HUMAN | z177e03.a1 Soares_fetal_liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460824 3' |
| 7427 | 19851 | 32816 | 4.48 | 2.0E-15 | W05084.1 | EST_HUMAN | z177d10.11 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:288875 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE ; |
| 8837 | 21376 | 34300 | 2.62 | 2.0E-15 | D14547.1 | NT | Human DNA, SINE repetitive element |
| 9002 | 21539 | 34468 | 0.87 | 2.0E-15 | AA397758.1 | EST_HUMAN | z177g08.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5' |
| 9002 | 21539 | 34468 | 0.87 | 2.0E-15 | AA397758.1 | EST_HUMAN | z177g08.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5' |
| 9325 | 21839 | 34790 | 1.13 | 2.0E-15 | AW379465.1 | EST_HUMAN | GM0-HT0244-201088-078-a12 HT0244 Homo sapiens cDNA |
| 9325 | 21839 | 34791 | 1.13 | 2.0E-15 | AW379465.1 | EST_HUMAN | GM0-HT0244-201088-078-a12 HT0244 Homo sapiens cDNA |
| 10718 | 23246 | | 3.59 | 2.0E-15 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 12487 | 16163 | 28845 | 2.97 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 12487 | 16163 | 28846 | 2.97 | 2.0E-15 | AF223391.1 | NT | Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced |
| 2803 | 15355 | | 2.08 | 1.0E-15 | A1888984.1 | EST_HUMAN | t28805.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ; |
| 3048 | 15862 | 28143 | 1.24 | 1.0E-15 | BE043594.1 | EST_HUMAN | tk40e02.y1 NCI_CGAP_Ox64 Homo sapiens cDNA clone IMAGE:2888182 5' |
| 3178 | 16789 | 28261 | 1.06 | 1.0E-15 | P08547 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 6510 | 19110 | 31868 | 1.71 | 1.0E-15 | T95763.1 | EST_HUMAN | ye40e10.s1 Soares_fetal_liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element ; |
| 7080 | 19652 | | 1.91 | 1.0E-15 | BE074217.1 | EST_HUMAN | QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA |
| 7105 | 19445 | 32262 | 0.77 | 1.0E-15 | P39057 | SWISSPROT | DYNEIN BETA CHAIN, CILIARY |
| 8174 | 20715 | 33631 | 0.88 | 1.0E-15 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 8359 | 20899 | 33819 | 4.97 | 1.0E-15 | A1200978.1 | EST_HUMAN | qf68h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3' |
| 8359 | 20899 | 33820 | 4.97 | 1.0E-15 | A1200978.1 | EST_HUMAN | qf68h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8969 | 21507 | 34428 | 0.51 | 1.0E-15 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 8972 | 21510 | 34432 | 1.99 | 1.0E-15 | 4507208 | NT | Homo sapiens spermidine synthase (SRM) mRNA |
| 9171 | 21748 | 34681 | 0.87 | 1.0E-15 | Q39575 | SWISSPROT | DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM |
| 9550 | 22050 | 35012 | 1.18 | 1.0E-15 | AA884653.1 | EST_HUMAN | chr37c03.s1 NCI_CGAP_K148 Homo sapiens cDNA clone IMAGE:1469872 3' similar to contains L1.13 L1 repetitive element; |
| 10698 | 23228 | 38242 | 6.66 | 1.0E-15 | AF044083.1 | NT | Homo sapiens major histocompatibility locus class III region |
| 12664 | 24820 | 30782 | 9.35 | 1.0E-15 | A1783944.1 | EST_HUMAN | ts31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2218912 3' similar to contains Alu repetitive element |
| 4417 | 17002 | | 0.63 | 9.0E-16 | BF689487.1 | EST_HUMAN | 602120192F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277422 5' |
| 4802 | 17185 | 29632 | 1.11 | 9.0E-16 | 4503168 | NT | Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA |
| 10873 | 23394 | 38409 | 2.68 | 9.0E-16 | F08688.1 | EST_HUMAN | HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23F05 |
| 5980 | 18502 | 31228 | 0.73 | 7.0E-16 | 4885120 | NT | Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA |
| 7379 | 19905 | 32769 | 1.36 | 7.0E-16 | O88807 | SWISSPROT | PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE M) (PAD-R4) |
| 7379 | 19905 | 32770 | 1.36 | 7.0E-16 | O88807 | SWISSPROT | PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE M) (PAD-R4) |
| 12509 | 24916 | | 33.75 | 7.0E-16 | T04149.1 | EST_HUMAN | (PEPTIDYLARGININE DEIMINASE TYPE ALPHA) |
| 2188 | 14762 | | 29.26 | 6.0E-16 | AW872611.1 | EST_HUMAN | ye28c12.11 Stratiogene lung (8937210) Homo sapiens cDNA clone IMAGE:118062 5' |
| 5436 | 17891 | 30397 | 0.94 | 6.0E-16 | BF365702.1 | EST_HUMAN | EST384702 MAGE resequences, MAGL Homo sapiens cDNA |
| 1539 | 14131 | 26687 | 1.21 | 5.0E-16 | AJ251154.1 | NT | QV2-NT0048-160800-316-412 NT0048 Homo sapiens cDNA |
| 2705 | 15262 | 27829 | 2.6 | 5.0E-16 | AA982176.1 | EST_HUMAN | Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene |
| 11398 | 23848 | 36914 | 3.76 | 5.0E-16 | BF217988.1 | EST_HUMAN | cd80c04.a1 Soares_t048_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element; |
| 12806 | 24680 | | 4.86 | 5.0E-16 | 11418127 | NT | 601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104128 5' |
| 2281 | 14855 | | 1.23 | 4.0E-16 | AB001523.1 | NT | Homo sapiens GTP binding protein 1 (GTPBP1), mRNA |
| 2419 | 14987 | 27561 | 1.68 | 4.0E-16 | AW797168.1 | EST_HUMAN | Homo sapiens gene for TMEM1 and PWP2, complete and partial cds |
| 2419 | 14987 | 27562 | 1.68 | 4.0E-16 | AW797168.1 | EST_HUMAN | QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA |
| 3503 | 18108 | 26584 | 6.73 | 4.0E-16 | Q16653 | SWISSPROT | QV1-UM0038-200300-115-g02 UM0038 Homo sapiens cDNA |
| 4223 | 18811 | 29258 | 4.28 | 4.0E-16 | BE083675.1 | EST_HUMAN | MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR |
| 4223 | 18811 | 29259 | 4.28 | 4.0E-16 | BE083675.1 | EST_HUMAN | PMA4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA |
| 7698 | 20207 | 33094 | 37.48 | 4.0E-16 | AL163284.2 | NT | PMA4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA |
| 9219 | 21736 | 34678 | 1.44 | 4.0E-16 | 11423191 | NT | Homo sapiens chromosome 21 segment HS21C084 |
| 11088 | 23808 | 36948 | 1.68 | 4.0E-16 | AV730030.1 | EST_HUMAN | Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA |
| | | | | | | | AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5' |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11800 | 24180 | | 1.34 | 4.0E-16 | P08548 | SWISSPROT | LINE-1 REVERSE TRANSCRIPTASE HOMOLOG |
| 11887 | 24232 | | 13.76 | 4.0E-16 | C05847.1 | EST_HUMAN | C05847 Human pancreatic islet Homo sapiens cDNA clone hbc3355 |
| 11887 | 24239 | 31008 | 2.91 | 4.0E-16 | | NT | Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA |
| 12178 | 24414 | | 1.8 | 4.0E-16 | R18591.1 | EST_HUMAN | Y68b11.11 Soares Infant Brain 1N1B Homo sapiens cDNA clone IMAGE:30489 5' |
| 138 | 12803 | 25292 | 0.93 | 3.0E-16 | AW022882.1 | EST_HUMAN | df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486378 5' |
| 138 | 12803 | 25293 | 0.93 | 3.0E-16 | AW022882.1 | EST_HUMAN | df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486378 5' |
| 491 | 13124 | | 1.24 | 3.0E-16 | AL046445.1 | EST_HUMAN | DKFZp434P037_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5' |
| 501 | 13133 | | 2.35 | 3.0E-16 | AF135446.1 | NT | Homo sapiens TSX (TSX) pseudogene, exon 5 |
| 1501 | 14093 | 26632 | 1.81 | 3.0E-16 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 3004 | 16820 | 28097 | 4.2 | 3.0E-16 | P03200 | SWISSPROT | ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220] |
| 4007 | 16905 | 29078 | 0.81 | 3.0E-16 | T08169.1 | EST_HUMAN | EST00600 Infant Brain, Berto Soares Homo sapiens cDNA clone HIBBA13 5' and |
| 4031 | 16828 | | 1.07 | 3.0E-16 | U03887.1 | NT | Human BXP-20 gene |
| 4689 | 17271 | 29720 | 0.97 | 3.0E-16 | AW160828.1 | EST_HUMAN | eu76606.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782163 5' similar to SW:KID1_MOUSE Q81751 RENAL TRANSCRIPTION FACTOR KID-1; |
| 5077 | 17650 | 30091 | 1.14 | 3.0E-16 | AV681393.1 | EST_HUMAN | AV681393 GLC Homo sapiens cDNA clone GLCSA01 3' |
| 6482 | 18116 | | 0.9 | 3.0E-16 | AA077226.1 | EST_HUMAN | 7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02 |
| 5801 | 18428 | 31144 | 1.57 | 3.0E-16 | AF003528.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 8592 | 21131 | 34047 | 4.08 | 3.0E-16 | A002838.1 | EST_HUMAN | en0805.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR_b2 THR repetitive element; |
| 9805 | 22303 | | 0.94 | 3.0E-16 | BF880617.1 | EST_HUMAN | 602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5' |
| 10027 | 22522 | 35518 | 5.15 | 3.0E-16 | L78810.1 | NT | Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds |
| 12637 | 25078 | 30516 | 9.33 | 3.0E-16 | AL043288.2 | EST_HUMAN | DKFZp434L1623_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5' |
| 1007 | 13818 | | 1.38 | 2.0E-16 | AL163278.2 | NT | Homo sapiens chromosome 21 segment HS21C079 |
| 2429 | 14996 | | 1.01 | 2.0E-16 | AA621791.1 | EST_HUMAN | af06d04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3' |
| 2713 | 15270 | | 1.53 | 2.0E-16 | J03081.1 | NT | Human SSAN-related endogenous retroviral LTR-like element |
| 4257 | 16843 | 29292 | 1.34 | 2.0E-16 | X89211.1 | NT | H. sapiens DNA for endogenous retroviral like element |
| 5370 | 17930 | 30344 | 0.57 | 2.0E-16 | BE001178.1 | EST_HUMAN | RC3-BT0048-131188-003-H12 BT0048 Homo sapiens cDNA |
| 6839 | 19429 | 32245 | 0.89 | 2.0E-16 | Q31125 | SWISSPROT | HISTIDINE-RICH PROTEIN KE4 |
| 7701 | 20210 | 33097 | 0.76 | 2.0E-16 | A470723.1 | EST_HUMAN | U18e11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element; |
| 7908 | 20450 | 33357 | 1.81 | 2.0E-16 | A1732837.1 | EST_HUMAN | nc4706.x6 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 ;contains MER7.11 MER7 repetitive element ;. |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 8099 | 20840 | 33551 | 0.7 | 2.0E-18 | BE858028.1 | EST_HUMAN | 782H09.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3303521 3' |
| 8099 | 20840 | 33552 | 0.7 | 2.0E-18 | BE858028.1 | EST_HUMAN | 782H09.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3303521 3' |
| 8464 | 21004 | 33921 | 0.6 | 2.0E-16 | AW877214.1 | EST_HUMAN | GM4-PT0034-180200-509-601 PT0034 Homo sapiens cDNA |
| 8464 | 21004 | 33922 | 0.6 | 2.0E-16 | AW877214.1 | EST_HUMAN | GM4-PT0034-180200-509-601 PT0034 Homo sapiens cDNA |
| 10808 | 23331 | 36343 | 2.71 | 2.0E-18 | 5802145 | NT | Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA |
| 197 | 12857 | 25339 | 2.56 | 1.0E-18 | AF200719.1 | NT | Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds |
| 405 | 13080 | | 29.83 | 1.0E-18 | AA628692.1 | EST_HUMAN | af39g11.s1 Soares_t048_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element; |
| 2014 | 14598 | 27159 | 1.78 | 1.0E-18 | BF327942.1 | EST_HUMAN | QV0-BND148-070700-283-a10 BN0148 Homo sapiens cDNA |
| 5986 | 18518 | 31243 | 0.85 | 1.0E-18 | AF163984.1 | NT | Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced |
| 6565 | 19163 | | 27.68 | 1.0E-18 | U45993.1 | NT | Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds |
| 6688 | 19284 | 32087 | 2.77 | 1.0E-18 | Q02779 | SWISSPROT | MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST) |
| 7556 | 19163 | | 6.98 | 1.0E-18 | U45993.1 | NT | Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds |
| 9207 | 21724 | 34867 | 1.15 | 1.0E-18 | AW875651.1 | EST_HUMAN | QV2-PT0012-040400-124-a05 PT0012 Homo sapiens cDNA |
| 3802 | 18402 | 28668 | 2.48 | 9.0E-17 | AW900048.1 | EST_HUMAN | GM1-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA |
| 6824 | 18414 | | 1.94 | 9.0E-17 | AI392884.1 | EST_HUMAN | tg22a-11.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12 MER28 repetitive element; |
| 8052 | 20584 | | 4.65 | 9.0E-17 | AW150257.1 | EST_HUMAN | xq48g12.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630850 3' similar to contains OFR.12 OFR repetitive element; |
| 10124 | 22818 | | 2.1 | 9.0E-17 | AF200719.1 | NT | Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds |
| 1056 | 13681 | | 1.56 | 8.0E-17 | AW880701.1 | EST_HUMAN | QV0-OT0032-080300-155-a01 OT0032 Homo sapiens cDNA |
| 3961 | 16559 | | 0.7 | 8.0E-17 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 5771 | 24748 | 31111 | 3.55 | 8.0E-17 | BE172081.1 | EST_HUMAN | MRO-HT0559-080300-003-a04 HT0559 Homo sapiens cDNA |
| 7319 | 18846 | | 1.82 | 8.0E-17 | AV730759.1 | EST_HUMAN | AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5' |
| 1505 | 14097 | | 3.4 | 7.0E-17 | 6753097 | NT | Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA |
| 5528 | 18158 | | 2.97 | 7.0E-17 | AF216650.1 | NT | Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced |
| 6789 | 16380 | 32186 | 7.15 | 7.0E-17 | AF229843.1 | NT | Mus musculus WNT-2 gene, partial cds; putative enkyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene |
| 217 | 12878 | 25365 | 7.43 | 6.0E-17 | AW963880.1 | EST_HUMAN | RC1-HN0003-220300-021-a04 HN0003 Homo sapiens cDNA |
| 6455 | 18056 | 31841 | 1.68 | 8.0E-17 | AW862772.1 | EST_HUMAN | h181d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878695 3' similar to contains L1.12 L1 repetitive element; |
| 10182 | 22887 | 35880 | 0.52 | 6.0E-17 | P20138 | SWISSPROT | MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67) |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 446 | 12675 | 25131 | 2.78 | 5.0E-17 | TG4110.1 | EST_HUMAN | y05h08.t1 Stratiogene lung (4937210) Homo sapiens cDNA clone IMAGE:79839 5' |
| 7586 | 20101 | 32876 | 1.82 | 5.0E-17 | TG1043.1 | EST_HUMAN | y126h04.t1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:108327 5' |
| 8284 | 21884 | 34829 | 1.12 | 4.0E-17 | AW128165.1 | EST_HUMAN | yf20e04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2818822 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element; |
| 11365 | 23817 | 36878 | 2.17 | 4.0E-17 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 11816 | 24188 | | 2.36 | 4.0E-17 | A1073546.1 | EST_HUMAN | 04f5e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR:Q16530 |
| 1540 | 14132 | | 1.03 | 3.0E-17 | D14547.1 | NT | Q16530 PMSS3 MRNA ; contains MER10.12 MER10 repetitive element ; |
| 2146 | 14723 | 27295 | 1.28 | 3.0E-17 | AW119123.1 | EST_HUMAN | Human DNA, SINE repetitive element |
| 3227 | 15839 | | 1.41 | 3.0E-17 | P35410 | EST_HUMAN | xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604764 3' |
| 3704 | 16305 | 28773 | 1.24 | 3.0E-17 | BE326522.1 | SWISSPROT | MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG |
| 3704 | 16305 | 28774 | 1.24 | 3.0E-17 | BE326522.1 | EST_HUMAN | hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181889 3' |
| 5181 | 17747 | | 1.02 | 3.0E-17 | BF511268.1 | EST_HUMAN | hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181889 3' |
| 8212 | 20753 | 33687 | 1.09 | 3.0E-17 | N88451.1 | EST_HUMAN | UI-H-B14-adj-c-08-Q-J1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3' |
| 9618 | 22118 | 35081 | 4.54 | 3.0E-17 | AB028898.1 | NT | z14802.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:282491 3' similar to contains PTR5.13 PTR5 repetitive element ; |
| 10282 | 22777 | 35767 | 0.65 | 3.0E-17 | BF327012.1 | EST_HUMAN | Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds) |
| 10282 | 22777 | 35768 | 0.65 | 3.0E-17 | BF327012.1 | EST_HUMAN | QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA |
| 11775 | 24163 | | 3.77 | 3.0E-17 | 11417888 | NT | QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA |
| 375 | 13024 | 25510 | 3.38 | 2.0E-17 | A1270080.1 | EST_HUMAN | Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA |
| 378 | 13024 | 25510 | 2.68 | 2.0E-17 | A1270080.1 | EST_HUMAN | q63e06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1958922 3' similar to contains Alu repetitive element; |
| 1025 | 13036 | | 1.12 | 2.0E-17 | AA72832.1 | EST_HUMAN | q63e08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1958922 3' similar to contains Alu repetitive element; |
| 2490 | 15055 | 27627 | 2.43 | 2.0E-17 | Q28983 | SWISSPROT | zg61d04.s1 Soares_fetal_heart_NBH10W Homo sapiens cDNA clone IMAGE:399751 3' |
| 2490 | 15055 | 27628 | 2.43 | 2.0E-17 | Q28983 | SWISSPROT | ZONADHESIN PRECURSOR |
| 2956 | 15572 | 28049 | 8.06 | 2.0E-17 | P12036 | SWISSPROT | ZONADHESIN PRECURSOR |
| 5568 | 18200 | 30648 | 1.57 | 2.0E-17 | M27885.1 | NT | NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H) |
| 5569 | 18200 | 30649 | 1.57 | 2.0E-17 | M27885.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| 6410 | 18013 | | 1.8 | 2.0E-17 | AF055088.1 | NT | Mus musculus ultra high sulfur keratin gene, complete cds |
| 6816 | 19213 | | 1.68 | 2.0E-17 | AL134881.1 | EST_HUMAN | Homo sapiens MHC class I region |
| 7773 | 20282 | 33178 | 0.65 | 2.0E-17 | AB037839.1 | NT | DKFZp762J0610 .r1 762 (synonym: hmla2) Homo sapiens cDNA clone DKFZp762J0610 5' |
| | | | | | | | Homo sapiens mRNA for KIAA1418 protein, partial cds |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO. | Exon SEQ ID NO. | ORF SEQ ID NO. | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 8028 | 20570 | 33474 | 1.84 | 2.0E-17 | Q85158 | SWISSPROT | OLFACTORY RECEPTOR-LIKE PROTEIN OLF3 |
| 8394 | 20834 | 33856 | 1.15 | 2.0E-17 | AA300840.1 | EST_HUMAN | EST13504 Testis tumor Homo sapiens cDNA 5' and similar to glycogenin |
| 9783 | 22281 | 35287 | 2.45 | 2.0E-17 | BE209888.1 | EST_HUMAN | 600944680F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860815 5' |
| 9818 | 22318 | 35297 | 3.38 | 2.0E-17 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 9818 | 22316 | 35298 | 3.38 | 2.0E-17 | AL163247.2 | NT | Homo sapiens chromosome 21 segment HS21C047 |
| 10180 | 22855 | 35650 | 7.23 | 2.0E-17 | D13391.1 | NT | Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements) |
| 10281 | 22778 | 35765 | 0.58 | 2.0E-17 | P88063 | SWISSPROT | BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1) |
| 10281 | 22778 | 35768 | 0.58 | 2.0E-17 | P88063 | SWISSPROT | BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1) |
| 10308 | 22800 | 35791 | 0.83 | 2.0E-17 | AI798802.1 | EST_HUMAN | we94b04.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2348719 3' |
| 10308 | 22800 | 35782 | 0.83 | 2.0E-17 | AI798802.1 | EST_HUMAN | we94b04.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2348719 3' |
| 780 | 13399 | 25902 | 3.38 | 1.0E-17 | P08183 | SWISSPROT | MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) |
| 1748 | 14338 | | 1.2 | 1.0E-17 | AJ271738.1 | NT | Homo sapiens Xq pseudautosomal region; segment 2/2 |
| 1804 | 14394 | 26839 | 2.89 | 1.0E-17 | AL163207.2 | NT | Homo sapiens chromosome 21 segment HS21C007 |
| 2182 | 14739 | 27309 | 2.11 | 1.0E-17 | P02461 | SWISSPROT | COLLAGEN ALPHA 1(III) CHAIN PRECURSOR |
| 2373 | 14943 | 27616 | 1.88 | 1.0E-17 | U78410.1 | NT | Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B |
| 3825 | 16228 | | 0.89 | 1.0E-17 | AF224689.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 4217 | 16805 | | 8.46 | 1.0E-17 | R09942.1 | EST_HUMAN | Y30a07.J1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5' |
| 6759 | 18352 | 32161 | 1.55 | 1.0E-17 | AI185842.1 | EST_HUMAN | qe65b05.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743825 3' |
| 6759 | 18352 | 32162 | 1.55 | 1.0E-17 | AI185842.1 | EST_HUMAN | qe65b05.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1743825 3' |
| 7146 | 18678 | 32520 | 1.28 | 1.0E-17 | Q16831 | SWISSPROT | URIDINE PHOSPHORYLASE (UDRPASE) |
| 8528 | 21067 | 33886 | 1.23 | 1.0E-17 | BE082744.1 | EST_HUMAN | QV0-BT0283-101298-072-d67 BT0283 Homo sapiens cDNA |
| 8919 | 22415 | 35390 | 0.94 | 1.0E-17 | AW986538.1 | EST_HUMAN | QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA |
| 11295 | 23747 | 36805 | 1.82 | 1.0E-17 | Q28824 | SWISSPROT | MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN] |
| 2510 | 15074 | 27647 | 1.13 | 9.0E-18 | AA174078.1 | EST_HUMAN | zp18g12.s1 Stratiogene fetal retina 93/202 Homo sapiens cDNA clone IMAGE:608862 3' |
| 9418 | 21927 | | 3.03 | 9.0E-18 | AI472167.1 | EST_HUMAN | ig66d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3' |
| 3854 | 18452 | 28915 | 1.58 | 8.0E-18 | 4758977 | NT | Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA |
| 371 | 13020 | 25504 | 32.68 | 7.0E-18 | AW316978.1 | EST_HUMAN | xc10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb.L20868 60S |
| 371 | 13020 | 25505 | 32.68 | 7.0E-18 | AW316978.1 | EST_HUMAN | xc10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb.L20868 60S |
| 7469 | 18891 | 32854 | 0.98 | 7.0E-18 | AW887542.1 | EST_HUMAN | RC3-OT0091-170300-011-d03 OT0091 Homo sapiens cDNA |

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Table 4
Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 12308 | 13020 | 25504 | 5.28 | 7.0E-18 | AW316978.1 | EST_HUMAN | xt10604.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN); |
| 12308 | 13020 | 25506 | 5.28 | 7.0E-18 | AW316978.1 | EST_HUMAN | xt10604.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN); |
| 3334 | 15944 | 28419 | 1.36 | 6.0E-18 | X71791.2 | NT | Rattus norvegicus partial GdhFr-1 gene for glia-derived neuroprotease within 1. enhancer region |
| 4857 | 17435 | | 3.95 | 6.0E-18 | P52181 | SWISSPROT | PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC) |
| 8182 | 20733 | | 2.75 | 6.0E-18 | 11428155 | NT | Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83448), mRNA |
| 8289 | 20830 | 33751 | 0.6 | 6.0E-18 | AL163210.2 | NT | Homo sapiens chromosome 21 segment HS21C010 |
| 11014 | 23528 | 36564 | 1.87 | 6.0E-18 | AL163246.2 | NT | Homo sapiens chromosome 21 segment HS21C046 |
| 11209 | 23713 | 36767 | 1.9 | 6.0E-18 | X87344.1 | NT | H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes |
| 11591 | 24034 | | 2.22 | 6.0E-18 | 11429885 | NT | Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC83091), mRNA |
| 12041 | 24328 | 30995 | 2.24 | 6.0E-18 | U87829.1 | NT | Human acornitide hydratase (ACO2) gene, exon 4 |
| 1187 | 13788 | 26299 | 11.3 | 5.0E-18 | AI280214.1 | EST_HUMAN | qm65g11.x1 Soares placenta 8t6weeks_2NHP8t69W Homo sapiens cDNA clone IMAGE:1893688 3' similar to contains Alu repetitive element; |
| 5284 | 17848 | 30273 | 0.94 | 5.0E-18 | D61517.1 | EST_HUMAN | HUM411F05B Clontech human fetal brain polyA+ mRNA (#8335) Homo sapiens cDNA clone GEN-411F05 5' |
| 5477 | 18111 | 30520 | 1.03 | 5.0E-18 | AF087813.1 | NT | Human endogenous retrovirus HERV-P-T47D |
| 8854 | 21193 | 34111 | 4.82 | 5.0E-18 | BE143312.1 | EST_HUMAN | MRO-HT0181-221089-002-c08 HT0181 Homo sapiens cDNA |
| 10857 | 23378 | 36396 | 3.68 | 5.0E-18 | 10242378 | NT | Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA |
| 10857 | 23378 | 36397 | 3.68 | 5.0E-18 | 10242378 | NT | Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA |
| 12170 | 24409 | | 6.6 | 6.0E-18 | AW887182.1 | EST_HUMAN | MRI-SN0035-060-400-001-g11 SN0035 Homo sapiens cDNA |
| 12531 | 24844 | | 51.19 | 5.0E-18 | AV650547.1 | EST_HUMAN | AV650547 GLC Homo sapiens cDNA clone GLOCGA02 3' |
| 130 | 12797 | 25283 | 1.98 | 4.0E-18 | BE044076.1 | EST_HUMAN | h338r04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element; |
| 130 | 12797 | 25284 | 1.98 | 4.0E-18 | BE044076.1 | EST_HUMAN | h338r04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element; |
| 1754 | 14344 | 28890 | 8.14 | 4.0E-18 | AA621814.1 | EST_HUMAN | h24f11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M283328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); |
| 1833 | 14517 | | 0.92 | 4.0E-18 | AI738592.1 | EST_HUMAN | w33h08.x1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:2392085 3' |
| 2242 | 14817 | 27390 | 1.23 | 4.0E-18 | Q06430 | SWISSPROT | N-ACETYL LACTOSAMINIDE BETA-1,6-N-ACETYL GLUCOSAMINYL TRANSFERASE (N-ACETYL GLUCOSAMINYL TRANSFERASE) (BRANCHING ENZYME) (IGNT) |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|--|
| 2242 | 14817 | 27391 | 1.23 | 4.0E-18 | Q06430 | SWISSPROT | N-ACETYL LACTOSAMINIDE BETA-1,6-N-ACETYL GLUCOSAMINYL TRANSFERASE (N-ACETYL GLUCOSAMINYL TRANSFERASE) (H-BRANCHING ENZYME) (IGNT) |
| 5568 | 18197 | 30643 | 2.32 | 4.0E-18 | A017565.1 | EST_HUMAN | cu23e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827138 3' |
| 5568 | 18197 | 30644 | 2.32 | 4.0E-18 | A017565.1 | EST_HUMAN | cu23e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827138 3' |
| 7787 | 20330 | | 0.81 | 4.0E-18 | AA746811.1 | EST_HUMAN | nc04e08.s1 NCI_CGAP_AW1 Homo sapiens cDNA clone IMAGE:1268698 similar to contains L1.12 L1 repetitive element; |
| 10884 | 23405 | 36424 | 7.68 | 4.0E-18 | AA371807.1 | EST_HUMAN | EST183633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat |
| 882 | 13496 | 26015 | 18.02 | 3.0E-18 | AA814106.1 | EST_HUMAN | cb23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW_RS5_HUMAN |
| 865 | 13576 | 26091 | 2.25 | 3.0E-18 | BE088634.1 | EST_HUMAN | PA6782 40S RIBOSOMAL PROTEIN S5.; |
| 4022 | 16620 | 28063 | 1.25 | 3.0E-18 | AL163247.2 | NT | CMO-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA |
| 6917 | 19578 | 32405 | 6.98 | 3.0E-18 | BE001671.1 | EST_HUMAN | Homo sapiens chromosome 21 segment HS21C047 |
| 12312 | 24504 | | 8.85 | 3.0E-18 | AW022015.1 | EST_HUMAN | PMO-BN0081-100300-001-008 BN0081 Homo sapiens cDNA |
| 272 | 12929 | 25410 | 2.57 | 2.0E-18 | AW636820.1 | EST_HUMAN | df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485128 5' |
| 1192 | 13793 | | 197.1 | 2.0E-18 | BE256097.1 | EST_HUMAN | QV1-LT0038-150200-070-e07 LT0038 Homo sapiens cDNA |
| 3157 | 15771 | 26238 | 1.15 | 2.0E-18 | Q39575 | SWISSPROT | 601114352F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5' |
| 5606 | 18235 | | 3.99 | 2.0E-18 | AA868610.1 | EST_HUMAN | DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM |
| 5687 | 18323 | 30623 | 3.16 | 2.0E-18 | D14547.1 | NT | ak53e07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577 |
| 5687 | 18323 | 30624 | 3.16 | 2.0E-18 | D14547.1 | NT | O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE.; |
| 6038 | 18957 | | 1.88 | 2.0E-18 | BF347229.1 | EST_HUMAN | Human DNA, SINE repetitive element |
| 6313 | 18920 | 31686 | 1 | 2.0E-18 | X60456.1 | NT | Human DNA, SINE repetitive element |
| 6313 | 18920 | 31686 | 1 | 2.0E-18 | X60456.1 | NT | Human IFNAR gene for Interferon alpha/beta receptor |
| 6424 | 19027 | 31810 | 0.84 | 2.0E-18 | BF352940.1 | EST_HUMAN | Human IFNAR gene for Interferon alpha/beta receptor |
| 6460 | 19061 | 31847 | 7.53 | 2.0E-18 | AW685853.1 | EST_HUMAN | IL3-HT0819-220700-222-G12 HT0819 Homo sapiens cDNA |
| 9960 | 22455 | 35437 | 1.39 | 2.0E-18 | AW151673.1 | EST_HUMAN | h84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879884 3' similar to contains MER10.12 |
| 9960 | 22455 | 35437 | 1.39 | 2.0E-18 | AW151673.1 | EST_HUMAN | MER10.12 MER19 repetitive element; |
| 9960 | 22455 | 35438 | 1.39 | 2.0E-18 | AW151673.1 | EST_HUMAN | x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 |
| 10854 | 23375 | 36394 | 4.96 | 2.0E-18 | AW470791.1 | EST_HUMAN | MER10 repetitive element; |
| | | | | | | | x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 |
| | | | | | | | MER10 repetitive element; |
| | | | | | | | h83d08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875469 3' similar to contains THR.b3 |
| | | | | | | | THR repetitive element; |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|---|--------------------------|-------------------------------|---|
| 11578 | 24026 | 37063 | 5.24 | 2.0E-18 | AW151289.1 | EST_HUMAN | xq47c08.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2830728 3' similar to contains MER8.b2 |
| 11870 | 13783 | | 20.18 | 2.0E-18 | BE256097.1 | EST_HUMAN | MER8 repetitive element ; 601114352F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5' |
| 4507 | 17091 | | 0.85 | 1.0E-18 | T85408.1 | EST_HUMAN | ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element ; |
| 5558 | 18190 | 30806 | 1.91 | 1.0E-18 | AV683405.1 | EST_HUMAN | AV683405 GLC Homo sapiens cDNA clone GLDKE11 3' |
| 5759 | 18385 | 31068 | 2.18 | 1.0E-18 | D00099.1 | NT | Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds |
| 5759 | 18385 | 31100 | 2.18 | 1.0E-18 | D00099.1 | NT | Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds |
| 6582 | 19180 | 31980 | 1.37 | 1.0E-18 | AL163280.2 | NT | Homo sapiens chromosome 21 segment HS21C080 |
| 8380 | 20820 | 33840 | 1.22 | 1.0E-18 | AI148288.1 | EST_HUMAN | cd69d09.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680503 3' similar to contains L1.11 L1 repetitive element ; |
| 9813 | 22311 | 35283 | 4.45 | 1.0E-18 | U91928.1 | NT | Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds |
| 11918 | 24255 | 31011 | 4.39 | 1.0E-18 | AF003529.1 | NT | Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions |
| 571 | 13202 | 25884 | 3.33 | 9.0E-19 | AA281961.1 | EST_HUMAN | z11d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 |
| 572 | 13202 | 25884 | 2.86 | 9.0E-19 | AA281961.1 | EST_HUMAN | MER19 repetitive element ; |
| 7790 | 20333 | | 5.83 | 9.0E-19 | F09688.1 | EST_HUMAN | z11d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 |
| 8822 | 21181 | 34078 | 2.46 | 9.0E-19 | AL163203.2 | NT | HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23F05 |
| 8822 | 21181 | 34077 | 2.46 | 9.0E-19 | AL163203.2 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 11007 | 23521 | 36556 | 3.82 | 9.0E-19 | AB032069.1 | NT | Homo sapiens chromosome 21 segment HS21C003 |
| 11678 | 13202 | 25884 | 28.32 | 9.0E-19 | AA281961.1 | EST_HUMAN | Homo sapiens mRNA for KIAA1143 protein, partial cds |
| 1088 | 13891 | | 1.38 | 8.0E-19 | AW974002.1 | EST_HUMAN | z11d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 |
| 8090 | 20631 | 33544 | 1 | 8.0E-19 | BE158836.1 | EST_HUMAN | MER19 repetitive element ; |
| 2287 | 14861 | 27436 | 1.72 | 7.0E-19 | 4758139 | NT | EST387007 MAGE resequences, MAGN Homo sapiens cDNA |
| 6584 | 19182 | 31982 | 1.91 | 7.0E-19 | AF092090.1 | NT | MRO-HT0404-210200-001-g08 HT0404 Homo sapiens cDNA |
| 7341 | 18888 | 32732 | 0.95 | 7.0E-19 | P28444 | SWISSPROT | Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA |
| 9025 | 22421 | 35395 | 0.47 | 7.0E-19 | AB344661.1 | EST_HUMAN | Rattus norvegicus cp151 mRNA, partial cds |
| 11823 | 25088 | | 2.85 | 7.0E-19 | AA705884.1 | EST_HUMAN | BETA CRYSTALLIN A2 |
| 3847 | 16446 | | 1.21 | 6.0E-19 | AW852930.1 | EST_HUMAN | 601c08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3' |
| | | | | | | | 260b01.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3' |
| | | | | | | | PMO-CT0248-131089-001-g01 CT0248 Homo sapiens cDNA |

Table 4

Single Exon Probes Expressed in Fetal Liver

| Probe SEQ ID NO: | Exon SEQ ID NO: | ORF SEQ ID NO: | Expression Signal | Most Similar (Top) Hit BLAST E- Value | Top Hit Accession No. | Top Hit Database Source | Top Hit Descriptor |
|------------------------|-----------------------|-------------------|----------------------|--|--------------------------|-------------------------------|--|
| 4562 | 17145 | 28562 | 1.39 | 6.0E-19 | P34986 | SWISSPROT | OLFACTORY RECEPTOR 6 (M50) |
| 4562 | 17145 | 28563 | 1.39 | 6.0E-19 | P34986 | SWISSPROT | OLFACTORY RECEPTOR 6 (M50) |
| 4919 | 17494 | | 1.15 | 6.0E-19 | AJ271735.1 | NT | Homo sapiens Xq pseudautosomal region; segment 1/2 |
| 6019 | 18638 | 31378 | 5.29 | 5.0E-19 | Q00183 | SWISSPROT | ZP-X) (RC55) |
| 6365 | 18689 | 31747 | 0.79 | 5.0E-19 | AW663302.1 | EST_HUMAN | h77606.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868767 5' |
| 10322 | 22818 | 35812 | 0.66 | 5.0E-19 | AJ297688.1 | NT | Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14 |
| 11412 | 23863 | 36924 | 7.61 | 5.0E-19 | AW163725.1 | EST_HUMAN | x87602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2884171 3' similar to contains element MSRT1 repetitive element; |
| 12544 | 24823 | | 1.36 | 5.0E-19 | U68060.1 | NT | Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S8A3N2T, TCRBV13S6A2T, TCRBV6S8P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV6S2, TCRBV6S8A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12 |
| 580 | 13210 | 25688 | 0.85 | 4.0E-19 | AB007970.1 | NT | Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501 |
| 2707 | 15264 | 27831 | 1.25 | 4.0E-19 | BF687362.1 | EST_HUMAN | 602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5' |
| 5583 | 18223 | 30872 | 1.1 | 4.0E-19 | AF224689.1 | NT | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds |
| 3919 | 16517 | 28982 | 1.58 | 3.0E-19 | Q28897 | SWISSPROT | BETA-2 ADRENERGIC RECEPTOR |
| 3919 | 16517 | 28983 | 1.58 | 3.0E-19 | Q28897 | SWISSPROT | BETA-2 ADRENERGIC RECEPTOR |
| 4373 | 16660 | 29405 | 0.9 | 3.0E-19 | O43900 | SWISSPROT | LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6) |
| 4373 | 16660 | 29406 | 0.9 | 3.0E-19 | O43900 | SWISSPROT | LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6) |
| 4544 | 17128 | 28571 | 1.33 | 3.0E-19 | AV708138.1 | EST_HUMAN | AV708138 ADC Homo sapiens cDNA clone ADCAMA11 5' |
| 6484 | 18118 | | 0.8 | 3.0E-19 | AF223467.1 | NT | Homo sapiens NPD008 protein (NPD008) mRNA, complete cds |
| 7418 | 18942 | | 1.83 | 3.0E-19 | 11432214 | NT | Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA |
| 9380 | 20319 | 33220 | 1.2 | 3.0E-19 | X99895.1 | NT | M.musculus mRNA for TPCP33 protein |
| 12084 | 24347 | | 16.44 | 3.0E-19 | AF165520.1 | NT | Homo sapiens phospholipid protein (PBI) mRNA, complete cds |
| 2585 | 15157 | 27725 | 7.09 | 2.0E-19 | AL163201.2 | NT | Homo sapiens chromosome 21 segment HS21C001 |
| 4542 | 17128 | | 1.28 | 2.0E-19 | AI311783.1 | EST_HUMAN | q961402.x1 NCI_CGAP_K45 Homo sapiens cDNA clone IMAGE:1915888 3' similar to TR-Q68398 Q68398 POL/ENV GENE: |
| 8272 | 20813 | 33735 | 8.35 | 2.0E-19 | AA012854.1 | EST_HUMAN | z634-c09.1 Soares retina N244HR Homo sapiens cDNA clone IMAGE:360880 5' |
| 9823 | 22321 | 35308 | 0.81 | 2.0E-19 | Q95155 | SWISSPROT | OLFACTORY RECEPTOR-LIKE PROTEIN OLF2 |
| 507 | 13140 | | 1.65 | 1.0E-19 | BE408611.1 | EST_HUMAN | 801304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5' |